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**Patentanmeldung Nr.** **Patent application No.** **Demande de brevet n°**

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PRIORITY DOCUMENT

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Der Präsident des Europäischen Patentamts;
Im Auftrag

For the President of the European Patent Office

Le Président de l'Office européen des brevets
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Streptococcus agalactiae antigens

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The present invention relates to isolated nucleic acid molecules, which encode antigens for *Streptococcus agalactiae*, which are suitable for use in preparation of pharmaceutical medicaments for the prevention and treatment of bacterial infections caused by *Streptococcus agalactiae*.

*Streptococcus agalactiae* is a gram-positive bacterium, and belongs to the Group B Streptococci (GBS) based on its hemolysis pattern in blood agar. The organism is encapsulated, and capsule is an important element of pathogenicity. Capsules are antigenic and form the basis for classifying GBS by serotypes. Nine distinct GBS serotypes have been identified: Ia, Ib, II, III, IV, V, VI, VII and VIII. Most *S. agalactiae* serotypes have been shown to cause serious disease, and the two most common serotypes - type III and V - are estimated to account for the majority of invasive disease worldwide. The ranking and serotype prevalence differs by age group and geographic area. In the US, GBS type III causes more than 50% of infant disease, type V about 40% of nonpregnant adult disease, and type Ia about a third of disease in any patient population.

*Streptococcus agalactiae* is an important agent of human disease at the extremities of age and in those who have underlying disease. Group B *Streptococci* are the major cause of generalized and focal infections in the newborn infant. GBS is the predominant pathogen in newborns in the US since the 1970's. Bacterial infection can lead to life threatening diseases, such as sepsis, pneumonia and meningitis. Survivers can become permanently handicapped with hearing, learning and visual disabilities. Newborns usually acquire the organism intrapartum or during delivery from their GBS-colonized mothers. In addition, GBS are also a frequent cause of infections in pregnant women and in chronically ill and elderly patients, such as those suffering from diabetes, malignancies, immunodeficiencies, etc., (reviewed by Balter, S. et al. in Gram positive pathogens ed. by Fischetti V.A. et al. ASM Press 2000, pp 154-160).

10-35% of pregnant women are colonized with GBS, but are asymptomatic. However, GBS colonization is important because of the risk of vertical transmission. 50-70% of neonates born to colonized women – that is 5-15% of all newborns - become colonized by GBS during delivery. Colonization is a prerequisite for infection and disease. The most preterm infants are at the highest risk for invasive disease due to low maternal transfer of antibodies and immature immune system. GBS carriage during pregnancy may be chronic, intermittent, or transient. It is difficult to assess the duration of carriage, since women are screened once during a prenatal visit from the late trimester. Several studies suggest that there is a correlation (~90%) between the colonization status in the third trimester and at the time of delivery. Serotyping of the isolates indicates that persistence of the same type is most common (reviewed by Balter, S. et al. in Gram positive pathogens ed. by Fischetti V.A. et al. ASM Press 2000, pp 154-160).

Without preventive intervention, 1 to 2% of all neonates and 15% of neonates born to heavily colonized women develop invasive disease (sepsis, pneumonia and/or meningitis). In the US, GBS infections affect 1-5 newborns/1000 live birth. About 17.000 cases of invasive GBS disease occurred in the US annually, and 7.500 occurred in newborns before prevention. GBS is the most common cause of bacterial meningitis accounting for ~ 40 % of all cases reported in this age group. The overall incidence of invasive GBS disease is 0.2-0.7/100.000 in the US. It is somewhat lower in Europe. Mortality without preventive intervention is 6% with invasive disease, every 16. infected newborn dies and 20% of survivers become permanently handicapped.

The rates of serious group B strep infections are much higher among newborns than among any other age group. Nonetheless, serious group B strep infections occur in other age groups in both men and women. Among non-pregnant adults, rates of serious disease range from 4.1 to 7.2 cases per 100,000 populations. The average death rate for invasive infections (infections where the bacteria have entered a part of the body that is normally not exposed to bacteria) is 8-10% for adult's ages 18-64 and 15-25% for adults 65 years of age and over. Mortality rates are lower among younger adults, and adults who do not have other medical conditions. The rate of serious group B strep disease increases with age. The average age of cases

in non-pregnant adults is about 60 years old. Most adult group B strep disease occurs in adults who have serious medical conditions. These include: diabetes mellitus; liver disease; history of stroke; history of cancer; or bedsores. Among the elderly, rates of serious group B strep disease are more common among residents of nursing facilities, and among bedridden hospitalized patients. Group B strep disease among non-pregnant adults may often be acquired after recent trauma, or after having certain invasive hospital procedures like surgery ({Farley, M., 2001}; {Jackson, L. et al., 1995}; www.cdc.gov/groupbstrep/).

Direct medical costs of neonatal disease before prevention were $294 million annually and GBS continues to pose a considerable economic burden.

A definitive diagnosis of infection with *Streptococcus agalactiae* generally relies on isolation of the organism from cervical swabs, blood or other normally sterile body sites. Tests are also available to detect capsular polysaccharide antigen in body fluids.

Penicillin G is the treatment of choice for established cases of GBS. Ten days of treatment is recommended for bacteremia, pneumonia and soft tissue infections, while 2-3 weeks is recommended for meningitis and 3-4 weeks for osteomyelitis.

Prevention has been established since 1994 in North America by screening pregnant women for carriage of GBS, taking vaginal and anorectal swabs at 35-37 weeks' gestation, or by identifying risk factors at admission for delivery without cultures. Women who are candidates for prophylaxis are given intrapartum antibiotic therapy during labor to prevent early-onset neonatal disease. This prevention method has decreased the incidence of GBS disease from 1.7 to 0.4/1000 live births between 1993 and 1999 in the US. Although most neonatal GBS disease can be prevented through intrapartum prophylaxis (Penicillin G or Ampicillin), currently available strategies are not ideal, especially for the prevention of late-onset (>7 days of age) infections and disease in premature babies. There are always individuals who escape of screening for carriage due to several reasons, such as intermittent carriers, who are tested negative at wks 32-35, but become positive during delivery, unattendance, negligence, or delivery before screening date (32-35 wks).

In the long run, widespread use of antibiotics usually induces resistant strains that appear after a period of time. Extensive use of Penicillin (every 3-5$^{th}$ women are treated with high dose), and other antibiotics has already been shown to steadily increase the percentage of antibotic resistant clinical isolates (ref). Moreover, efficiency of antibiotic based prevention is not that effective for late onset disease, as it is for early onset (within 48 hrs after delivery). An additional concern is that prevention in susceptible adult populations has not been addressed.

Vaccine development is hindered by the lack of sufficient knowledge about the elements of protective immunity against GBS carriage and disease. The relationship of carriage to the development of natural immunity is poorly understood. In addition, the immunologic mechanism that allows disease to occur in a carrier is ill defined. However, it is suggested that the maternal serum levels of pathogen-specific antibodies are correlated with neonatal GBS disease. It has been firmly established that there is an inverse correlation between maternal anti-capsular polysaccharide antibody levels at delivery and the frequency of invasive neonatal diseases {Campbell, J. et al., 2000}.

Although the group B carbohydrate antigen is common to all strains of GBS, unfortunately, it is not strongly immunogenic and antibodies are not protective from lethal challenge in experimental models. The GBS capsule itself that is made of polysaccharides, is immunogenic and is able to induce protective antibodies. However, this protection is type-specific. Although capsular specific antibodies have been shown to be highly protective, it remains unclear what concentration of these serotype-specific antibodies protect against disease and more recently it has become clear that opsonic activity and avidity of these

antibodies are more critical determinants of protection than concentration.

The importance of surface proteins in human immunity to *S. agalactiae* already has been appreciated. It is apparent that all serotypes express surface proteins with activity relevant to host immune defense. The alpha C protein, beta C protein, Rib and Sip proteins are well-characterized biochemically and genetically, and have also been shown to immunogenic and protective in animal models ({Michel, J. et al., 1991}; {Brodeur, B. et al., 2000}; {Larsson, C. et al., 1999}; {Cheng, Q. et al., 2002}). The major problem with these proteins as vaccine candidates seems to be their variability in prevalenve among the different clinical isolates of GBS. The Rib protein for example is present in serotype III GBS, but missing from type V, which responsible for significant portion of disease worldwide. Some other surface proteins are characterized as being immunogenic, but there is a limited systematic work done to identify most of the immunogenic proteins of GBS.

Thus, there remains a need for an effective treatment to prevent or ameliorate GBS infections. A vaccine could not only prevent infections by GBS, but more specifically prevent or ameliorate colonization of host tissues (esp. in the birth canal), thereby reducing the incidence of transmission from mother to fetus. Reducing the incidence of acute infection and carriage of the organism would lead to prevention of invasive diseases in newborns - pneumonia, bacteremia, meningitis, and sepsis. Vaccines capable of showing cross-protection against the majority of *S. agalactiae* strains causing human infections could also be useful to prevent or ameliorate infections caused by all other streptococcal species, namely groups A, C and G.

A vaccine can contain a whole variety of different antigens. Examples of antigens are whole-killed or attenuated organisms, subfractions of these organisms/tissues, proteins, or, in their most simple form, peptides. Antigens can also be recognized by the immune system in form of glycosylated proteins or peptides and may also be or contain polysaccharides or lipids. Short peptides can be used since for example cytotoxic T-cells (CTL) recognize antigens in form of short usually 8-11 amino acids long peptides in conjunction with major histocompatibility complex (MHC). B-cells can recognize linear epitopes as short as 4-5 amino acids, as well as three-dimensional structures (conformational epitopes). In order to obtain sustained, antigen-specific immune responses, adjuvants need to trigger immune cascades that involve all cells of the immune system. Primarily, adjuvants are acting, but are not restricted in their mode of action, on so-called antigen presenting cells (APCs). These cells usually first encounter the antigen(s) followed by presentation of processed or unmodified antigen to immune effector cells. Intermediate cell types may also be involved. Only effector cells with the appropriate specificity are activated in a productive immune response. The adjuvant may also locally retain antigens and co-injected factors. In addition, the adjuvant may act as a chemoattractant for other immune cells or may act locally and/or systemically as a stimulating agent for the immune system.

Vaccine development since the late 1970s has focused on the capsular polysaccharides, but a safe, effective product is still not available. However, vaccine against *S. agalactiae* is ranked as one of the most important for development and administration to infants and high-risk adults. Currently vaccines against this infection are only in the research stages of development. Efforts are focused on using capsular polysaccharide (CPS) as immunogens, either with or without conjugation to protein {Paoletti, L. et al., 2002}. However, there are several arguments against the use of polysaccharide-based vaccine. Polysaccharides induce IgG2 antibodies, which cross the placenta less efficiently then IgG1 or IgG3 antibodies. It is especially a problem for the most susceptible neonates, the still-borns since placental antibody transfer is low before weeks 32-34. It is estimated that ~10% of deliveries occur before the 34$^{th}$ pregnancy week.

Protein conjugate vaccines are no doubt a great new addition to the amarmatorium in the battle against GBS disease, but the vaccine can contain only a limited number of GBS serotypes and given adequate ecological pressure, replacement disease by non-vaccine serotypes remains a real threat, particularly in

areas with very high disease burden. Morover polysaccharide antigens used for active immunization do not provide immunological memory in humans. Conjugation of CPS to non-GBS related immunogenic protein carriers (e.g. tetanus toxoid, cholera toxin B subunit, etc.) has been shown to beneficial in inducing higher concentrations of antibodies in vaccinees, but it does not provide pathogen-specific B cell and T cell epitopes which would recruit memory B and T cells during a real infection to support the most effective host response. To be able to supplement the CPS vaccines with proteins fulfilling these criteria it is necessary to identify conserved immunogenic GBS-specific surface proteins.

All these insufficiencies suggest that there is a need to develop new generation vaccines composed of proteins, or their derivatives, expressed by all strains under *in vivo* conditions with the ability to induce opsonizing and/or neutralizing antibodies in humans.

There is a great potential for passive antibody-based therapy. There have been already attempts to use human intravenous immunoglobulin (IVIG) preparations for prevention. Recent advances in the technology of monoclonal antibody production provide the means to generate human antibody reagents and reintroduce antibody therapies, while avoiding the toxicities associated with serum therapy. Immunoglobulins are an extremely versatile class of antimicrobial proteins that can be used to prevent and treat emerging infectious diseases. Antibody therapy has been effective against a variety of diverse microorganisms (reviewed in {Burnie, J. et al., 1998}). Anti-GBS mAbs could be given therapeutically to every newborn that develop invasive diseases or preventively to low birth-weight and premature neonates.

During the last decade the immunogenicity and protective capacity of several GBS proteins have been described in animal models and these are now being explored for the development of species-common protein based vaccines. Such proteins are the GBS surface proteins Sip {Brodeur, B. et al., 2000}, rib, α-protein and {Michel, J. et al., 1991}.

Certain proteins or enzymes displayed on the surface of gram-positive organisms significantly contribute to pathogenesis, are involved in the disease process caused by these pathogens. Often, these proteins are involved in direct interactions with host tissues or in conceiling the bacterial surface from the host defense mechanisms {Navarre, W. et al., 1999}. *S. agalactiae* is not an exception in this regard. Several surface proteins are characterized as virulence factors, important for GBS pathogenicity ((reviewed in (Paoletti L.C. et al. in Gram positive pathogens, ed. by Fischetti V.A et al., ASM Press 2000, pp 137-153); {Paoletti, L. et al., 2002}). If antibodies to these proteins could offer better protection to humans then polysaccharides, they could provide the source of a novel, protein-based GBS vaccine to be used in conjunction with or in place of the more traditional capsular polysaccharise vaccine. The use of some of the above-described proteins as antigens for a potential vaccine as well as a number of additional candidates resulted mainly from a selection based on easiness of identification or chance of availability. There is a demand to identify relevant antigens for *S. agalactiae* in a more comprehensive way.

The present inventors have developed a method for identification, isolation and production of hyperimmune serum reactive antigens from a specific pathogen, especially from *Staphylococcus aureus* and *Staphylococcus epidermidis* (WO 02/059148). However, given the differences in biological property, pathogenic function and genetic background, *Streptococcus agalactiae* is distinctive from *Staphylococcus* strains. Importantly, the selection of sera for the identification of antigens from *S. agalactiae* is different from that applied to the *S. aureus* screens. Four major types of human antibody sources were collected for that purpose. First, healthy pregnant women who were tested negative for cervical and anorectal carriage of GBS. This donor group represents the most important source of antibodies. In addition to their serum samples, human cervical secretions collected with cervical wicks, containing secretory IgA (sIgA) were also used for antigen idntification and validation. The main value of this collection is that sIgA can be considered the major immune effector molecule on mucosal surfaces. Second, healthy pregnant women

colonized with GBS whos newborn remained GBS-free (although with antibiotic prevention). Third, adults below <45 years of age without clinical disease. Four, naïve individuals, youg children between 5 and 10 months of age, after they already lost maternal antibodies and have not acquired GBS-specific ones due to the lack of GBS disease.

To be able to select for relevant serum sources, a series of ELISAs and immunoblotting experiments measuring anti-*S. agalactiae* IgG and IgA antibody levels were performed with bacterial lysates and culture supernatant proteins. Sera from high titer carriers and non-carriers were included in the genomic-based antigen identification. This approach for selection of human sera is basically very different from that used for *S. aureus*, where carriage or non-carriage state couldn't be associated with antibody levels.

The present invention uses high throughput genomic method to identify *in vivo* expressed pathogen-specific proteins with the ability to induce antibodies in humans during the course of infections and colonization.

The genomes of the two bacterial species *S. agalactiae* and *S. aureus* by itself show a number of important differences. The genome of *S. agalactiae* contains app. 2.2 Mb, while *S. aureus* harbours 2.85 Mb. They have an average GC content of 35.7 and 33%, respectively and approximately 30 to 45% of the encoded genes are not shared between the two pathogens. In addition, the two bacterial species require different growth conditions and media for propagation. A list of the most important diseases, which can be inflicted by the two pathogens is presented below. *S. aureus* causes mainly nosocomial, opportunistic infections: impetigo, folliculitis, abscesses, boils, infected lacerations, endocarditis, meningitis, septic arthritis, pneumonia, osteomyelitis, scalded skin syndrome (SSS), toxic shock syndrome. *S. agalactiae* causes mainly neonatal infections and diseases in elderly, such as bacteremia, sepsis, wound infection, osteomyelitis and meningitis.

The complete genome sequence of a capsular serotype III isolate of *S. agalactiae*, designated NEM316 (ATCC 12403) was determined by the random shotgun sequencing strategy (GenBank accession number AL732656; see www.tigr.org/tigrscripts/CMR2/CMRHomePage.spl). {Glaser, P. et al., 2002}.

The problem underlying the present invention was to provide means for the development of medicaments such as vaccines against *S. agalactiae* infection. More particularly, the problem was to provide an efficient, relevant and comprehensive set of nucleic acid molecules or hyperimmune serum reactive antigens from *S. agalactiae* that can be used for the manufacture of said medicaments.

Therefore, the present invention provides an isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence, which is selected from the group consisting of:

a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule selected from Seq ID No 14, 90, 157-216.
b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b), or c)
e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid molecule defined in a), b), c) or d).

According to a preferred embodiment of the present invention the sequence identity is at least 80%, preferably at least 95%, especially 100%.

Furthermore, the present invention provides an isolated nucleic acid molecule encoding a hyperimmune

serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of

a) a nucleic acid molecule having at least 96% sequence identity to a nucleic acid molecule selected from **Seq ID No** 1, 3, 5-13, 15, 18-25, 27-31, 33-36, 39-68, 70-85, 92-100, 103-126, 128-145, 147, 149-156, 217, 435-448.
b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

According to another aspect, the present invention provides an isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of

a) a nucleic acid molecule selected from **Seq ID No** 32, 86, 91, 101, 127.
b) a nucleic acid molecule which is complementary to the nucleic acid of a),
c) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

Preferably, the nucleic acid molecule is DNA or RNA.

According to a preferred embodiment of the present invention, the nucleic acid molecule is isolated from a genomic DNA, especially from a S. *agalactiae* genomic DNA.

According to the present invention a vector comprising a nucleic acid molecule according to any of the present invention is provided.

In a preferred embodiment the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragments thereof encoded by the nucleic acid molecule according to the present invention.

The present invention also provides a host cell comprising the vector according to the present invention.

According to another aspect the present invention further provides a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to the present invention.

In a preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of **Seq ID No** 231, 307, 374-433.

In another preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of **Seq ID No** 218, 220, 222-230, 232, 235-242, 244-248, 250-253, 256-285, 287-302, 309-317, 320-343, 345-362, 364, 366-373, 434, 449-462.

In a further preferred embodiment the amino acid sequence (polypeptide) is selected from the group consisting of **Seq ID No** 249, 303, 308, 318, 344.

According to a further aspect the present invention provides fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table **1A**, **especially peptides comprising amino acid** 4-20, 35-44, 65-70, 73-87, 92-98, 112-137, 152-161, 177-186, 193-200, 206-

213, 229-255, 282-294, 308-313, 320-326, 349-355, 373-384, 388-406, 420-425 and 115-199 of Seq ID No 218; 5-24, 35-41, 44-70, 73-89, 103-109, 127-143, 155-161, 185-190, 192-207, 212-219, 246-262, 304-336, 372-382, 384-393, 398-407, 412-418, 438-444, 1-75, 76-161 and 164-239 of Seq ID No 219; 4-10, 16-58, 60-71, 77-92, 100-126, 132-146, 149-164, 166-172, 190-209, 214-220, 223-229, 241-256, 297-312, 314-319, 337-343, 351-359, 378-387, 398-418, 421-428, 430-437, 440-448, 462-471, 510-519, 525-536, 552-559, 561-568, 573-582, 596-602, 608-630, 637-649, 651-665, 681-702, 714-732, 739-745, 757-778, 790-805, 807-815, 821-829, 836-842, 846-873, 880-903, 908-914, 916-923, 931-940, 943-948, 956-970, 975-986, 996-1015, 1031-1040, 1051-1069, 1072-1095, 1114-1119, 1130-1148, 1150-1157, 1169-1176, 1229-1238 and 802-812 of Seq ID No 220; 5-12, 14-26, 35-47, 52-67, 72-78, 83-98, 121-141, 152-159, 163-183, 186-207, 209-257, 264-277, 282-299, 301-309, 312-318, 324-339, 358-368, 372-378, 387-397, 425-431 and 46-291 of Seq ID No 221; 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12-28, 41-91, 98-107, 112-120, 125-131, 151-193, 215-221, 240-250, 263-280 and 128-138 of Seq ID No 368; 16-24, 32-38, 46-62, 68-81, 90-105, 127-133, 144-150, 160-166, 178-184, 186-202, 210-219, 232-240, 252-258, 264-273, 293-324, 337-344, 349-357, 360-369, 385-398, 410-416, 419-427, 441-449, 458-476, 508-515, 523-539, 544-549, 562-569, 571-579, 96-109 and 127-139 of Seq ID No 369; 19-25, 28-34, 56-61, 85-97, 110-116 and 39-53 of Seq ID No 370; 4-37, 41-50, 62-72, 91-97, 99-109, 114-125, 136-141, 149-158, 160-166, 201-215 and 27-225 of Seq ID No 371; 15-31, 44-51, 96-105, 122-130, 149-157, 162-168, 178-183, 185-192, 198-204, 206-213, 221-234, 239-245, 248-255, 257-266, 289-335, 349-357, 415-422, 425-441, 448-454, 462-468 and 463-481 of Seq ID No 372; 5-31, 39-55, 63-72, 76-99, 106-155, 160-177, 179-199, 207-217, 223-240, 245-255, 261-267, 294-316, 321-343, 354-378, 382-452, 477-488, 529-536, 555-569, 584-591, 593-612, 620-627, 632-640, 647-654, 671-680, 698-704, 723-730, 732-750, 769-775, 781-788, 822-852 and 505-525 of Seq ID No 373; 3-18 of Seq ID No 374; 4-14 and 12-24 of Seq ID No 375; 4-11, 22-30 and 12-25 of Seq ID No 376; 5-12 and 4-18 of Seq ID No 377; 4-28 and 7-14 of Seq ID No 378; 6-16 and 8-16 of Seq ID No 379; 4-15, 18-33 and 24-36 of Seq ID No 380; 4-10, 16-21 and 20-31 of Seq ID No 381; 6-19 of Seq ID No 382; 11-18 and 3-10 of Seq ID No 383; 13-24 and 3-15 of Seq ID No 384; 15-27 and 7-16 of Seq ID No 385; 11-16 and 1-15 of Seq ID No 386; 4-16 and 9-21 of Seq ID No 387; 4-24, 40-48, 54-67 and 22-39 of Seq ID No 388; 6-30, 34-55, 62-68, 78-106 and 68-74 of Seq ID No 389; 3-14 of Seq ID No 390; 9-19 and 6-21 of Seq ID No 391; 4-17 and 1-9 of Seq ID No 392; 5-30 and 1-8 of Seq ID No 393; 4-16, 23-46, 51-56 and 45-55 of Seq ID No 394; 7-16 of Seq ID No 395; 2-14 of Seq ID No 396; 4-36, 43-65 and 50-62 of Seq ID No 397; 10-30 and 14-21 of Seq ID No 398; 9-17 and 1-10 of Seq ID No 399; 4-12

and 3-16 of Seq ID No 400; 4-15 and 5-23 of Seq ID No 401; 10-21 of Seq ID No 402; 6-16 of Seq ID No 403; 4-29, 31-38 and 2-14 of Seq ID No 404; 4-35 and 33-42 of Seq ID No 405; 2-17 of Seq ID No 406; 9-18, 30-35 and 15-33 of Seq ID No 407; 4-9 and 6-12 of Seq ID No 408; 3-17 of Seq ID No 409; 12-21, 37-44, 52-61, 72-80 and 38-48 of Seq ID No 410; 4-10, 29-44, 54-61, 69-78 and 13-27 of Seq ID No 411; 13-23, 36-53 and 2-15 of Seq ID No 412; 4-25, 28-46, 56-72, 81-99, 120-132, 134-142, 154-160 and 129-141 of Seq ID No 413; 4-15, 24-33, 35-41, 64-86 and 21-33 of Seq ID No 414; 9-15 and 4-13 of Seq ID No 415; 4-11, 13-19, 34-48 and 15-32 of Seq ID No 416; 4-21 and 11-31 of Seq ID No 417; 23-57 and 38-50 of Seq ID No 418; 4-32 and 3-13 of Seq ID No 419; 4-10, 13-25, 32-42, 56-68, 72-84 and 26-38 of Seq ID No 420; 4-20, 31-48, 52-58, 65-71, 80-93, 99-108, 114-123 and 37-49 of Seq ID No 421; 6-12, 14-20 and 3-25 of Seq ID No 422; 14-25, 27-38 and 5-14 of Seq ID No 423; 4-41, 57-105, 109-118, 123-136, 144-152 and 86-99 of Seq ID No 424; 6-19 of Seq ID No 425; 2-19 of Seq ID No 426; 14-47 and 1-14 of Seq ID No 427; 4-21, 29-44 and 2-18 of Seq ID No 428; 23-29 and 10-28 of Seq ID No 429; 6-16, 22-36 and 11-22 of Seq ID No 430; 4-19, 30-44 and 18-27 of Seq ID No 431; 5-15, 37-45, 58-65 and 38-47 of Seq ID No 432; 4-15, 23-34 and 4-15 of Seq ID No 433; 30-36, 44-54, 79-85, 101-114, 138-152, 154-164, 170-175, 179-200, 213-220, 223-240, 243-255, 258-264, 268-284 and 10-28 of Seq ID No 434; the peptides comprising amino acid sequences of column "Identical region" of the Table 1B, especially peptides comprising amino acid 210-226 and 738-753 of Seq ID No 449; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 450; 893-906 of Seq ID No 451; 51-69 of Seq ID No 452; 110-125 of Seq ID No 453; 291-305 of Seq ID No 454; 210-226 and 738-753 of Seq ID No 455; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 456; 893-906 of Seq ID No 457; 51-69 of Seq ID No 458; 110-125 of Seq ID No 459; 291-305 of Seq ID No 460; 32-44 of Seq ID No 461; 399-410 of Seq ID No 462; the serum reactive epitopes as specified in the column of "aa from" to "aa to" of Table 2, especially peptides comprising amino acid 120-143, 138-161 and 156-179 of Seq ID No 218; 110-129 and 168-184 of Seq ID No 219; 74-90 of Seq ID No 222; 759-773 of Seq ID No 223; 237-260 of Seq ID No 224; 265-284 of Seq ID No 225; 65-74 of Seq ID No 226; 41-50 of Seq ID No 227; 163-174 of Seq ID No 229; 26-37 of Seq ID No 230; 174-189 of Seq ID No 232; 240-256 of Seq ID No 234; 285-297 of Seq ID No 236; 238-247 of Seq ID No 238; 491-519 of Seq ID No 239; 114-140 of Seq ID No 243; 267-284 of Seq ID No 250; 439-453 of Seq ID No 252; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 60-71 of Seq ID No 256; 244-257 of Seq ID No 257; 44-63 and 57-76 of Seq ID No 258; 185-196 of Seq ID No 260; 119-129 of Seq ID No 263; 182-195 of Seq ID No 266; 32-44 and 424-442 of Seq ID No 267; 247-256 of Seq ID No 268; 678-694, 785-805, 55-77 and 72-94 of Seq ID No 269; 210-226 of Seq ID No 281; 37-59 of Seq ID No 289; 13-29 of Seq ID No 296; 136-159 of Seq ID No 348; 205-222 of Seq ID No 349; 99-110 of Seq ID No 350; 160-176 of Seq ID No 351; 457-470 of Seq ID No 355; 221-237 of Seq ID No 356; 167-190 of Seq ID No 357; 96-120 of Seq ID No 361; 399-417, 503-519 and 544-563 of Seq ID No 364; 46-68, 159-183 and 184-198 of Seq ID No 371; 463-481 of Seq ID No 372; the immunogenic epitopes as specified in the column of "aa from" to "aa to" of Table 4; especially peptides comprising amino acid 110-129 and 168-184 of Seq ID No 219; 877-901, 333-354, 326-344 and 801-809 of Seq ID No 277; 1-54 of Seq ID No 347; 544-563, 31-51, 107-119, 399-417 and 503-519 of Seq ID No 364; 120-198 of Seq ID No 218; 20-35 of Seq ID No 219; 118-201 of Seq ID No 221; 48-132 of Seq ID No 242; 118-136 of Seq ID No 249; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 50-76 of Seq ID No 258; 785-819 and 44-128 of Seq ID No 269; 90-128 of Seq ID No 274; 314-384 of Seq ID No 289; 327-349 of Seq ID No 293; 242-314, 405-478 and 23-100 of Seq ID No 304; 129-210 of Seq ID No 305; 162-188 of Seq ID No 307; 750-772 of Seq ID No 310; 1-56 of Seq ID No 335; 322-337 of Seq ID No 337; 72-90 of Seq ID No 339; 374-395 of Seq ID No 345; 136-159 of Seq ID No 348; 141-164 of Seq ID No 358; 96-157 of Seq ID No 361; 1-82 of Seq ID No 363; 489-556 of Seq ID No 364; 159-183 and 49-133 of Seq ID No 371.

The present invention also provides a process for producing a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof according to the present invention comprising expressing one or more of the nucleic acid molecules according to the present invention in a suitable expression system.

Moreover, the present invention provides a process for producing a cell, which expresses a *S agalactiae* hyperimmune serum reactive antigen or a fragment thereof according to the present invention

comprising transforming or transfecting a suitable host cell with the vector according to the present invention.

According to the present invention a pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reactive antigen or a fragment thereof as defined in the present invention or a nucleic acid molecule as defined in the present invention is provided.

In a preferred embodiment the pharmaceutical composition further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, especially KLKL5KLK, neuroactive compounds, especially human growth hormone, alumn, Freund's complete or incomplete adjuvants or combinations thereof.

In a more preferred embodiment the immunostimulatory substance is a combination of either a polycationic polymer and immunostimulatory deoxynucleotides or of a peptide containing at least two LysLeuLys motifs and immunostimulatory deoxynucleotides.

In a still more preferred embodiment the polycationic polymer is a polycationic peptide, especially polyarginine.

According to the present invention the use of a nucleic acid molecule according to the present invention or a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a pharmaceutical preparation, especially for the manufacture of a vaccine against *S. agalactiae* infection, is provided.

Also an antibody, or at least an effective part thereof, which binds at least to a selective part of the hyperimmune serum-reactive antigen or a fragment thereof according to the present invention, is provided herewith.

In a preferred embodiment the antibody is a monoclonal antibody.

In another preferred embodiment the effective part of the antibody comprises Fab fragments.

In a further preferred embodiment the antibody is a chimeric antibody.

In a still preferred embodiment the antibody is a humanized antibody.

The present invention also provides a hybridoma cell line, which produces an antibody according to the present invention.

Moreover, the present invention provids a method for producing an antibody according to the present invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in the invention, to said animal,
- removing an antibody containing body fluid from said animal, and
- producing the antibody by subjecting said antibody containing body fluid to further purification steps.

Accordingly, the present invention also provides a method for producing an antibody according to the present invention, characterized by the following steps:

- initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in the present invention, to said animal,

- removing the spleen or spleen cells from said animal,
- producing hybridoma cells of said spleen or spleen cells,
- selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens or a fragment thereof,
- producing the antibody by cultivation of said cloned hybridoma cells and optionally further purification steps.

The antibodies provided or produced according to the above methods may be used for the preparation of a medicament for treating or preventing *S. agalactiae* infections.

According to another aspect the present invention provides an antagonist, which binds to a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention.

Such an antagonist capable of binding to a hyperimmune serum-reactive antigen or fragment thereof according to the present invention may be identified by a method comprising the following steps:

a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragment thereof according to the present invention with a candidate antagonist under conditions to permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen or fragment, in the presence of a component capable of providing a detectable signal in response to the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragment thereof; and
b) detecting the presence or absence of a signal generated in response to the binding of the antagonist to the hyperimmune serum reactive antigen or the fragment thereof.

An antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention to its interaction partner may be identified by a method comprising the following steps:

a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof according to the present invention,
b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragment thereof, especially an antibody according to the present invention,
c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form an interaction complex,
d) providing a candidate antagonist,
e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex ,
f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.

The hyperimmune serum reactive antigens or fragments thereof according to the present invention may be used for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.

The present invention also provides a process for *in vitro* diagnosing a disease related to expression of a hyperimmune serum-reactive antigen or a fragment thereof according to the present invention comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

The present invention also provides a process for *in vitro* diagnosis of a bacterial infection, especially a *S. agalactiae* infection, comprising analyzing for the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen or fragment thereof according to the present invention or the

presence of the hyperimmune serum reactive antigen or fragment thereof according to the present invention.

Moreover, the present invention provides the use of a hyperimmune serum reactive antigen or fragment thereof according to the present invention for the generation of a peptide binding to said hyperimmune serum reactive antigen or fragment thereof, wherein the peptide is an anticaline.

The present invention also provides the use of a hyperimmune serum-reactive antigen or fragment thereof according to the present invention for the manufacture of a functional nucleic acid, wherein the functional nucleic acid is selected from the group comprising aptamers and spiegelmers.

The nucleic acid molecule according to the present invention may also be used for the manufacture of a functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the group comprising ribozymes, antisense nucleic acids and siRNA.

The present invention advantageously provides an efficient, relevant and comprehensive set of isolated nucleic acid molecules and their encoded hyperimmune serum reactive antigens or fragments thereof identified from *S. agalactiae* using an antibody preparation from multiple human plasma pools and surface expression libraries derived from the genome of *S. agalactiae*. Thus, the present invention fulfils a widely felt demand for *S. agalactiae* antigens, vaccines, diagnostics and products useful in procedures for preparing antibodies and for identifying compounds effective against *S. agalactiae* infection.

An effective vaccine should be composed of proteins or polypeptides, which are expressed by all strains and are able to induce high affinity, abundant antibodies against cell surface components of S. *agalactiae*. The antibodies should be IgG1 and/or IgG3 for opsonization, and any IgG subtype and IgA for neutralisation of adherence and toxin action. A chemically defined vaccine must be definitely superior compared to a whole cell vaccine (attenuated or killed), since components of S. *agalactiae*, which cross-react with human tissues or inhibit opsonization can be eliminated, and the individual proteins inducing protective antibodies and/or a protective immune response can be selected.

The approach, which has been employed for the present invention, is based on the interaction of GBS proteins or peptides with the antibodies present in human sera. The antibodies produced against *S. agalactiae* by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. In addition, the antigenic proteins as identified by the bacterial surface display expression libraries using pools of pre-selected sera, are processed in a second and third round of screening by individual selected or generated sera. Thus the present invention supplies an efficient, relevant, comprehensive set of GBS antigens as a pharmaceutical composition, especially a vaccine preventing infection by *S. agalactiae*.

In the antigen identification program for identifying a comprehensive set of antigens according to the present invention, at least two different bacterial surface expression libraries are screened with several serum pools or plasma fractions or other pooled antibody containing body fluids (antibody pools). The antibody pools are derived from a serum collection, which has been tested against antigenic compounds of *S. agalactiae*, such as whole cell extracts and culture supernatant proteins. Preferably, three distinct serum collections are used, obtained ad 1. from healthy pregnant women tested negative for cervical and anorectal carriage of GBS, ad 2. healthy pregnant women tested positive for cervical and/or anorectal carriage of GBS who's newborn remained GBS-free (although with antibiotic prevention), ad 3. from adults below <45 years of age without clinical disease. Sera have to react with multiple GBS-specific antigens in order to be considered hyperimmune and therefore relevant in the screening method applied for the present invention.

The expression libraries as used in the present invention should allow expression of all potential antigens,

e.g. derived from all secreted and surface proteins of *S. agalactiae*. Bacterial surface display libraries will be represented by a recombinant library of a bacterial host displaying a (total) set of expressed peptide sequences of *S. agalactiae* on two selected outer membrane proteins (LamB and FhuA) at the bacterial host membrane {Georgiou, G., 1997}; {Etz, H. et al., 2001}. One of the advantages of using recombinant expression libraries is that the identified hyperimmune serum-reactive antigens may be instantly produced by expression of the coding sequences of the screened and selected clones expressing the hyperimmune serum-reactive antigens without further recombinant DNA technology or cloning steps necessary.

The comprehensive set of antigens identified by the described program according to the present invention is analysed further by one or more additional rounds of screening. Therefore individual antibody preparations or antibodies generated against selected peptides, which were identified as immunogenic are used. According to a preferred embodiment the individual antibody preparations for the second round of screening are derived from pregnant women and non-pregant adults who show an antibody titer above a certain minimum level, for example an antibody titer being higher than 80 percentile, preferably higher than 90 percentile, especially higher than 95 percentile of the human (patient or healthy individual) sera tested. Using such high titer individual antibody preparations in the second screening round allows a very selective identification of the hyperimmune serum-reactive antigens and fragments thereof from *S. agalactiae*.

Following the comprehensive screening procedure, the selected antigenic proteins, expressed as recombinant proteins or *in vitro* translated products, in case it can not be expressed in prokaryotic expression systems, or the identified antigenic peptides (produced synthetically) are tested in a second screening by a series of ELISA and Western blotting assays for the assessment of their immunogenicity with a large human serum collection (minimum ~150 healthy and patients sera).

It is important that the individual antibody preparations (which may also be the selected serum) allow a selective identification of the most promising candidates of all the hyperimmune serum-reactive antigens from all the promising candidates from the first round. Therefore, preferably at least 10 individual antibody preparations (i.e. antibody preparations (e.g. sera) from at least 10 different individuals having suffered from an infection to the chosen pathogen) should be used in identifying these antigens in the second screening round. Of course, it is possible to use also less than 10 individual preparations, however, selectivity of the step may not be optimal with a low number of individual antibody preparations. On the other hand, if a given hyperimmune serum-reactive antigen (or an antigenic fragment thereof) is recognized by at least 10 individual antibody preparations, preferably at least 30, especially at least 50 individual antibody preparations, identification of the hyperimmune serum-reactive antigen is also selective enough for a proper identification. Hyperimmune serum-reactivity may of course be tested with as many individual preparations as possible (e.g. with more than 100 or even with more than 1,000).

Therefore, the relevant portion of the hyperimmune serum-reactive antibody preparations according to the method of the present invention should preferably be at least 10, more preferred at least 30, especially at least 50 individual antibody preparations. Alternatively (or in combination) hyperimmune serum-reactive antigens may preferably be also identified with at least 20%, preferably at least 30%, especially at least 40% of all individual antibody preparations used in the second screening round.

According to a preferred embodiment of the present invention, the sera from which the individual antibody preparations for the second round of screening are prepared (or which are used as antibody preparations), are selected by their titer against *S. agalactiae* (e.g. against a preparation of this pathogen, such as a lysate, cell wall components and recombinant proteins). Preferably, some are selected with a total IgA titer above 300 U, especially above 500 U, and/or an IgG titer above 5,000 U, especially above 10,000 U (U = units, calculated from the $OD_{405nm}$ reading at a given dilution) when the whole organism

(total lysate or whole cells) is used as antigen in the ELISA.

The antibodies produced against streptococci by the human immune system and present in human sera are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. The recognition of linear epitopes recognized by serum antibodies can be based on sequences as short as 4-5 amino acids. Of course it does not necessarily mean that these short peptides are capable of inducing the given antibody *in vivo*. For that reason the defined epitopes, polypeptides and proteins are further to be tested in animals (mainly in mice) for their capacity to induce antibodies against the selected proteins *in vivo*.

The preferred antigens are located on the cell surface or secreted, and are therefore accessible extracellularly. Antibodies against cell wall proteins are expected to serve multiple purposes: to inhibit adhesion, to interfere with nutrient acquisition, to inhibit immune evasion nand to promote phagocytosis {Hornef, M. et al., 2002}. Antibodies against secreted proteins are beneficial in neutralisation of their function as toxin or virulence component. It is also known that bacteria communicate with each other through secreted proteins. Neutralizing antibodies against these proteins will interrupt growth-promoting cross-talk between or within streptococcal species. Bioinformatic analyses (signal sequences, cell wall localisation signals, transmembrane domains) proved to be very useful in assessing cell surface localisation or secretion. The experimental approach includes the isolation of antibodies with the corresponding epitopes and proteins from human serum, and the generation of immune sera in mice against (poly) peptides selected by the bacterial surface display screens. These sera are then used in a third round of screening as reagents in the following assays: cell surface staining of *S. agalactiae* grown under different conditions (FACS or microscopy), determination of neutralizing capacity (toxin, adherence), and promotion of opsonization and phagocytosis (*in vitro* phagocytosis assay).

For that purpose, bacterial *E. coli* clones are directly injected into mice and immune sera are taken and tested in the relevant *in vitro* assay for functional opsonic or neutralizing antibodies. Alternatively, specific antibodies may be purified from human or mouse sera using peptides or proteins as substrate.

Host defence against *S. agalactiae* relies mainly on opsonophagocytic killing mechanism. Inducing high affinity antibodies of the opsonic and neutralizing type by vaccination helps the innate immune system to eliminate bacteria and toxins. This makes the method according to the present invention an optimal tool for the identification of GBS antigenic proteins.

The skin and mucous membranes are formidable barriers against invasion by streptococci. However, once the skin or the mucous membranes are breached the first line of non-adaptive cellular defence begins its co-ordinate action through complement and phagocytes, especially the polymorphonuclear leukocytes (PMNs). These cells can be regarded as the cornerstones in eliminating invading bacteria. As *Streptococcus agalactiae* is a primarily extracellular pathogen, the major anti-streptococcal adaptive response comes from the humoral arm of the immune system, and is mediated through three major mechanisms: promotion of opsonization, toxin neutralisation, and inhibition of adherence. It is believed that opsonization is especially important, because of its requirement for an effective phagocytosis. For efficient opsonization the microbial surface has to be coated with antibodies and complement factors for recognition by PMNs through receptors to the Fc fragment of the IgG molecule or to activated C3b. After opsonization, streptococci are phagocytosed and killed. Antibodies bound to specific antigens on the cell surface of bacteria serve as ligands for the attachment to PMNs and to promote phagocytosis. The very same antibodies bound to the adhesins and other cell surface proteins are expected to neutralize adhesion and prevent colonization. The selection of antigens as provided by the present invention is thus well suited to identify those that will lead to protection against infection in an animal model or in humans.

According to the antigen identification method used herein, the present invention can surprisingly provide a set of comprehensive novel nucleic acids and novel hyperimmune serum reactive antigens and

fragments thereof of *S. agalactiae*, among other things, as described below. According to one aspect, the invention particularly relates to the nucleotide sequences encoding hyperimmune serum reactive antigens which sequences are set forth in the Sequence listing **Seq ID No**: 1-217 and 435-448 and the corresponding encoded amino acid sequences representing hyperimmune serum reactive antigens are set forth in the Sequence Listing **Seq ID No** 218-434 and 449-462.

In a preferred embodiment of the present invention, a nucleic acid molecule is provided which exhibits 70% identity over their entire length to a nucleotide sequence set forth with **Seq ID No** 14, 90, 157-216.. Most highly preferred are nucleic acids that comprise a region that is at least 80% or at least 85% identical over their entire length to a nucleic acid molecule set forth with **Seq ID No** 14, 90, 157-216. In this regard, nucleic acid molecules at least 90%, 91%, 92%, 93%, 94%, 95%, or 96% identical over their entire length to the same are particularly preferred. Furthermore, those with at least 97% are highly preferred, those with at least 98% and at least 99% are particularly highly preferred, with at least 99% or 99.5% being the more preferred, with 100% identity being especially preferred. Moreover, preferred embodiments in this respect are nucleic acids which encode hyperimmune serum reactive antigens or fragments thereof (polypeptides) which retain substantially the same biological function or activity as the mature polypeptide encoded by said nucleic acids set forth in the **Seq ID No** 14, 90, 157-216.

Identity, as known in the art and used herein, is the relationship between two or more polypeptide sequences or two or more polynucleotide sequences, as determined by comparing the sequences. In the art, identity also means the degree of sequence relatedness between polypeptide or polynucleotide sequences, as the case may be, as determined by the match between strings of such sequences. Identity can be readily calculated. While there exist a number of methods to measure identity between two polynucleotide or two polypeptide sequences, the term is well known to skilled artisans (e.g. *Sequence Analysis in Molecular Biology*, von Heinje, G., Academic Press, 1987). Preferred methods to determine identity are designed to give the largest match between the sequences tested. Methods to determine identity are codified in computer programs. Preferred computer program methods to determine identity between two sequences include, but are not limited to, GCG program package {Devereux, J. et al., 1984}, BLASTP, BLASTN, and FASTA {Altschul, S. et al., 1990}.

According to another aspect of the invention, nucleic acid molecules are provided which exhibit at least 96% identity to the nucleic acid sequence set forth with **Seq ID No** 1, 3, 5-13, 15, 18-25, 27-31, 33-36, 39-68, 70-85, 92-100, 103-126, 128-145, 147, 149-156, 217, 435-448.

According to a further aspect of the present invention, nucleic acid molecules are provided which are identical to the nucleic acid sequences set forth with **Seq ID No** 32, 86, 91, 101, 127.

The nucleic acid molecules according to the present invention can as a second alternative also be a nucleic acid molecule which is at least essentially complementary to the nucleic acid described as the first alternative above. As used herein complementary means that a nucleic acid strand is base pairing via Watson-Crick base pairing with a second nucleic acid strand. Essentially complementary as used herein means that the base pairing is not occurring for all of the bases of the respective strands but leaves a certain number or percentage of the bases unpaired or wrongly paired. The percentage of correctly pairing bases is preferably at least 70 %, more preferably 80 %, even more preferably 90 % and most preferably any percentage higher than 90 %. It is to be noted that a percentage of 70 % matching bases is considered as homology and the hybridization having this extent of matching base pairs is considered as stringent. Hybridization conditions for this kind of stringent hybridization may be taken from Current Protocols in Molecular Biology (John Wiley and Sons, Inc., 1987). More particularly, the hybridization conditions can be as follows:

- Hybridization performed e.g. in 5 x SSPE, 5 x Denhardt's reagent, 0.1% SDS, 100 g/mL sheared DNA at 68°C

- Moderate stringency wash in 0.2xSSC, O.1% SDS at 42°C
- High stringency wash in 0.1xSSC, 0.1% SDS at 68°C

Genomic DNA with a GC content of 50% has an approximate $T_M$ of 96°C. For 1% mismatch, the $T_M$ is reduced by approximately 1°C.

In addition, any of the further hybridization conditions described herein are in principle applicable as well.

Of course, all nucleic acid sequence molecules which encode the same polypeptide molecule as those identified by the present invention are encompassed by any disclosure of a given coding sequence, since the degeneracy of the genetic code is directly applicable to unambiguously determine all possible nucleic acid molecules which encode a given polypeptide molecule, even if the number of such degenerated nucleic acid molecules may be high. This is also applicable for fragments of a given polypeptide, as long as the fragments encode a polypeptide being suitable to be used in a vaccination connection, e.g. as an active or passive vaccine.

The nucleic acid molecule according to the present invention can as a third alternative also be a nucleic acid which comprises a stretch of at least 15 bases of the nucleic acid molecule according to the first and second alternative of the nucleic acid molecules according to the present invention as outlined above. Preferably, the bases form a contiguous stretch of bases. However, it is also within the scope of the present invention that the stretch consists of two or more moieties, which are separated by a number of bases.

The present nucleic acids may preferably consist of at least 20, even more preferred at least 30, especially at least 50 contiguous bases from the sequences disclosed herein. The suitable length may easily be optimized due to the planned area of use (e.g. as (PCR) primers, probes, capture molecules (e.g. on a (DNA) chip), etc.). Preferred nucleic acid molecules contain at least a contiguous 15 base portion of one or more of the predicted immunogenic amino acid sequences listed in tables 1 and 2, especially the sequences of table 2 with scores of more than 10, preferably more than 20, especially with a score of more than 25. Specifically preferred are nucleic acids containing a contiguous portion of a DNA sequence of any sequence in the sequence protocol of the present application which shows 1 or more, preferably more than 2, especially more than 5, non-identical nucleic acid residues compared to the published *Streptococcus agalactiae* strain NEM316 (ATCC 12403) genome ({Glaser, P. et al., 2002}; GenBank accession AL732656) and/or any other published *S. agalactiae* genome sequence or parts thereof, especially of the serotype V 2603 V/R (A909) strain {Tettelin, H. et al., 2002}); GenBank accession AE009948). Specifically preferred non-identical nucleic acid residues are residues, which lead to a non-identical amino acid residue. Preferably, the nucleic acid sequences encode polypeptides having at least 1, preferably at least 2, preferably at least 3 different amino acid residues compared to the published *S. agalactiae* counterparts mentioned above. Also such isolated polypeptides, being fragments of the proteins (or the whole protein) mentioned herein e.g. in the sequence listing, having at least 6, 7, or 8 amino acid residues and being encoded by these nucleic acids are preferred.

The nucleic acid molecule according to the present invention can as a fourth alternative also be a nucleic acid molecule which anneals under stringent hybridisation conditions to any of the nucleic acids of the present invention according to the above outlined first, second, and third alternative. Stringent hybridisation conditions are typically those described herein.

Finally, the nucleic acid molecule according to the present invention can as a fifth alternative also be a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to any of the nucleic acid molecules according to any nucleic acid molecule of the present invention according to the first, second, third, and fourth alternative as outlined above. This kind of nucleic acid molecule refers to

the fact that preferably the nucleic acids according to the present invention code for the hyperimmune serum reactive antigens or fragments thereof according to the present invention. This kind of nucleic acid molecule is particularly useful in the detection of a nucleic acid molecule according to the present invention and thus the diagnosis of the respective microorganisms such as *S. agalactiae* and any disease or diseased condition where this kind of microorganims is involved. Preferably, the hybridisation would occur or be preformed under stringent conditions as described in connection with the fourth alternative described above.

Nucleic acid molecule as used herein generally refers to any ribonucleic acid molecule or deoxyribonucleic acid molecule, which may be unmodified RNA or DNA or modified RNA or DNA. Thus, for instance, nucleic acid molecule as used herein refers to, among other, single-and double-stranded DNA, DNA that is a mixture of single- and double-stranded RNA, and RNA that is a mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded, or triple-stranded, or a mixture of single- and double-stranded regions. In addition, nucleic acid molecule as used herein refers to triple-stranded regions comprising RNA or DNA or both RNA and DNA. The strands in such regions may be from the same molecule or from different molecules. The regions may include all of one or more of the molecules, but more typically involve only a region of some of the molecules. One of the molecules of a triple-helical region often is an oligonucleotide. As used herein, the term nucleic acid molecule includes DNAs or RNAs as described above that contain one or more modified bases. Thus, DNAs or RNAs with backbones modified for stability or for other reasons are "nucleic acid molecule" as that term is intended herein. Moreover, DNAs or RNAs comprising unusual bases, such as inosine, or modified bases, such as tritylated bases, to name just two examples, are nucleic acid molecule as the term is used herein. It will be appreciated that a great variety of modifications have been made to DNA and RNA that serve many useful purposes known to those of skill in the art. The term nucleic acid molecule as it is employed herein embraces such chemically, enzymatically or metabolically modified forms of nucleic acid molecule, as well as the chemical forms of DNA and RNA characteristic of viruses and cells, including simple and complex cells, *inter alia*. The term nucleic acid molecule also embraces short nucleic acid molecules often referred to as oligonucleotide(s). "Polynucleotide" and "nucleic acid" or "nucleic acid molecule" are often used interchangeably herein.

Nucleic acid molecules provided in the present invention also encompass numerous unique fragments, both longer and shorter than the nucleic acid molecule sequences set forth in the sequencing listing of the *S. agalactiae* coding regions, which can be generated by standard cloning methods. To be unique, a fragment must be of sufficient size to distinguish it from other known nucleic acid sequences, most readily determined by comparing any selected *S. agalactiae* fragment to the nucleotide sequences in computer databases such as GenBank.

Additionally, modifications can be made to the nucleic acid molecules and polypeptides that are encompassed by the present invention. For example, nucleotide substitutions can be made which do not affect the polypeptide encoded by the nucleic acid, and thus any nucleic acid molecule which encodes a hyperimmune serum reactive antigen or fragments thereof is encompassed by the present invention.

Furthermore, any of the nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof provided by the present invention can be functionally linked, using standard techniques such as standard cloning techniques, to any desired regulatory sequences, whether a *S. agalactiae* regulatory sequence or a heterologous regulatory sequence, heterologous leader sequence, heterologous marker sequence or a heterologous coding sequence to create a fusion protein.

Nucleic acid molecules of the present invention may be in the form of RNA, such as mRNA or cRNA, or in the form of DNA, including, for instance, cDNA and genomic DNA obtained by cloning or produced by chemical synthetic techniques or by a combination thereof. The DNA may be triple-stranded, double-

stranded or single-stranded. Single-stranded DNA may be the coding strand, also known as the sense strand, or it may be the non-coding strand, also referred to as the anti-sense strand.

The present invention further relates to variants of the herein above described nucleic acid molecules which encode fragments, analogs and derivatives of the hyperimmune serum reactive antigens and fragments thereof having a deducted *S. agalactiae* amino acid sequence set forth in the Sequence Listing. A variant of the nucleic acid molecule may be a naturally occurring variant such as a naturally occurring allelic variant, or it may be a variant that is not known to occur naturally. Such non-naturally occurring variants of the nucleic acid molecule may be made by mutagenesis techniques, including those applied to nucleic acid molecules, cells or organisms.

Among variants in this regard are variants that differ from the aforementioned nucleic acid molecules by nucleotide substitutions, deletions or additions. The substitutions, deletions or additions may involve one or more nucleotides. The variants may be altered in coding or non-coding regions or both. Alterations in the coding regions may produce conservative or non-conservative amino acid substitutions, deletions or additions. Preferred are nucleic acid molecules encoding a variant, analog, derivative or fragment, or a variant, analogue or derivative of a fragment, which have a *S. agalactiae* sequence as set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid(s) is substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the *S. agalactiae* polypeptides set forth in the Sequence Listing. Also especially preferred in this regard are conservative substitutions.

The peptides and fragments according to the present invention also include modified epitopes wherein preferably one or two of the amino acids of a given epitope are modified or replaced according to the rules disclosed in e.g. {Tourdot, S. et al., 2000}, as well as the nucleic acid sequences encoding such modified epitopes.

It is clear that also epitopes derived from the present epitopes by amino acid exchanges improving, conserving or at least not significantly impeding the T cell activating capability of the epitopes are covered by the epitopes according to the present invention. Therefore the present epitopes also cover epitopes, which do not contain the original sequence as derived from *S. agalactiae*, but trigger the same or preferably an improved T cell response. These epitope are referred to as "heteroclitic"; they need to have a similar or preferably greater affinity to MHC/HLA molecules, and the need the ability to stimulate the T cell receptors (TCR) directed to the original epitope in a similar or preferably stronger manner.

Heteroclitic epitopes can be obtained by rational design i.e. taking into account the contribution of individual residues to binding to MHC/HLA as for instance described by {Rammensee, H. et al., 1999}, combined with a systematic exchange of residues potentially interacting with the TCR and testing the resulting sequences with T cells directed against the original epitope. Such a design is possible for a skilled man in the art without much experimentation.

Another possibility includes the screening of peptide libraries with T cells directed against the original epitope. A preferred way is the positional scanning of synthetic peptide libraries. Such approaches have been described in detail for instance by {Hemmer, B. et al., 1999}and the references given therein.

As an alternative to epitopes represented by the present derived amino acid sequences or heteroclitic epitopes, also substances mimicking these epitopes e.g. "peptidemimetica" or "retro-inverso-peptides" can be applied.

Another aspect of the design of improved epitopes is their formulation or modification with substances increasing their capacity to stimulate T cells. These include T helper cell epitopes, lipids or liposomes or preferred modifications as described in WO 01/78767.

Another way to increase the T cell stimulating capacity of epitopes is their formulation with immune stimulating substances for instance cytokines or chemokines like interleukin-2, -7, -12, -18, class I and II interferons (IFN), especially IFN-gamma, GM-CSF, TNF-alpha, flt3-ligand and others.

As discussed additionally herein regarding nucleic acid molecule assays of the invention, for instance, nucleic acid molecules of the invention as discussed above, may be used as a hybridization probe for RNA, cDNA and genomic DNA to isolate full-length cDNAs and genomic clones encoding polypeptides of the present invention and to isolate cDNA and genomic clones of other genes that have a high sequence similarity to the nucleic acid molecules of the present invention. Such probes generally will comprise at least 15 bases. Preferably, such probes will have at least 20, at least 25 or at least 30 bases, and may have at least 50 bases. Particularly preferred probes will have at least 30 bases, and will have 50 bases or less, such as 30, 35, 40, 45, or 50 bases.

For example, the coding region of a nucleic acid molecule of the present invention may be isolated by screening a relevant library using the known DNA sequence to synthesize an oligonucleotide probe. A labeled oligonucleotide having a sequence complementary to that of a gene of the present invention is then used to screen a library of cDNA, genomic DNA or mRNA to determine to which members of the library the probe hybridizes.

The nucleic acid molecules and polypeptides of the present invention may be employed as reagents and materials for development of treatments of and diagnostics for disease, particularly human disease, as further discussed herein relating to nucleic acid molecule assays, *inter alia.*

The nucleic acid molecules of the present invention that are oligonucleotides can be used in the processes herein as described, but preferably for PCR, to determine whether or not the *S. agalactiae* genes identified herein in whole or in part are present and/or transcribed in infected tissue such as blood. It is recognized that such sequences will also have utility in diagnosis of the stage of infection and type of infection the pathogen has attained. For this and other purposes the arrays comprising at least one of the nucleic acids according to the present invention as described herein, may be used.

The nucleic acid molecules according to the present invention may be used for the detection of nucleic acid molecules and organisms or samples containing these nucleic acids. Preferably such detection is for diagnosis, more preferable for the diagnosis of a disease related or linked to the present or abundance of *S. agalactiae.*

Eukaryotes (herein also "individual(s)"), particularly mammals, and especially humans, infected with *S. agalactiae* may be identifiable by detecting any of the nucleic acid molecules according to the present invention detected at the DNA level by a variety of techniques. Preferred nucleic acid molecules candidates for distinguishing a *S. agalactiae* from other organisms can be obtained.

The invention provides a process for diagnosing disease, arising from infection with *S. agalactiae,* comprising determining from a sample isolated or derived from an individual an increased level of expression of a nucleic acid molecule having the sequence of a nucleic acid molecule set forth in the Sequence Listing. Expression of nucleic acid molecules can be measured using any one of the methods well known in the art for the quantitation of nucleic acid molecules, such as, for example, PCR, RT-PCR, Rnase protection, Northern blotting, other hybridisation methods and the arrays described herein.

Isolated as used herein means separated "by the hand of man" from its natural state; i.e., that, if it occurs in nature, it has been changed or removed from its original environment, or both. For example, a naturally occurring nucleic acid molecule or a polypeptide naturally present in a living organism in its natural state is not "isolated," but the same nucleic acid molecule or polypeptide separated from the

coexisting materials of its natural state is "isolated", as the term is employed herein. As part of or following isolation, such nucleic acid molecules can be joined to other nucleic acid molecules, such as DNAs, for mutagenesis, to form fusion proteins, and for propagation or expression in a host, for instance. The isolated nucleic acid molecules, alone or joined to other nucleic acid molecules such as vectors, can be introduced into host cells, in culture or in whole organisms. Introduced into host cells in culture or in whole organisms, such DNAs still would be isolated, as the term is used herein, because they would not be in their naturally occurring form or environment. Similarly, the nucleic acid molecules and polypeptides may occur in a composition, such as a media formulations, solutions for introduction of nucleic acid molecules or polypeptides, for example, into cells, compositions or solutions for chemical or enzymatic reactions, for instance, which are not naturally occurring compositions, and, therein remain isolated nucleic acid molecules or polypeptides within the meaning of that term as it is employed herein.

The nucleic acids according to the present invention may be chemically synthesized. Alternatively, the nucleic acids can be isolated from *S. agalactiae* by methods known to the one skilled in the art.

According to another aspect of the present invention, a comprehensive set of novel hyperimmune serum reactive antigens and fragments thereof are provided by using the herein described antigen identification method. In a preferred embodiment of the invention, a hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by any one of the nucleic acids molecules herein described and fragments thereof are provided. In another preferred embodiment of the invention a novel set of hyperimmune serum-reactive antigens which comprises amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 231, 307, 374-433 and fragments thereof are provided. In a further preferred embodiment of the invention hyperimmune serum-reactive antigens which comprise amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 218, 220, 222-230, 232, 235-242, 244-248, 250-253, 256-285, 287-302, 309-317, 320-343, 345-362, 364, 366-373, 434, 449-462 and fragments thereof are provided. In a still preferred embodiment of the invention hyperimmune serum-reactive antigens which comprise amino acid sequences selected from a group consisting of the polypeptide sequences as represented in Seq ID No 249, 303, 308, 318, 344 and fragments thereof are provided.

The hyperimmune serum reactive antigens and fragments thereof as provided in the invention include any polypeptide set forth in the Sequence Listing as well as polypeptides which have at least 70% identity to a polypeptide set forth in the Sequence Listing, preferably at least 80% or 85% identity to a polypeptide set forth in the Sequence Listing, and more preferably at least 90% similarity (more preferably at least 90% identity) to a polypeptide set forth in the Sequence Listing and still more preferably at least 95%, 96%, 97%, 98%, 99% or 99.5% similarity (still more preferably at least 95%, 96%, 97%, 98%, 99%, or 99.5% identity) to a polypeptide set forth in the Sequence Listing and also include portions of such polypeptides with such portion of the polypeptide generally containing at least 4 amino acids and more preferably at least 8, still more preferably at least 30, still more preferably at least 50 amino acids, such as 4, 8, 10, 20, 30, 35, 40, 45 or 50 amino acids.

The invention also relates to fragments, analogs, and derivatives of these hyperimmune serum reactive antigens and fragments thereof. The terms "fragment", "derivative" and "analog" when referring to an antigen whose amino acid sequence is set forth in the Sequence Listing, means a polypeptide which retains essentially the same or a similar biological function or activity as such hyperimmune serum reactive antigen and fragment thereof.

The fragment, derivative or analog of a hyperimmune serum reactive antigen and fragment thereof may be 1) one in which one or more of the amino acid residues are substituted with a conserved or non-conserved amino acid residue (preferably a conserved amino acid residue) and such substituted amino acid residue may or may not be one encoded by the genetic code, or 2) one in which one or more of the amino acid residues includes a substituent group, or 3) one in which the mature hyperimmune serum

reactive antigen or fragment thereof is fused with another compound, such as a compound to increase the half-life of the hyperimmune serum reactive antigen and fragment thereof (for example, polyethylene glycol), or 4) one in which the additional amino acids are fused to the mature hyperimmune serum reactive antigen or fragment thereof, such as a leader or secretory sequence or a sequence which is employed for purification of the mature hyperimmune serum reactive antigen or fragment thereof or a proprotein sequence. Such fragments, derivatives and analogs are deemed to be within the scope of those skilled in the art from the teachings herein.

The present invention also relates to antigens of different *S. agalactiae* isolates. Such homologues may easily be isolated based on the nucleic acid and amino acid sequences disclosed herein. There are 9 serotypes distinguished to date and the typing is based on serotype specific antisera. The presence of any antigen can accordingly be determined for every serotype. In addition it is possible to determine the variability of a particular antigen in the various serotypes as described for the *S. pyogenes* sic gene (Hoe, N. et al., 2001). The contribution of the various serotypes to the different GBS infections varies in the different age groups and geographical regions. It is an important aspect that the most valuable protective antigens are expected to be conserved among various clinical strains.

Among the particularly preferred embodiments of the invention in this regard are the hyperimmune serum reactive antigens set forth in the Sequence Listing, variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of fragments. Additionally, fusion polypeptides comprising such hyperimmune serum reactive antigens, variants, analogs, derivatives and fragments thereof, and variants, analogs and derivatives of the fragments are also encompassed by the present invention. Such fusion polypeptides and proteins, as well as nucleic acid molecules encoding them, can readily be made using standard techniques, including standard recombinant techniques for producing and expression of a recombinant polynucleic acid encoding a fusion protein.

Among preferred variants are those that vary from a reference by conservative amino acid substitutions. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr.

Further particularly preferred in this regard are variants, analogs, derivatives and fragments, and variants, analogs and derivatives of the fragments, having the amino acid sequence of any polypeptide set forth in the Sequence Listing, in which several, a few, 5 to 10, 1 to 5, 1 to 3, 2, 1 or no amino acid residues are substituted, deleted or added, in any combination. Especially preferred among these are silent substitutions, additions and deletions, which do not alter the properties and activities of the polypeptide of the present invention. Also especially preferred in this regard are conservative substitutions. Most highly preferred are polypeptides having an amino acid sequence set forth in the Sequence Listing without substitutions.

The hyperimmune serum reactive antigens and fragments thereof of the present invention are preferably provided in an isolated form, and preferably are purified to homogeneity.

Also among preferred embodiments of the present invention are polypeptides comprising fragments of the polypeptides having the amino acid sequence set forth in the Sequence Listing, and fragments of variants and derivatives of the polypeptides set forth in the Sequence Listing.

In this regard a fragment is a polypeptide having an amino acid sequence that entirely is the same as part but not all of the amino acid sequence of the afore mentioned hyperimmune serum reactive antigen and fragment thereof, and variants or derivative, analogs, fragments thereof. Such fragments may be "free-

standing", i.e., not part of or fused to other amino acids or polypeptides, or they may be comprised within a larger polypeptide of which they form a part or region. Also preferred in this aspect of the invention are fragments characterised by structural or functional attributes of the polypeptide of the present invention, i.e. fragments that comprise alpha-helix and alpha-helix forming regions, beta-sheet and beta-sheet forming regions, turn and turn-forming regions, coil and coil-forming regions, hydrophilic regions, hydrophobic regions, alpha amphipathic regions, beta-amphipathic regions, flexible regions, surface-forming regions, substrate binding regions, and high antigenic index regions of the polypeptide of the present invention, and combinations of such fragments. Preferred regions are those that mediate activities of the hyperimmune serum reactive antigens and fragments thereof of the present invention. Most highly preferred in this regard are fragments that have a chemical, biological or other activity of the hyperimmune serum reactive antigen and fragments thereof of the present invention, including those with a similar activity or an improved activity, or with a decreased undesirable activity. Particularly preferred are fragments comprising receptors or domains of enzymes that confer a function essential for viability of *S. agalactiae* or the ability to cause disease in humans. Further preferred polypeptide fragments are those that comprise or contain antigenic or immunogenic determinants in an animal, especially in a human.

An antigenic fragment is defined as a fragment of the identified antigen, which is for itself antigenic or may be made antigenic when provided as a hapten. Therefore, also antigens or antigenic fragments showing one or (for longer fragments) only a few amino acid exchanges are enabled with the present invention, provided that the antigenic capacities of such fragments with amino acid exchanges are not severely deteriorated on the exchange(s), i.e., suited for eliciting an appropriate immune response in an individual vaccinated with this antigen and identified by individual antibody preparations from individual sera.

Preferred examples of such fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table 1A, **especially peptides comprising amino acid** 4-20, 35-44, 65-70, 73-87, 92-98, 112-137, 152-161, 177-186, 193-200, 206-213, 229-255, 282-294, 308-313, 320-326, 349-355, 373-384, 388-406, 420-425 and 115-199 of **Seq ID No** 218; 5-24, 35-41, 44-70, 73-89, 103-109, 127-143, 155-161, 185-190, 192-207, 212-219, 246-262, 304-336, 372-382, 384-393, 398-407, 412-418, 438-444, 1-75, 76-161 and 164-239 of **Seq ID No** 219; 4-10, 16-58, 60-71, 77-92, 100-126, 132-146, 149-164, 166-172, 190-209, 214-220, 223-229, 241-256, 297-312, 314-319, 337-343, 351-359, 378-387, 398-418, 421-428, 430-437, 440-448, 462-471, 510-519, 525-536, 552-559, 561-568, 573-582, 596-602, 608-630, 637-649, 651-665, 681-702, 714-732, 739-745, 757-778, 790-805, 807-815, 821-829, 836-842, 846-873, 880-903, 908-914, 916-923, 931-940, 943-948, 956-970, 975-986, 996-1015, 1031-1040, 1051-1069, 1072-1095, 1114-1119, 1130-1148, 1150-1157, 1169-1176, 1229-1238 and 802-812 of **Seq ID No** 220; 5-12, 14-26, 35-47, 52-67, 72-78, 83-98, 121-141, 152-159, 163-183, 186-207, 209-257, 264-277, 282-299, 301-309, 312-318, 324-339, 358-368, 372-378, 387-397, 425-431 and 46-291 of **Seq ID No** 221; 29-38, 44-64, 70-76, 78-87, 94-100, 102-112, 119-134, 140-149, 163-173, 178-186, 188-194, 207-234, 247-262, 269-290 and 73-92 of **Seq ID No** 222; 10-28, 36-63, 77-87, 103-119, 127-136, 141-169, 171-183, 195-200, 207-232, 236-246, 251-265, 268-283, 287-297, 314-322, 335-343, 354-363, 384-390, 405-411, 419-436, 443-455, 467-473, 480-513, 518-529, 550-557, 565-585, 602-608, 616-625, 632-660, 665-677, 685-701, 726-736, 738-747, 752-761, 785-796, 801-813, 838-853, 866-871 and 757-774 of **Seq ID No** 223; 31-38, 61-66, 74-81, 90-115, 123-145, 154-167, 169-179, 182-193, 200-206, 238-244, 267-272 and 235-251 of **Seq ID No** 224; 19-25, 38-54, 56-64, 66-72, 74-92, 94-100, 116-129, 143-149, 156-183, 204-232, 253-266, 269-275, 294-307 and 241-313 of **Seq ID No** 225; 5-34, 50-56, 60-65, 74-85, 89-97, 108-119, 159-165, 181-199, 209-225, 230-240, 245-251, 257-262, 274-282, 300-305 and 64-75 of **Seq ID No** 226; 5-13, 16-21, 27-42, 45-52, 58-66, 74-87, 108-114, 119-131 and 39-51 of **Seq ID No** 227; 6-23, 46-54, 59-65, 78-84, 100-120, 128-133, 140-146, 159-165, 171-183, 190-204, 224-232, 240-248, 250-259, 274-280, 288-296, 306-315 and 267-274 of **Seq ID No** 228; 5-12, 15-24, 26-36, 42-65, 68-80, 82-104, 111-116, 125-144, 159-167, 184-189, 209-218, 235-243, 254-265, 269-283, 287-300, 306-316, 318-336, 338-352, 374-392 and 162-174 of **Seq ID No** 229; 30-42, 45-54 and 25-37 of **Seq ID No** 230; 10-30, 53-59, 86-95, 116-130, 132-147, 169-189, 195-201, 212-221, 247-256, 258-265, 278-

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12-28, 41-91, 98-107, 112-120, 125-131, 151-193, 215-221, 240-250, 263-280 and 128-138 of Seq ID No 368; 16-24, 32-38, 46-62, 68-81, 90-105, 127-133, 144-150, 160-166, 178-184, 186-202, 210-219, 232-240, 252-258, 264-273, 293-324, 337-344, 349-357, 360-369, 385-398, 410-416, 419-427, 441-449, 458-476, 508-515, 523-539, 544-549, 562-569, 571-579, 96-109 and 127-139 of Seq ID No 369; 19-25, 28-34, 56-61, 85-97, 110-116 and 39-53 of Seq ID No 370; 4-37, 41-50, 62-72, 91-97, 99-109, 114-125, 136-141, 149-158, 160-166, 201-215 and 27-225 of Seq ID No 371; 15-31, 44-51, 96-105, 122-130, 149-157, 162-168, 178-183, 185-192, 198-204, 206-213, 221-234, 239-245, 248-255, 257-266, 289-335, 349-357, 415-422, 425-441, 448-454, 462-468 and 463-481 of Seq ID No 372; 5-31, 39-55, 63-72, 76-99, 106-155, 160-177, 179-199, 207-217, 223-240, 245-255, 261-267, 294-316, 321-343, 354-378, 382-452, 477-488, 529-536, 555-569, 584-591, 593-612, 620-627, 632-640, 647-654, 671-680, 698-704, 723-730, 732-750, 769-775, 781-788, 822-852 and 505-525 of Seq ID No 373; 3-18 of Seq ID No 374; 4-14 and 12-24 of Seq ID No 375; 4-11, 22-30 and 12-25 of Seq ID No 376; 5-12 and 4-18 of Seq ID No 377; 4-28 and 7-14 of Seq ID No 378; 6-16 and 8-16 of Seq ID No 379; 4-15, 18-33 and 24-36 of Seq ID No 380; 4-10, 16-21 and 20-31 of Seq ID No 381; 6-19 of Seq ID No 382; 11-18 and 3-10 of Seq ID No 383; 13-24 and 3-15 of Seq ID No 384; 15-27 and 7-16 of Seq ID No 385; 11-16 and 1-15 of Seq ID No 386; 4-16 and 9-21 of Seq ID No 387; 4-24, 40-48, 54-67 and 22-39 of Seq ID No 388; 6-30, 34-55, 62-68, 78-106 and 68-74 of Seq ID No 389; 3-14 of Seq ID No 390; 9-19 and 6-21 of Seq ID No 391; 4-17 and 1-9 of Seq ID No 392; 5-30 and 1-8 of Seq ID No 393; 4-16, 23-46, 51-56 and 45-55 of Seq ID No 394; 7-16 of Seq ID No 395; 2-14 of Seq ID No 396; 4-36, 43-65 and 50-62 of Seq ID No 397; 10-30 and 14-21 of Seq ID No 398; 9-17 and 1-10 of Seq ID No 399; 4-12 and 3-16 of Seq ID No 400; 4-15 and 5-23 of Seq ID No 401; 10-21 of Seq ID No 402; 6-16 of Seq ID No 403; 4-29, 31-38 and 2-14 of Seq ID No 404; 4-35 and 33-42 of Seq ID No 405; 2-17 of Seq ID No 406; 9-18, 30-35 and 15-33 of Seq ID No 407; 4-9 and 6-12 of Seq ID No 408; 3-17 of Seq ID No 409; 12-21, 37-44, 52-61, 72-80 and 38-48 of Seq ID No 410; 4-10, 29-44, 54-61, 69-78 and 13-27 of Seq ID No 411; 13-23, 36-53 and 2-15 of Seq ID No 412; 4-25, 28-46, 56-72, 81-99, 120-132, 134-142, 154-160 and 129-141 of Seq ID No 413; 4-15, 24-33, 35-41, 64-86 and 21-33 of Seq ID No 414; 9-15 and 4-13 of Seq ID No 415; 4-11, 13-19, 34-48 and 15-32 of Seq ID No 416; 4-21 and 11-31 of Seq ID No 417; 23-57 and 38-50 of Seq ID No 418; 4-32 and 3-13 of Seq ID No 419; 4-10, 13-25, 32-42, 56-68, 72-84 and 26-38 of Seq ID No 420; 4-20, 31-48, 52-58, 65-71, 80-93, 99-108, 114-123 and 37-49 of Seq ID No 421; 6-12, 14-20 and 3-25 of Seq ID No 422; 14-25, 27-38 and 5-14 of Seq ID No 423; 4-41, 57-105, 109-118, 123-136, 144-152 and 86-99 of Seq ID No 424; 6-19 of Seq ID No 425; 2-19 of Seq ID No 426; 14-47 and 1-14 of Seq ID No 427; 4-21, 29-44 and 2-18 of Seq ID No 428; 23-29 and 10-28 of Seq ID No 429; 6-16, 22-36 and 11-22 of Seq ID No 430; 4-19, 30-44 and 18-27 of Seq ID No 431; 5-15, 37-45, 58-65 and 38-47 of Seq ID No 432; 4-15, 23-34 and 4-15 of Seq ID No 433; 30-36, 44-54, 79-85, 101-114, 138-152, 154-164, 170-175, 179-200, 213-220, 223-240, 243-255, 258-264, 268-284 and 10-28 of Seq ID No 434; the peptides comprising amino acid sequences of column "Identical region" of the Table 1B, especially peptides comprising amino acid 210-226 and 738-753 of Seq ID No 449; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 450; 893-906 of Seq ID No 451; 51-69 of Seq ID No 452; 110-125 of Seq ID No 453; 291-305 of Seq ID No 454; 210-226 and 738-753 of Seq ID No 455; 326-344, 326-348, 338-354, 371-392, 801-809 and 877-901 of Seq ID No 456; 893-906 of Seq ID No 457; 51-69 of Seq ID No 458; 110-125 of Seq ID No 459; 291-305 of Seq ID No 460; 32-44 of Seq ID No 461; 399-410 of Seq ID No 462; the serum reactive epitopes as specified in the column of "aa from" to "aa to" of Table 2, especially peptides comprising amino acid 120-143, 138-161 and 156-179 of Seq ID No 218; 110-129 and 168-184 of Seq ID No 219; 74-90 of Seq ID No 222; 759-773 of Seq ID No 223; 237-260 of Seq ID No 224;

265-284 of Seq ID No 225; 65-74 of Seq ID No 226; 41-50 of Seq ID No 227; 163-174 of Seq ID No 229; 26-37 of Seq ID No 230; 174-189 of Seq ID No 232; 240-256 of Seq ID No 234; 285-297 of Seq ID No 236; 238-247 of Seq ID No 238; 491-519 of Seq ID No 239; 114-140 of Seq ID No 243; 267-284 of Seq ID No 250; 439-453 of Seq ID No 252; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 60-71 of Seq ID No 256; 244-257 of Seq ID No 257; 44-63 and 57-76 of Seq ID No 258; 185-196 of Seq ID No 260; 119-129 of Seq ID No 263; 182-195 of Seq ID No 266; 32-44 and 424-442 of Seq ID No 267; 247-256 of Seq ID No 268; 678-694, 785-805, 55-77 and 72-94 of Seq ID No 269; 210-226 of Seq ID No 281; 37-59 of Seq ID No 289; 13-29 of Seq ID No 296; 136-159 of Seq ID No 348; 205-222 of Seq ID No 349; 99-110 of Seq ID No 350; 160-176 of Seq ID No 351; 457-470 of Seq ID No 355; 221-237 of Seq ID No 356; 167-190 of Seq ID No 357; 96-120 of Seq ID No 361; 399-417, 503-519 and 544-563 of Seq ID No 364; 46-68, 159-183 and 184-198 of Seq ID No 371; 463-481 of Seq ID No 372; the immunogenic epitopes as specified in the column of "aa from" to "aa to" of Table 4; especially peptides comprising amino acid 110-129 and 168-184 of Seq ID No 219; 877-901, 333-354, 326-344 and 801-809 of Seq ID No 277; 1-54 of Seq ID No 347; 544-563, 31-51, 107-119, 399-417 and 503-519 of Seq ID No 364; 120-198 of Seq ID No 218; 20-35 of Seq ID No 219; 118-201 of Seq ID No 221; 48-132 of Seq ID No 242; 118-136 of Seq ID No 249; 162-178 of Seq ID No 253; 347-364 of Seq ID No 254; 699-715 of Seq ID No 255; 50-76 of Seq ID No 258; 785-819 and 44-128 of Seq ID No 269; 90-128 of Seq ID No 274; 314-384 of Seq ID No 289; 327-349 of Seq ID No 293; 242-314, 405-478 and 23-100 of Seq ID No 304; 129-210 of Seq ID No 305; 162-188 of Seq ID No 307; 750-772 of Seq ID No 310; 1-56 of Seq ID No 335; 322-337 of Seq ID No 337; 72-90 of Seq ID No 339; 374-395 of Seq ID No 345; 136-159 of Seq ID No 348; 141-164 of Seq ID No 358; 96-157 of Seq ID No 361; 1-82 of Seq ID No 363; 489-556 of Seq ID No 364; 159-183 and 49-133 of Seq ID No 371 and fragments comprising at least 6, preferably more than 8, especially more than 10 aa of said sequences. All these fragments individually and each independently form a preferred selected aspect of the present invention.

All linear hyperimmune serum reactive fragments of a particular antigen may be identified by analysing the entire sequence of the protein antigen by a set of peptides overlapping by 1 amino acid with a length of at least 10 amino acids. Subsequently, non-linear epitopes can be identified by analysis of the protein antigen with hyperimmune sera using the expressed full-length protein or domain polypeptides thereof. Assuming that a distinct domain of a protein is sufficient to form the 3D structure independent from the native protein, the analysis of the respective recombinant or synthetically produced domain polypeptide with hyperimmune serum would allow the identification of conformational epitopes within the individual domains of multi-domain proteins. For those antigens where a domain possesses linear as well as conformational epitopes, competition experiments with peptides corresponding to the linear epitopes may be used to confirm the presence of conformational epitopes.

It will be appreciated that the invention also relates to, among others, nucleic acid molecules encoding the aforementioned fragments, nucleic acid molecules that hybridise to nucleic acid molecules encoding the fragments, particularly those that hybridise under stringent conditions, and nucleic acid molecules, such as PCR primers, for amplifying nucleic acid molecules that encode the fragments. In these regards, preferred nucleic acid molecules are those that correspond to the preferred fragments, as discussed above.

The present invention also relates to vectors, which comprise a nucleic acid molecule or nucleic acid molecules of the present invention, host cells which are genetically engineered with vectors of the invention and the production of hyperimmune serum reactive antigens and fragments thereof by recombinant techniques.

A great variety of expression vectors can be used to express a hyperimmune serum reactive antigen or fragment thereof according to the present invention. Generally, any vector suitable to maintain, propagate or express nucleic acids to express a polypeptide in a host may be used for expression in this regard. In accordance with this aspect of the invention the vector may be, for example, a plasmid vector,

a single or double-stranded phage vector, a single or double-stranded RNA or DNA viral vector. Starting plasmids disclosed herein are either commercially available, publicly available, or can be constructed from available plasmids by routine application of well-known, published procedures. Preferred among vectors, in certain respects, are those for expression of nucleic acid molecules and hyperimmune serum reactive antigens or fragments thereof of the present invention. Nucleic acid constructs in host cells can be used in a conventional manner to produce the gene product encoded by the recombinant sequence. Alternatively, the hyperimmune serum reactive antigens and fragments thereof of the invention can be synthetically produced by conventional peptide synthesizers. Mature proteins can be expressed in mammalian cells, yeast, bacteria, or other cells under the control of appropriate promoters. Cell-free translation systems can also be employed to produce such proteins using RNAs derived from the DNA construct of the present invention.

Host cells can be genetically engineered to incorporate nucleic acid molecules and express nucleic acid molecules of the present invention. Representative examples of appropriate hosts include bacterial cells, such as streptococci, staphylococci, *E. coli*, *Streptomyces* and *Bacillus subtillis* cells; fungal cells, such as yeast cells and *Aspergillus* cells; insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, Hela, C127, 3T3, BHK, 293 and Bowes melanoma cells; and plant cells.

The invention also provides a process for producing a *S. agalactiae* hyperimmune serum reactive antigen and a fragment thereof comprising expressing from the host cell a hyperimmune serum reactive antigen or fragment thereof encoded by the nucleic acid molecules provided by the present invention. The invention further provides a process for producing a cell, which expresses a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof comprising transforming or transfecting a suitable host cell with the vector according to the present invention such that the transformed or transfected cell expresses the polypeptide encoded by the nucleic acid contained in the vector.

The polypeptide may be expressed in a modified form, such as a fusion protein, and may include not only secretion signals but also additional heterologous functional regions. Thus, for instance, a region of additional amino acids, particularly charged amino acids, may be added to the N- or C-terminus of the polypeptide to improve stability and persistence in the host cell, during purification or during subsequent handling and storage. Also, regions may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to polypeptides to engender secretion or excretion, to improve stability or to facilitate purification, among others, are familiar and routine techniques in the art. A preferred fusion protein comprises a heterologous region from immunoglobulin that is useful to solubilize or purify polypeptides. For example, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobin molecules together with another protein or part thereof. In drug discovery, for example, proteins have been fused with antibody Fc portions for the purpose of high-throughout screening assays to identify antagonists. See for example, {Bennett, D. et al., 1995} and {Johanson, K. et al., 1995}.

The *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, hydroxylapatite chromatography and lectin chromatography.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention can be produced by chemical synthesis as well as by biotechnological means. The latter comprise the transfection or transformation of a host cell with a vector containing a nucleic acid according to the present invention and the cultivation of the transfected or transformed host cell under conditions, which are known to the ones skilled in the art. The production method may also comprise a purification step in

order to purify or isolate the polypeptide to be manufactured. In a preferred embodiment the vector is a vector according to the present invention.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may be used for the detection of the organism or organisms in a sample containing these organisms or polypeptides derived thereof. Preferably such detection is for diagnosis, more preferable for the diagnosis of a disease, most preferably for the diagnosis of a diseases related or linked to the presence or abundance of Gram-positive bacteria, especially bacteria selected from the group comprising streptococci, staphylococci and lactococci. More preferably, the microorganisms are selected from the group comprising *Streptococcus pneumoniae*, *Streptococcus pyogenes* and *Streptococcus mutans*, especially the microorganism is *Streptococcus pyogenes*.

The present invention also relates to diagnostic assays such as quantitative and diagnostic assays for detecting levels of the hyperimmune serum reactive antigens and fragments thereof of the present invention in cells and tissues, including determination of normal and abnormal levels. Thus, for instance, a diagnostic assay in accordance with the invention for detecting over-expression of the polypeptide compared to normal control tissue samples may be used to detect the presence of an infection, for example, and to identify the infecting organism. Assay techniques that can be used to determine levels of a polypeptide, in a sample derived from a host are well known to those of skill in the art. Such assay methods include radioimmunoassays, competitive-binding assays, Western Blot analysis and ELISA assays. Among these, ELISAs frequently are preferred. An ELISA assay initially comprises preparing an antibody specific to the polypeptide, preferably a monoclonal antibody. In addition, a reporter antibody generally is prepared which binds to the monoclonal antibody. The reporter antibody is attached to a detectable reagent such as radioactive, fluorescent or enzymatic reagent, such as horseradish peroxidase enzyme.

The hyperimmune serum reactive antigens and fragments thereof according to the present invention may also be used for the purpose of or in connection with an array. More particularly, at least one of the hyperimmune serum reactive antigens and fragments thereof according to the present invention may be immobilized on a support. Said support typically comprises a variety of hyperimmune serum reactive antigens and fragments thereof whereby the variety may be created by using one or several of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and/or hyperimmune serum reactive antigens and fragments thereof being different. The characterizing feature of such array as well as of any array in general is the fact that at a distinct or predefined region or position on said support or a surface thereof, a distinct polypeptide is immobilized. Because of this any activity at a distinct position or region of an array can be correlated with a specific polypeptide. The number of different hyperimmune serum reactive antigens and fragments thereof immobilized on a support may range from as little as 10 to several 1000 different hyperimmune serum reactive antigens and fragments thereof. The density of hyperimmune serum reactive antigens and fragments thereof per $cm^2$ is in a preferred embodiment as little as 10 peptides/polypeptides per $cm^2$ to at least 400 different peptides/polypeptides per $cm^2$ and more particularly at least 1000 different hyperimmune serum reactive antigens and fragments thereof per $cm^2$.

The manufacture of such arrays is known to the one skilled in the art and, for example, described in US patent 5,744,309. The array preferably comprises a planar, porous or non-porous solid support having at least a first surface. The hyperimmune serum reactive antigens and fragments thereof as disclosed herein, are immobilized on said surface. Preferred support materials are, among others, glass or cellulose. It is also within the present invention that the array is used for any of the diagnostic applications described herein. Apart from the hyperimmune serum reactive antigens and fragments thereof according to the present invention also the nucleic acid molecules according to the present invention may be used for the generation of an array as described above. This applies as well to an array made of antibodies, preferably monoclonal antibodies as, among others, described herein.

In a further aspect the present invention relates to an antibody directed to any of the hyperimmune serum reactive antigens and fragments thereof, derivatives or fragments thereof according to the present invention. The present invention includes, for example, monoclonal and polyclonal antibodies, chimeric, single chain, and humanized antibodies, as well as Fab fragments, or the product of a Fab expression library. It is within the present invention that the antibody may be chimeric, i. e. that different parts thereof stem from different species or at least the respective sequences are taken from different species.

Antibodies generated against the hyperimmune serum reactive antigens and fragments thereof corresponding to a sequence of the present invention can be obtained by direct injection of the hyperimmune serum reactive antigens and fragments thereof into an animal or by administering the hyperimmune serum reactive antigens and fragments thereof to an animal, preferably a non-human. The antibody so obtained will then bind the hyperimmune serum reactive antigens and fragments thereof itself. In this manner, even a sequence encoding only a fragment of a hyperimmune serum reactive antigen and fragments thereof can be used to generate antibodies binding the whole native hyperimmune serum reactive antigen and fragments thereof. Such antibodies can then be used to isolate the hyperimmune serum reactive antigens and fragments thereof from tissue expressing those hyperimmune serum reactive antigens and fragments thereof.

For preparation of monoclonal antibodies, any technique known in the art, which provides antibodies produced by continuous cell line cultures can be used (as described originally in {Kohler, G. et al., 1975}.

Techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778) can be adapted to produce single chain antibodies to immunogenic hyperimmune serum reactive antigens and fragments thereof according to this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies to immunogenic hyperimmune serum reactive antigens and fragments thereof according to this invention.

Alternatively, phage display technology or ribosomal display could be utilized to select antibody genes with binding activities towards the hyperimmune serum reactive antigens and fragments thereof either from repertoires of PCR amplified v-genes of lymphocytes from humans screened for possessing respective target antigens or from naïve libraries {McCafferty, J. et al., 1990}; {Marks, J. et al., 1992}. The affinity of these antibodies can also be improved by chain shuffling {Clackson, T. et al., 1991}.

If two antigen binding domains are present, each domain may be directed against a different epitope – termed 'bispecific' antibodies.

The above-described antibodies may be employed to isolate or to identify clones expressing the hyperimmune serum reactive antigens and fragments thereof or purify the hyperimmune serum reactive antigens and fragments thereof of the present invention by attachment of the antibody to a solid support for isolation and/or purification by affinity chromatography.

Thus, among others, antibodies against the hyperimmune serum reactive antigens and fragments thereof of the present invention may be employed to inhibit and/or treat infections, particularly bacterial infections and especially infections arising from *S. agalactiae*.

Hyperimmune serum reactive antigens and fragments thereof include antigenically, epitopically or immunologically equivalent derivatives, which form a particular aspect of this invention. The term "antigenically equivalent derivative" as used herein encompasses a hyperimmune serum reactive antigen and fragments thereof or its equivalent which will be specifically recognized by certain antibodies which, when raised to the protein or hyperimmune serum reactive antigen and fragments thereof according to the present invention, interfere with the interaction between pathogen and mammalian host. The term

"immunologically equivalent derivative" as used herein encompasses a peptide or its equivalent which when used in a suitable formulation to raise antibodies in a vertebrate, the antibodies act to interfere with the interaction between pathogen and mammalian host.

The hyperimmune serum reactive antigens and fragments thereof, such as an antigenically or immunologically equivalent derivative or a fusion protein thereof can be used as an antigen to immunize a mouse or other animal such as a rat or chicken. The fusion protein may provide stability to the hyperimmune serum reactive antigens and fragments thereof. The antigen may be associated, for example by conjugation, with an immunogenic carrier protein, for example bovine serum albumin (BSA) or keyhole limpet haemocyanin (KLH). Alternatively, an antigenic peptide comprising multiple copies of the protein or hyperimmune serum reactive antigen and fragments thereof, or an antigenically or immunologically equivalent hyperimmune serum reactive antigen and fragments thereof, may be sufficiently antigenic to improve immunogenicity so as to obviate the use of a carrier.

Preferably the antibody or derivative thereof is modified to make it less immunogenic in the individual. For example, if the individual is human the antibody may most preferably be "humanized", wherein the complimentarity determining region(s) of the hybridoma-derived antibody has been transplanted into a human monoclonal antibody, for example as described in {Jones, P. et al., 1986} or {Tempest, P. et al., 1991}.

The use of a polynucleotide of the invention in genetic immunization will preferably employ a suitable delivery method such as direct injection of plasmid DNA into muscle, delivery of DNA complexed with specific protein carriers, coprecipitation of DNA with calcium phosphate, encapsulation of DNA in various forms of liposomes, particle bombardment {Tang, D. et al., 1992}, {Eisenbraun, M. et al., 1993} and *in vivo* infection using cloned retroviral vectors {Seeger, C. et al., 1984}.

In a further aspect the present invention relates to a peptide binding to any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, and a method for the manufacture of such peptides whereby the method is characterized by the use of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and the basic steps are known to the one skilled in the art.

Such peptides may be generated by using methods according to the state of the art such as phage display or ribosome display. In case of phage display, basically a library of peptides is generated, in form of phages, and this kind of library is contacted with the target molecule, in the present case a hyperimmune serum reactive antigen and fragments thereof according to the present invention. Those peptides binding to the target molecule are subsequently removed, preferably as a complex with the target molecule, from the respective reaction. It is known to the one skilled in the art that the binding characteristics, at least to a certain extent, depend on the particularly realized experimental set-up such as the salt concentration and the like. After separating those peptides binding to the target molecule with a higher affinity or a bigger force, from the non-binding members of the library, and optionally also after removal of the target molecule from the complex of target molecule and peptide, the respective peptide(s) may subsequently be characterised. Prior to the characterisation optionally an amplification step is realized such as, e. g. by propagating the peptide encoding phages. The characterisation preferably comprises the sequencing of the target binding peptides. Basically, the peptides are not limited in their lengths, however, preferably peptides having a lengths from about 8 to 20 amino acids are preferably obtained in the respective methods. The size of the libraries may be about $10^2$ to $10^{18}$, preferably $10^8$ to $10^{15}$ different peptides, however, is not limited thereto.

A particular form of target binding hyperimmune serum reactive antigens and fragments thereof are the so-called "anticalines" which are, among others, described in German patent application DE 197 42 706.

In a further aspect the present invention relates to functional nucleic acids interacting with any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, and a method for the manufacture of such functional nucleic acids whereby the method is characterized by the use of the hyperimmune serum reactive antigens and fragments thereof according to the present invention and the basic steps are known to the one skilled in the art. The functional nucleic acids are preferably aptamers and spiegelmers.

Aptamers are D-nucleic acids, which are either single stranded or double stranded and which specifically interact with a target molecule. The manufacture or selection of aptamers is, e.g. described in European patent EP 0 533 838. Basically the following steps are realized. First, a mixture of nucleic acids, i. e. potential aptamers, is provided whereby each nucleic acid typically comprises a segment of several, preferably at least eight subsequent randomised nucleotides. This mixture is subsequently contacted with the target molecule whereby the nucleic acid(s) bind to the target molecule, such as based on an increased affinity towards the target or with a bigger force thereto, compared to the candidate mixture. The binding nucleic acid(s) are/is subsequently separated from the remainder of the mixture. Optionally, the thus obtained nucleic acid(s) is amplified using, e.g. polymerase chain reaction. These steps may be repeated several times giving at the end a mixture having an increased ratio of nucleic acids specifically binding to the target from which the final binding nucleic acid is then optionally selected. These specifically binding nucleic acid(s) are referred to as aptamers. It is obvious that at any stage of the method for the generation or identification of the aptamers samples of the mixture of individual nucleic acids may be taken to determine the sequence thereof using standard techniques. It is within the present invention that the aptamers may be stabilized such as, e. g., by introducing defined chemical groups which are known to the one skilled in the art of generating aptamers. Such modification may for example reside in the introduction of an amino group at the 2'-position of the sugar moiety of the nucleotides. Aptamers are currently used as therapeutical agents. However, it is also within the present invention that the thus selected or generated aptamers may be used for target validation and/or as lead substance for the development of medicaments, preferably of medicaments based on small molecules. This is actually done by a competition assay whereby the specific interaction between the target molecule and the aptamer is inhibited by a candidate drug whereby upon replacement of the aptamer from the complex of target and aptamer it may be assumed that the respective drug candidate allows a specific inhibition of the interaction between target and aptamer, and if the interaction is specific, said candidate drug will, at least in principle, be suitable to block the target and thus decrease its biological availability or activity in a respective system comprising such target. The thus obtained small molecule may then be subject to further derivatisation and modification to optimise its physical, chemical, biological and/or medical characteristics such as toxicity, specificity, biodegradability and bioavailability.

Spiegelmers and their generation or manufacture is based on a similar principle. The manufacture of spiegelmers is described in international patent application WO 98/08856. Spiegelmers are L-nucleic acids, which means that they are composed of L-nucleotides rather than D-nucleotides as aptamers are. Spiegelmers are characterized by the fact that they have a very high stability in biological systems and, comparable to aptamers, specifically interact with the target molecule against which they are directed. In the process of generating spiegelmers, a heterogeonous population of D-nucleic acids is created and this population is contacted with the optical antipode of the target molecule, in the present case for example with the D-enantiomer of the naturally occurring L-enantiomer of the hyperimmune serum reactive antigens and fragments thereof according to the present invention. Subsequently, those D-nucleic acids are separated which do not interact with the optical antipode of the target molecule. But those D-nucleic acids interacting with the optical antipode of the target molecule are separated, optionally identified and/or sequenced and subsequently the corresponding L-nucleic acids are synthesized based on the nucleic acid sequence information obtained from the D-nucleic acids. These L-nucleic acids which are identical in terms of sequence with the aforementioned D-nucleic acids interacting with the optical antipode of the target molecule, will specifically interact with the naturally occurring target molecule rather than with the optical antipode thereof. Similar to the method for the generation of aptamers it is

also possible to repeat the various steps several times and thus to enrich those nucleic acids specifically interacting with the optical antipode of the target molecule.

In a further aspect the present invention relates to functional nucleic acids interacting with any of the nucleic acid molecules according to the present invention, and a method for the manufacture of such functional nucleic acids whereby the method is characterized by the use of the nucleic acid molecules and their respective sequences according to the present invention and the basic steps are known to the one skilled in the art. The functional nucleic acids are preferably ribozymes, antisense oligonucleotides and siRNA.

Ribozymes are catalytically active nucleic acids, which preferably consist of RNA, which basically comprises two moieties. The first moiety shows a catalytic activity whereas the second moiety is responsible for the specific interaction with the target nucleic acid, in the present case the nucleic acid coding for the hyperimmune serum reactive antigens and fragments thereof according to the present invention. Upon interaction between the target nucleic acid and the second moiety of the ribozyme, typically by hybridisation and Watson-Crick base pairing of essentially complementary stretches of bases on the two hybridising strands, the catalytically active moiety may become active which means that it catalyses, either intramolecularly or intermolecularly, the target nucleic acid in case the catalytic activity of the ribozyme is a phosphodiesterase activity. Subsequently, there may be a further degradation of the target nucleic acid, which in the end results in the degradation of the target nucleic acid as well as the protein derived from the said target nucleic acid. Ribozymes, their use and design principles are known to the one skilled in the art, and, for example described in {Doherty, E. et al., 2001} and {Lewin, A. et al., 2001}.

The activity and design of antisense oligonucleotides for the manufacture of a medicament and as a diagnostic agent, respectively, is based on a similar mode of action. Basically, antisense oligonucleotides hybridise based on base complementarity, with a target RNA, preferably with a mRNA, thereby activating RNase H. RNase H is activated by both phosphodiester and phosphorothioate-coupled DNA. Phosphodiester-coupled DNA, however, is rapidly degraded by cellular nucleases with the exception of phosphorothioate-coupled DNA. These resistant, non-naturally occurring DNA derivatives do not inhibit RNase H upon hybridisation with RNA. In other words, antisense polynucleotides are only effective as DNA RNA hybride complexes. Examples for this kind of antisense oligonucleotides are described, among others, in US-patent US 5,849,902 and US 5,989,912. In other words, based on the nucleic acid sequence of the target molecule which in the present case are the nucleic acid molecules for the hyperimmune serum reactive antigens and fragments thereof according to the present invention, either from the target protein from which a respective nucleic acid sequence may in principle be deduced, or by knowing the nucleic acid sequence as such, particularly the mRNA, suitable antisense oligonucleotides may be designed base on the principle of base complementarity.

Particularly preferred are antisense-oligonucleotides, which have a short stretch of phosphorothioate DNA (3 to 9 bases). A minimum of 3 DNA bases is required for activation of bacterial RNase H and a minimum of 5 bases is required for mammalian RNase H activation. In these chimeric oligonucleotides there is a central region that forms a substrate for RNase H that is flanked by hybridising "arms" comprised of modified nucleotides that do not form substrates for RNase H. The hybridising arms of the chimeric oligonucleotides may be modified such as by 2′-O-methyl or 2′-fluoro. Alternative approaches used methylphosphonate or phosphoramidate linkages in said arms. Further embodiments of the antisense oligonucleotide useful in the practice of the present invention are P-methoxyoligonucleotides, partial P-methoxyoligodeoxyribonucleotides or P-methoxyoligonucleotides.

Of particular relevance and usefulness for the present invention are those antisense oligonucleotides as more particularly described in the above two mentioned US patents. These oligonucleotides contain no naturally occurring 5′→3′-linked nucleotides. Rather the oligonucleotides have two types of nucleotides:

2′-deoxyphosphorothioate, which activate RNase H, and 2′-modified nucleotides, which do not. The linkages between the 2′-modified nucleotides can be phosphodiesters, phosphorothioate or P-ethoxyphosphodiester. Activation of RNase H is accomplished by a contiguous RNase H-activating region, which contains between 3 and 5 2′-deoxyphosphorothioate nucleotides to activate bacterial RNase H and between 5 and 10 2′- deoxyphosphorothioate nucleotides to activate eucaryotic and, particularly, mammalian RNase H. Protection from degradation is accomplished by making the 5′ and 3′ terminal bases highly nuclease resistant and, optionally, by placing a 3′ terminal blocking group.

More particularly, the antisense oligonucleotide comprises a 5′ terminus and a 3′ terminus; and from position 11 to 59 5′→3′-linked nucleotides independently selected from the group consisting of 2′-modified phosphodiester nucleotides and 2′-modified P-alkyloxyphosphotriester nucleotides; and wherein the 5′-terminal nucleoside is attached to an RNase H-activating region of between three and ten contiguous phosphorothioate-linked deoxyribonucleotides, and wherein the 3′-terminus of said oligonucleotide is selected from the group consisting of an inverted deoxyribonucleotide, a contiguous stretch of one to three phosphorothioate 2′-modified ribonucleotides, a biotin group and a P-alkyloxyphosphotriester nucleotide.

Also an antisense oligonucleotide may be used wherein not the 5′ terminal nucleoside is attached to an RNase H-activating region but the 3′ terminal nucleoside as specified above. Also, the 5′ terminus is selected from the particular group rather than the 3′ terminus of said oligonucleotide.

The nucleic acids as well as the hyperimmune serum reactive antigens and fragments thereof according to the present invention may be used as or for the manufacture of pharmaceutical compositions, especially vaccines. Preferably such pharmaceutical composition, preferably vaccine is for the prevention or treatment of diseases caused by, related to or associated with S. *agalactiae*. In so far another aspect of the invention relates to a method for inducing an immunological response in an individual, particularly a mammal, which comprises inoculating the individual with the hyperimmune serum reactive antigens and fragments thereof of the invention, or a fragment or variant thereof, adequate to produce antibodies to protect said individual from infection, particularly *streptococcal* infection and most particularly *S. agalactiae* infections.

Yet another aspect of the invention relates to a method of inducing an immunological response in an individual which comprises, through gene therapy or otherwise, delivering a nucleic acid functionally encoding hyperimmune serum reactive antigens and fragments thereof, or a fragment or a variant thereof, for expressing the hyperimmune serum reactive antigens and fragments thereof, or a fragment or a variant thereof *in vivo* in order to induce an immunological response to produce antibodies or a cell mediated T cell response, either cytokine-producing T cells or cytotoxic T cells, to protect said individual from disease, whether that disease is already established within the individual or not. One-way of administering the gene is by accelerating it into the desired cells as a coating on particles or otherwise.

A further aspect of the invention relates to an immunological composition which, when introduced into a host capable of having induced within it an immunological response, induces an immunological response in such host, wherein the composition comprises recombinant DNA which codes for and expresses an antigen of the hyperimmune serum reactive antigens and fragments thereof of the present invention. The immunological response may be used therapeutically or prophylactically and may take the form of antibody immunity or cellular immunity such as that arising from CTL or CD4+ T cells.

The hyperimmune serum reactive antigens and fragments thereof of the invention or a fragment thereof may be fused with a co-protein which may not by itself produce antibodies, but is capable of stabilizing the first protein and producing a fused protein which will have immunogenic and protective properties. This fused recombinant protein preferably further comprises an antigenic co-protein, such as Glutathione-S-transferase (GST) or beta-galactosidase, relatively large co-proteins which solubilise the

protein and facilitate production and purification thereof. Moreover, the co-protein may act as an adjuvant in the sense of providing a generalized stimulation of the immune system. The co-protein may be attached to either the amino or carboxy terminus of the first protein.

Also, provided by this invention are methods using the described nucleic acid molecule or particular fragments thereof in such genetic immunization experiments in animal models of infection with *S. agalactiae*. Such fragments will be particularly useful for identifying protein epitopes able to provoke a prophylactic or therapeutic immune response. This approach can allow for the subsequent preparation of monoclonal antibodies of particular value from the requisite organ of the animal successfully resisting or clearing infection for the development of prophylactic agents or therapeutic treatments of *S. agalactiae* infection in mammals, particularly humans.

The hyperimmune serum reactive antigens and fragments thereof may be used as an antigen for vaccination of a host to produce specific antibodies which protect against invasion of bacteria, for example by blocking adherence of bacteria to damaged tissue. Examples of tissue damage include wounds in skin or connective tissue and mucosal tissues caused e.g. by viral infection (esp. respiratory, such as the flu) mechanical, chemical or thermal damage or by implantation of indwelling devices, or wounds in the mucous membranes, such as the mouth, mammary glands, urethra or vagina.

The present invention also includes a vaccine formulation, which comprises the immunogenic recombinant protein together with a suitable carrier. Since the protein may be broken down in the stomach, it is preferably administered parenterally, including, for example, administration that is subcutaneous, intramuscular, intravenous, intradermal intranasal or tramsdermal. Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain anti-oxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the bodily fluid, preferably the blood, of the individual; and aqueous and non-aqueous sterile suspensions which may include suspending agents or thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampoules and vials, and may be stored in a freeze-dried condition requiring only the addition of the sterile liquid carrier immediately prior to use. The vaccine formulation may also include adjuvant systems for enhancing the immunogenicity of the formulation, such as oil-in-water systems and other systems known in the art. The dosage will depend on the specific activity of the vaccine and can be readily determined by routine experimentation.

According to another aspect, the present invention relates to a pharmaceutical composition comprising such a hyperimmune serum-reactive antigen or a fragment thereof as provided in the present invention for *S. agalactiae*. Such a pharmaceutical composition may comprise one or more hyperimmune serum reactive antigens or fragments thereof against *S. agalactiae*. Optionally, such *S. agalactiae* hyperimmune serum reactive antigens or fragments thereof may also be combined with antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *S. agalactiae* and/or other pathogens against which the antigens have been included in the vaccine.

According to a further aspect, the present invention relates to a pharmaceutical composition comprising a nucleic acid molecule encoding a hyperimmune serum-reactive antigen or a fragment thereof as identified above for *S. agalactiae*. Such a pharmaceutical composition may comprise one or more nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof against *S. agalactiae*. Optionally, such *S. agalactiae* nucleic acid molecules encoding hyperimmune serum reactive antigens or fragments thereof may also be combined with nucleic acid molecules encoding antigens against other pathogens in a combination pharmaceutical composition. Preferably, said pharmaceutical composition is a vaccine for preventing or treating an infection caused by *S. agalactiae* and/or other pathogens against which the antigens have been included in the vaccine.

The pharmaceutical composition may contain any suitable auxiliary substances, such as buffer substances, stabilisers or further active ingredients, especially ingredients known in connection of pharmaceutical composition and/or vaccine production.

A preferable carrier/or excipient for the hyperimmune serum-reactive antigens, fragments thereof or a coding nucleic acid molecule thereof according to the present invention is an immunostimulatory compound for further stimulating the immune response to the given hyperimmune serum-reactive antigen, fragment thereof or a coding nucleic acid molecule thereof. Preferably the immunostimulatory compound in the pharmaceutical preparation according to the present invention is selected from the group of polycationic substances, especially polycationic peptides, immunostimulatory nucleic acids molecules, preferably immunostimulatory deoxynucleotides, alum, Freund's complete adjuvants, Freund's incomplete adjuvants, neuroactive compounds, especially human growth hormone, or combinations thereof.

It is also within the scope of the present invention that the pharmaceutical composition, especially vaccine, comprises apart from the hyperimmune serum reactive antigens, fragments thereof and/or coding nucleic acid molecules thereof according to the present invention other compounds which are biologically or pharmaceutically active. Preferably, the vaccine composition comprises at least one polycationic peptide. The polycationic compound(s) to be used according to the present invention may be any polycationic compound, which shows the characteristic effects according to the WO 97/30721. Preferred polycationic compounds are selected from basic polyppetides, organic polycations, basic polyamino acids or mixtures thereof. These polyamino acids should have a chain length of at least 4 amino acid residues (WO 97/30721). Especially preferred are substances like polylysine, polyarginine and polypeptides containing more than 20 %, especially more than 50 % of basic amino acids in a range of more than 8, especially more than 20, amino acid residues or mixtures thereof. Other preferred polycations and their pharmaceutical compositions are described in WO 97/30721 (e.g. polyethyleneimine) and WO 99/38528. Preferably these polypeptides contain between 20 and 500 amino acid residues, especially between 30 and 200 residues.

These polycationic compounds may be produced chemically or recombinantly or may be derived from natural sources.

Cationic (poly)peptides may also be anti-microbial with properties as reviewed in {Ganz, T., 1999}. These (poly)peptides may be of prokaryotic or animal or plant origin or may be produced chemically or recombinantly (WO 02/13857). Peptides may also belong to the class of defensins (WO 02/13857). Sequences of such peptides can be, for example, found in the Antimicrobial Sequences Database under the following internet address:

http://www.bbcm.univ.trieste.it/~tossi/pag2.html

Such host defence peptides or defensives are also a preferred form of the polycationic polymer according to the present invention. Generally, a compound allowing as an end product activation (or down-regulation) of the adaptive immune system, preferably mediated by APCs (including dendritic cells) is used as polycationic polymer.

Especially preferred for use as polycationic substances in the present invention are cathelicidin derived antimicrobial peptides or derivatives thereof (International patent application WO 02/13857, incorporated herein by reference), especially antimicrobial peptides derived from mammalian cathelicidin, preferably from human, bovine or mouse.

Polycationic compounds derived from natural sources include HIV-REV or HIV-TAT (derived cationic peptides, antennapedia peptides, chitosan or other derivatives of chitin) or other peptides derived from

these peptides or proteins by biochemical or recombinant production. Other preferred polycationic compounds are cathelin or related or derived substances from cathelin. For example, mouse cathelin is a peptide which has the amino acid sequence $NH_2$-RLAGLLRKGGEKIGEKLKKIGOKIKNFFQKLVPQPE-COOH. Related or derived cathelin substances contain the whole or parts of the cathelin sequence with at least 15-20 amino acid residues. Derivations may include the substitution or modification of the natural amino acids by amino acids which are not among the 20 standard amino acids. Moreover, further cationic residues may be introduced into such cathelin molecules. These cathelin molecules are preferred to be combined with the antigen. These cathelin molecules surprisingly have turned out to be also effective as an adjuvant for an antigen without the addition of further adjuvants. It is therefore possible to use such cathelin molecules as efficient adjuvants in vaccine formulations with or without further immunactivating substances.

Another preferred polycationic substance to be used according to the present invention is a synthetic peptide containing at least 2 KLK-motifs separated by a linker of 3 to 7 hydrophobic amino acids (International patent application WO 02/32451, incorporated herein by reference).

The pharmaceutical composition of the present invention may further comprise immunostimulatory nucleic acid(s). Immunostimulatory nucleic acids are e. g. neutral or artificial CpG containing nucleic acids, short stretches of nucleic acids derived from non-vertebrates or in form of short oligonucleotides (ODNs) containing non-methylated cytosine-guanine di-nucleotides (CpG) in a certain base context (e.g. described in WO 96/02555). Alternatively, also nucleic acids based on inosine and cytidine as e.g. described in the WO 01/93903, or deoxynucleic acids containing deoxy-inosine and/or deoxyuridine residues (described in WO 01/93905 and PCT/EP 02/05448, incorporated herein by reference) may preferably be used as immunostimulatory nucleic acids for the present invention. Preferablly, the mixtures of different immunostimulatory nucleic acids may be used according to the present invention.

It is also within the present invention that any of the aforementioned polycationic compounds is combined with any of the immunostimulatory nucleic acids as aforementioned. Preferably, such combinations are according to the ones as described in WO 01/93905, WO 02/32451, WO 01/54720, WO 01/93903, WO 02/13857 and PCT/EP 02/05448 and the Austrian patent application A 1924/2001, incorporated herein by reference.

In addition or alternatively such vaccine composition may comprise apart from the hyperimmune serum reactive antigens and fragments thereof, and the coding nucleic acid molecules thereof according to the present invention a neuroactive compound. Preferably, the neuroactive compound is human growth factor as, e.g. described in WO 01/24822. Also preferably, the neuroactive compound is combined with any of the polycationic compounds and/or immunostimulatory nucleic acids as afore-mentioned.

In a further aspect the present invention is related to a pharmaceutical composition. Such pharmaceutical composition is, for example, the vaccine described herein. Also a pharmaceutical composition is a pharmaceutical composition which comprises any of the following compounds or combinations thereof: the nucleic acid molecules according to the present invention, the hyperimmune serum reactive antigens and fragments thereof according to the present invention, the vector according to the present invention, the cells according to the present invention, the antibody according to the present invention, the functional nucleic acids according to the present invention and the binding peptides such as the anticalines according to the present invention, any agonists and antagonists screened as described herein. In connection therewith any of these compounds may be employed in combination with a non-sterile or sterile carrier or carriers for use with cells, tissues or organisms, such as a pharmaceutical carrier suitable for administration to a subject. Such compositions comprise, for instance, a media additive or a therapeutically effective amount of a hyperimmune serum reactive antigen and fragments thereof of the invention and a pharmaceutically acceptable carrier or excipient. Such carriers may include, but are not

limited to, saline, buffered saline, dextrose, water, glycerol, ethanol and combinations thereof. The formulation should suit the mode of administration.

The pharmaceutical compositions may be administered in any effective, convenient manner including, for instance, administration by topical, oral, anal, vaginal, intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intratracheal or intradermal routes among others.

In therapy or as a prophylactic, the active agent may be administered to an individual as an injectable composition, for example as a sterile aqueous dispersion, preferably isotonic.

Alternatively the composition may be formulated for topical application, for example in the form of ointments, creams, lotions, eye ointments, eye drops, ear drops, mouthwash, impregnated dressings and sutures and aerosols, and may contain appropriate conventional additives, including, for example, preservatives, solvents to assist drug penetration, and emollients in ointments and creams. Such topical formulations may also contain compatible conventional carriers, for example cream or ointment bases, and ethanol or oleyl alcohol for lotions. Such carriers may constitute from about 1 % to about 98 % by weight of the formulation; more usually they will constitute up to about 80 % by weight of the formulation.

In addition to the therapy described above, the compositions of this invention may be used generally as a wound treatment agent to prevent adhesion of bacteria to matrix proteins exposed in wound tissue and for prophylactic use in dental treatment as an alternative to, or in conjunction with, antibiotic prophylaxis.

A vaccine composition is conveniently in injectable form. Conventional adjuvants may be employed to enhance the immune response. A suitable unit dose for vaccination is 0.05-5 μg antigen / per kg of body weight, and such dose is preferably administered 1-3 times and with an interval of 1-3 weeks.

With the indicated dose range, no adverse toxicological effects should be observed with the compounds of the invention, which would preclude their administration to suitable individuals.

In a further embodiment the present invention relates to diagnostic and pharmaceutical packs and kits comprising one or more containers filled with one or more of the ingredients of the aforementioned compositions of the invention. The ingredient(s) can be present in a useful amount, dosage, formulation or combination. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, reflecting approval by the agency of the manufacture, use or sale of the product for human administration.

In connection with the present invention any disease related use as disclosed herein such as, e. g. use of the pharmaceutical composition or vaccine, is particularly a disease or diseased condition which is caused by, linked or associated with Streptococci, more preferably, *S. pyogens and pneumoniae*. In connection therewith it is to be noted that *S. agalactiae* comprises several strains including those disclosed herein. A disease related, caused or associated with the bacterial infection to be prevented and/or treated according to the present invention includes besides others bacterial pharyngitis, otitis media, pneumonia, bacteremia, meningitis, peritonitis, wound infection and sepsis in humans.

In a still further embodiment the present invention is related to a screening method using any of the hyperimmune serum reactive antigens or nucleic acids according to the present invention. Screening methods as such are known to the one skilled in the art and can be designed such that an agonist or an antagonist is screened. Preferably an antagonist is screened which in the present case inhibits or prevents the binding of any hyperimmune serum reactive antigen and fragment thereof according to the present

invention to an interaction partner. Such interaction partner can be a naturally occurring interaction partner or a non-naturally occurring interaction partner.

The invention also provides a method of screening compounds to identify those, which enhance (agonist) or block (antagonist) the function of hyperimmune serum reactive antigens and fragments thereof or nucleic acid molecules of the present invention, such as its interaction with a binding molecule. The method of screening may involve high-throughput.

For example, to screen for agonists or antagonists, the interaction partner of the nucleic acid molecule and nucleic acid, respectively, according to the present invention, maybe a synthetic reaction mix, a cellular compartment, such as a membrane, cell envelope or cell wall, or a preparation of any thereof, may be prepared from a cell that expresses a molecule that binds to the hyperimmune serum reactive antigens and fragments thereof of the present invention. The preparation is incubated with labelled hyperimmune serum reactive antigens and fragments thereof in the absence or the presence of a candidate molecule, which may be an agonist or antagonist. The ability of the candidate molecule to bind the binding molecule is reflected in decreased binding of the labelled ligand. Molecules which bind gratuitously, i. e., without inducing the functional effects of the hyperimmune serum reactive antigens and fragments thereof, are most likely to be good antagonists. Molecules that bind well and elicit functional effects that are the same as or closely related to the hyperimmune serum reactive antigens and fragments thereof are good agonists.

The functional effects of potential agonists and antagonists may be measured, for instance, by determining the activity of a reporter system following interaction of the candidate molecule with a cell or appropriate cell preparation, and comparing the effect with that of the hyperimmune serum reactive antigens and fragments thereof of the present invention or molecules that elicit the same effects as the hyperimmune serum reactive antigens and fragments thereof. Reporter systems that may be useful in this regard include but are not limited to colorimetric labelled substrate converted into product, a reporter gene that is responsive to changes in the functional activity of the hyperimmune serum reactive antigens and fragments thereof, and binding assays known in the art.

Another example of an assay for antagonists is a competitive assay that combines the hyperimmune serum reactive antigens and fragments thereof of the present invention and a potential antagonist with membrane-bound binding molecules, recombinant binding molecules, natural substrates or ligands, or substrate or ligand mimetics, under appropriate conditions for a competitive inhibition assay. The hyperimmune serum reactive antigens and fragments thereof can be labelled such as by radioactivity or a colorimetric compound, such that the molecule number of hyperimmune serum reactive antigens and fragments thereof bound to a binding molecule or converted to product can be determined accurately to assess the effectiveness of the potential antagonist.

Potential antagonists include small organic molecules, peptides, polypeptides and antibodies that bind to a hyperimmune serum reactive antigen and fragments thereof of the invention and thereby inhibit or extinguish its acitivity. Potential antagonists also may be small organic molecules, a peptide, a polypeptide such as a closely related protein or antibody that binds to the same sites on a binding molecule without inducing functional activity of the hyperimmune serum reactive antigens and fragments thereof of the invention.

Potential antagonists include a small molecule, which binds to and occupies the binding site of the hyperimmune serum reactive antigens and fragments thereof thereby preventing binding to cellular binding molecules, such that normal biological activity is prevented. Examples of small molecules include but are not limited to small organic molecules, peptides or peptide-like molecules.

Other potential antagonists include antisense molecules (see {Okano, H. et al., 1991};

OLIGODEOXYNUCLEOTIDES AS ANTISENSE INHIBITORS OF GENE EXPRESSION; CRC Press, Boca Ration, FL (1988), for a description of these molecules).

Preferred potential antagonists include derivatives of the hyperimmune serum reactive antigens and fragments thereof of the invention.

As used herein the activity of a hyperimmune serum reactive antigen and fragment thereof according to the present invention is its capability to bind to any of its interaction partner or the extent of such capability to bind to its or any interaction partner.

In a particular aspect, the invention provides the use of the hyperimmune serum reactive antigens and fragments thereof, nucleic acid molecules or inhibitors of the invention to interfere with the initial physical interaction between a pathogen and mammalian host responsible for sequelae of infection. In particular the molecules of the invention may be used: i) in the prevention of adhesion of *S. agalactiae* to mammalian extracellular matrix proteins at mucosal surfaces and on in-dwelling devices or to extracellular matrix proteins in wounds; ii) to block bacterial adhesion between mammalian extracellular matrix proteins and bacterial proteins which mediate tissue damage or invasion iii) or lead to evasion of immune defense; iv) to block the normal progression of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or by other surgical techniques, e.g. through inhibiting nutrient acquisition.

Each of the DNA coding sequences provided herein may be used in the discovery and development of antibacterial compounds. The encoded protein upon expression can be used as a target for the screening of antibacterial drugs. Additionally, the DNA sequences encoding the amino terminal regions of the encoded protein or Shine-Delgarno or other translation facilitating sequences of the respective mRNA can be used to construct antisense sequences to control the expression of the coding sequence of interest.

The antagonists and agonists may be employed, for instance, to inhibit diseases arising from infection with Streptococcus, especially *S. agalactiae*, such as sepsis.

In a still further aspect the present invention is related to an affinity device such affinity device comprises as least a support material and any of the hyperimmune serum reactive antigens and fragments thereof according to the present invention, which is attached to the support material. Because of the specificity of the hyperimmune serum reactive antigens and fragments thereof according to the present invention for their target cells or target molecules or their interaction partners, the hyperimmune serum reactive antigens and fragments thereof allow a selective removal of their interaction partner(s) from any kind of sample applied to the support material provided that the conditions for binding are met. The sample may be a biological or medical sample, including but not limited to, fermentation broth, cell debris, cell preparation, tissue preparation, organ preparation, blood, urine, lymph liquid, liquor and the like.

The hyperimmune serum reactive antigens and fragments thereof may be attached to the matrix in a covalent or non-covalent manner. Suitable support material is known to the one skilled in the art and can be selected from the group comprising cellulose, silicon, glass, aluminium, paramagnetic beads, starch and dextrane.

The present invention is further illustrated by the following figures, examples and the sequence listing, from which further features, embodiments and advantages may be taken. It is to be understood that the present examples are given by way of illustration only and not by way of limitation of the disclosure.

In connection with the present invention

Figure 1 shows the characterization of human antibody sources for *S. agalactiae*.

Figure 2 shows the characterization of the small fragment genomic library, LSAg-70, from *Streptococcus agalactiae* ATCC 12403.

Figure 3 shows the selection of bacterial cells by MACS using biotinylated human IgGs.

Figure 4 shows the serotypes of the applied strains and an example for the gene distribution analysis with one of the identified antigens.

Figure 5 shows examples for induction of epitope-specific antibodies in mice by immunization with *E. coli* lysates.

Figure 6 shows examples for cell surface staining with epitope-specific antisera by flow cytometry.

Figure 7 shows the determination of bactericidal activity of antibodies induced by selected epitopes in an *in vitro* assay.

Table 1A shows the summary of all screens performed with genomic *S. agalactiae* libraries and human serum. Table 1B shows antigenic proteins identified by sequence identity within antigenic regions of the proteins listed in Table 1A.

Table 2 shows the summary of epitope serology analysis with human sera.

Table 3 shows the summary of the gene distribution analysis for the identified antigens in 46 *S. agalactiae* strains.

Table 4 shows the summary of mouse imunogenicity experiments.

The figures to which it might be referred to in the specification are described in the following in more details.

**Figure 1** shows the characterization of human sera and cervical secretions for anti-*S. agalactiae* antibodies as measured by immune assays. Total anti-*S. agalactiae* IgG and IgA antibody levels were measured by standard ELISA using total bacterial lysates or culture supernant fractions prepared from *S. agalactiae* serotype III strain ATCC 12403 as coating antigens. **(A)** Results of representative experiments are shown with healthy adult sera with total bacterial lysate proteins. Data are expressed as ELISA units calculated from absorbance at 405nm at a serum dilution in the linear range of detection (2.000X for IgA, 10,000 for IgG). Selected sera (out of 52) included in the healthy adult non-pregnant serum pool (NSag8-IgG,-IgA) are indicated by bold numbers. **(B)** Immunoblot analysis was performed on high titer sera selected by ELISA in order to ensure multiple immune reactivity with protein antigens. Results of a representative experiment using total bacterial lysate prepared from *S. agalactiae* serotype III ATCC 12403 strain and selected patients' sera at 5.000X dilution are shown. Blots were developed with anti-human IgG secondary antibody reagent. Low titer sera were included as negative controls. Mw: molecular weight markers. **(C)** shows selection of cervical secretions from noncolonized pregnant women by immunoblot analysis. Antibodies exctracted from cervical wicks were quantitated for IgA content. 2 μg IgA from each prepaprations were tested for immunoreactivity using total bacterial lysate in a multi-well blotting apparatus. Blots were developed with anti-human IgA secondary antibodies. IgA preparation showing reactivity with GBS proteins (inidicated by arrows) were selected and pooled.

**Figure 2** **(A)** shows the fragment size distribution of the *Streptococcus agalactiae* ATCC 12403 small fragment genomic library, LSAg-70. After sequencing 576 randomly selected clones, sequences were trimmed (464) to eliminate vector residues and the numbers of clones with various genomic fragment

sizes were plotted. (B) shows the graphic illustration of the distribution of the same set of randomly sequenced clones of LSAg-70 over the *S. agalactiae* ATCC 12403 chromosome. Rectangles indicate matching sequences to annotated ORFs and diamonds represent fully matched clones to non-coding chromosomal sequences in +/+ or +/- orientation. Circles position all clones with chimeric sequences. Numeric distances in base pairs are indicated over the circular genome for orientation. Partitioning of various clone sets within the library is given in numbers and percentage at the bottom of the figure.

**Figure 3** (A) shows the MACS selection with biotinylated human IgGs. The LSAg-70 library in pMAL9.1 was screened with 15-20 μg biotinylated IgG (PSag11-IgG, purified from human serum). As negative control, no serum was added to the library cells for screening. Number of cells selected after the 1st, 2nd and 3rd elution are shown for each selection round (upper, middle and lower panel, respectively). (B) shows the reactivity of specific clones (1-26) selected by bacterial surface display as analysed by immunoblot analysis with the human serum IgG pool (PSag11-IgG, 4 μg/μl) used for selection by MACS at a dilution of 1:3,000. As a loading control the same blot was also analysed with antibodies directed against the platform protein LamB at a dilution of 1:5,000 of hyperimmune rabbit serum. M, Molecular weigth marker; L, Extract from a clone expressing LamB without foreign peptide insert.

**Figure 4** (A) shows the representation of different serotypes of *S. agalactiae* clinical isolates analysed for the gene distribution study. A number of the strains were not typable and may represent additional serotypes. (B) shows the PCR analysis for the gene distribution of gbs0061 with the respective oligonucleotides and 46 *S. agalactiae* strains. The predicted size of the PCR fragments is 814 bp. 1-46, *S. agalactiae* strains, clinical isolates as shown under A; -, no genomic DNA added; +, genomic DNA from *S. agalactiae* ATCC 12403, which served as template for library construction.

**Figure 5** shows the measurement of epitope-specific mouse serum IgG antibody levels induced by total bacterial lysates of Lamb or FhuA expressing *E. coli* clones with *S. agalactiae*-derived epitopes. (A) shows representative peptide ELISA experiments with three sets of mouse sera (5 mice in each group, 1-5) generated by gbs0428, gbs0628 and gbs632 epitopes, respectively. Sera were tested at two different dilutions: black bars: 100X; grey bars; 1000X. Biotin-labeled synthetic peptides corresponding to the respective epitopes were used in the peptide ELISA. Sera induced with E. coli lysate without *S. agalactiae* derived epitopes are indicated as FhuA or LamB. (B) shows a typical immunoblotting experiment using lysates prepared from individual *E. coli* clones selected for mouse injections. Sera were depleted by *E. coli* lysate not carrying epitope to remove antibodies against *E. coli* proteins. Examples are shown for gbs0918, gbs0428, gbs0628 and gbs632 epitopes. Negative controls (-) are *E. coli* clones with empty platform proteins. Location of platform proteins LamB and FhuA is indicated by arrows.

**Figure 6** shows the detection of specific antibody binding on the cell surface of *Streptococcus agalactiae* by flow cytometry. In Figure 6A preimmune mouse sera and polyclonal sera raised against *S. agalactiae* serotype III lysate were incubated with *S. agalactiae* strain serotype III and analysed by flow cytometry. Control shows the level of non-specific binding of the secondary antibody to the surface of *S. agalactiae* cells. The histograms in figure 5B indicates the increased fluorescence due to specific binding of anti-gbs0031, anti-gbs1925 and anti-gbs0012 antibodies in comparison to the control sera generated against E. coli lysate containing only the 'empty' platform protein FhuA.

**Figure 7** shows the bactericidal activity of epitope specific antibodies as determined in *in vitro* killing assay. The killing activity of immune sera is measured parallel with and calculated relative to the appropriate control sera. Data are expressed as percentage of killing, that is the reduction on bacterial cfu numbers as a consequence of the presence of specific antibodies. Hyperimmune polyclonal mouse sera generated with *S. agalactiae* lysate and sera from non-immunized mice served as positive and negative controls for the assay, respectively. Immune sera generated with gbs0012, gbs0016, gbs0031, gbs0428, gbs1306 and gbs2018 epitopes were tested for bactericidal activity and data are expressed relative to appropriate controls, such as sera induced with Lamb or FhuA expressing *E. coli* clones without *S.*

*agalactiae*-derived epitopes. *S. agalactiae* serotype III cells were incubated with mouse phagocytic cells for 60 min, and surviving bacteria were quantified by counting cfus after plating on blood agar.

**Table 1: Immunogenic proteins identified by bacterial surface display.**
**(A)** Columns **A**, 300bp library of *S.agalactiae* ATCC 12403 in fhuA with NSag8-IgA (826), **B**, 300bp library in fhuA with PSag10-IgA (768), C, 300bp library in fhuA with PSag10-IgG (711), **D**, 300bp library in fhuA with PSag11-IgG (640), **E**, 70bp library in lamB with NSag8-IgA (1057), **F**, 70bp library in lamB with NSag8-IgG (869), **G**, 70bp library in lamB with PSag10-IgA (904), **H**, 70bp library in lamB with PSag10-IgA-adsorbed (493), **I**, 70bp library in lamB with PSag10-IgG (910), **J**, 70bp library in lamB with PSag11-IgA (631), **K**, 70bp library in lamB with PSag11-IgG (926), **L**, 70bp library in lamB with PSag18-IgA (691), **M**, 70bp library in lamB with PSag-sIgA (628); *, prediction of antigenic sequences longer than 5 amino acids was performed with the program ANTIGENIC (Kolaskar and Tongaonkar, 1990). **Table 1B** lists the immunogenic proteins identified by amino acid sequence identity with peptides identified by bacterial surface display. Antigenic peptides, which have been identified by bacterial surface-display possess identical counterparts in the listed proteins from *S. agalactiae*. The peptides have been shown to react with multiple human sera (see Table 2). Sera directed against these peptides can therefore recognize multiple proteins.

**Table 2: Epitope serology with human sera.**
Immune reactivity of individual synthetic peptides representing selected epitopes with human sera is shown. Extent of reactivity is expressed as +, ++ or +++, and summed from individual reactivities of peptides with individual sera (13 patient and 9 healthy adult, 22 total). A total score for each peptide was calculated based on ELISA units as the sum of all reactivities. Scores were 2-8 for +, 9-16 for ++ and 17-26 for +++. ELISA units were calculated from $OD_{405nm}$ readings and the serum dilution after correction for background. Location of synthetic peptides within the antigenic ORFs according to the genome annotation of ATCC 12403 strain is given in columns **aa from** and **aa to** indicating the first and last amino acid residues, respectively. Peptide names: gbs0012.1 present in annotated ORF: gbs0012.

**Table 3: Gene distribution in *S. agalactiae* strains.**
Fourty six *S. agalactiae* strains as shown in Figure 4A were tested by PCR with oligonucleotides specific for the genes encoding relevant antigens. The PCR fragment of one selected PCR reaction was sequenced in order to confirm the amplification of the correct DNA fragment. *, number of amino acid substitutions in a serotype IA strain as derived from sequencing as compared to *S. agalactiae* ATCC 12403. #, alternative strain used for sequencing, because gene was not present in the serotype IA strain.

**Table 4: Immunogenicity of antigenic epitopes.**
*S. agalactiae* antigens were tested for immunogenicity by immunization with *E. coli* clones harboring plasmids encoding the platform proteins LamB or FhuA fused to *S. agalactiae* peptides. The presence of epitope-specific antibodies were detected and measured by peptide ELISA and/or immunoblotting using the corresponding *E. coli* clone lysate, which served as immunogen. Results are expressed as + to ++++, and calculated for peptide ELISA as the sum of the reactivity of individual mouse sera based on ELISA units (as indicated on Fig. 5A) and for immunoblotting (IB) as the strength of reactivity of pooled (5 individual) mouse sera with the epitope containing platform protein (as indicated on Fig. 5B). Location of synthetic peptides within the antigenic ORFs according to the genome annotation of ATCC 12403 strain is given in columns **aa from** and **aa to** indicating the first and last amino acid residues, respectively.

## EXAMPLES

**Example 1: Characterization and selection of human serum sources based on anti-*S. agalactiae* antibodies, preparation of antibody screening reagents**

*Experimental procedures*

*Enzyme linked immune assay (ELISA).*
ELISA plates (Maxisorb, Millipore) were coated with 5-10 μg/ml total protein diluted in coating buffer (0.1M sodium carbonate pH 9.2). Three dilutions of sera (2,000X, 10,000X, 50,000X) were made in PBS-BSA. Highly specific Horse Radish Peroxidase (HRP)-conjugated anti-human IgG or anti-human IgA secondary antibodies (Southern Biotech) were used according to the manufacturers' recommendations (dilution: 1,000x). Antigen-antibody complexes were quantified by measuring the conversion of the substrate (ABTS) to colored product based on $OD_{405nm}$ readings by automatic ELIAS reader (TECAN SUNRISE).

*Preparation of bacterial antigen extracts*
Total bacterial lysate: Bacteria were grown overnight in THB (Todd-Hewitt Broth) and lysed by repeated freeze-thaw cycles: incubation on dry ice/ethanol-mixture until frozen (1 min), then thawed at 37°C (5 min): repeated 3 times. This was followed by sonication and collection of supernatant by centrifugation (3,500 rpm, 15 min, 4°C).
Culture supernatant: After removal of bacteria by centrifugation, the supernatant of overnight grown bacterial cultures was precipitated with ice-cold ethanol by mixing 1 part supernatant with 3 parts absolute ethanol and incubated overnight at -20°C. Precipitates were collected by centrifugation (2,600 g, for 15 min). Dry pellets were dissolved either in PBS for ELISA, or in urea and SDS-sample buffer for SDS-PAGE and immunoblotting. The protein concentration of samples was determined by Bradford assay.

*Immunoblotting*
Total bacterial lysate and culture supernatant samples were prepared from *in vitro* grown *S. agalactiae* serotype III strain. 10 to 25μg total protein/lane was separated by SDS-PAGE using the BioRad Mini-Protean Cell electrophoresis system and proteins transferred to nitrocellulose membrane (ECL, Amersham Pharmacia). After overnight blocking in 5% milk, human sera were added at 2,000x dilution, and HRPO labeled anti-human IgG was used for detection.

*Extraction of antibodies from cervical wicks*
Cervical secretions were collected by absorbent cylindrical wicks (Polyfiltronics) which were introduced into the cervical canal during speculum examination and thereafter kept frozen until extraction. Extraction was done according to Hordnes *et al*, 1998 (provider of the samples). Briefly, wicks were mixed with PBS containing protease inhibitors, vortexed and fluid was drained from the tubes containing the wicks. The concentrations of total IgA and IgG antibodies in extracts were determined.

*Purification of antibodies for genomic screening.* Five sera from both the patient and the healthy group were selected based on the overall anti-GBS titers for serum or cervical secretion pools used in the screening procedure. Antibodies against *E. coli* proteins were removed by incubating the heat-inactivated sera with whole cell *E. coli* cells (DH5alpha, transformed with pHIE11, grown under the same condition as used for bacterial surface display). Highly enriched preparations of IgGs from the pooled, depleted sera were generated by protein G affinity chromatography, according to the manufacturer's instructions (UltraLink Immobilized Protein G, Pierce). IgA antibodies were purified also by affinity chromatography using biotin-labeled anti-human IgA (Southern Biotech) immobilized on Streptavidin-agarose (GIBCO BRL). The efficiency of depletion and purification was checked by SDS-PAGE, Western blotting, ELISA and protein concentration measurements.

*Results*

The antibodies produced against *S. agalactiae* by the human immune system and present in human sera

are indicative of the *in vivo* expression of the antigenic proteins and their immunogenicity. These molecules are essential for the identification of individual antigens in the approach as described in the present invention, which is based on the interaction of the specific anti-GBS antibodies and the corresponding *S. agalactiae* peptides or proteins. To gain access to relevant antibody repertoires, human sera were collected from

I. healthy pregnant women tested negative for cervical and anorectal carriage of GBS

II. healthy pregnant women tested positive for cervical and/or anorectal carriage of GBS who's newborn remained GBS-free (although with antibiotic prevention).

III. adults below <45 years of age without clinical disease.

IV. naïve individuals, youg children between 5 and 10 months of age, after they already lost maternal antibodies and have not acquired GBS-specific ones due to the lack of GBS disease.

In addition cervical secretions were also collected from the first two groups of donors. The extrem value of these antibody sources is mainly the secretory IgA component, which is directly implicated as protective effector moluecule on mucosal surfaces.

It is important to screen with antibodies from at least two different populations, pregnant women and nonpregnant adults, since GBS disease affects elderly and immunocompromised adults, as well. Within the pregnant study group, there are again two different patient categories, women who are GBS colonized and those who are noncolonized, to be included in the antigen screen.

Antibodies in serum and other body fluids, such as mucosal secretions induced in individuals exposed to the pathogens are crucial for antigen identification. The exposure to GBS results in asymptomatic colonization, current or past acute or chronic infection. *S. agalactiae* colonization and infections are common, and antibodies are present as a consequence of natural immunization from previous encounters. It is likely that sera from high titer noncolonized individuals contain functional antibodies, which are able to eliminate carriage. At the same time certain antibodies might be induced against GBS components only if the antigen persist. For that reason sera from colonized individuals were also included. It has been shown that colonization is associated with capsular polysaccahride (CPS)-specific antibody responses. However, it is not clear whether sufficient level of antibodies to CPS's would prevent GBS colonization, since there are colonized women with both high and low levels of anti-CPS antibody, and the same is true for noncolonized pregnant women.

However, there are reports that effector function and avidity of antibodies produced during pregnancy might be altered. It is important to recognize that most healthy adults are protected from invasive GBS disease and are less susceptible than newborns and the elderly. Antibodies from these individuals seem to be especially valuable for identification of the corresponding antigens. It is known that anti-GBS antibody levels increase with age.

GBS is a mucosal pathogen and should induce IgA response; for that reason it was important to perform IgA-based screens, as well as IgG-based screens. The fact that some *S. agalactiae* strains express high affinity IgA-binding receptor also points to the importance of IgA in host response. Recently it was reported that not only IgG, but also IgA serum antibodies can be recognized by the FcRIII receptors of PMNs and promote opsonization {Phillips-Quagliata, J. et al., 2000}; {Shibuya, A. et al., 2000}. The primary role of IgA antibodies is neutralization, mainly at the mucosal surface. The level of serum IgA reflects the quality, quantity and specificity of the dimeric secretory IgA. For that reason the serum collection was not only analyzed for anti-streptococcal IgG, but also for IgA levels. In the ELISA assays highly specific secondary reagents were used to detect antibodies from the high affinity types, such as IgG and IgA, but avoided IgM. Production of IgM antibodies occurs during the primary adaptive humoral response, and results in low affinity antibodies, while IgG and IgA antibodies had already undergone affinity maturation, and are more valuable in fighting or preventing disease.

127 serum samples and 97 cervical secretions from pregnant women and 50 sera from healthy adults were characterized for anti-*S. agalactiae* antibodies by a series of immune assays. Primary characterization was done by ELISA using two different antigen preparations, such as total bacterial extract and culture supernatant proteins prepared from *S. agalactiae* serotype III ATCC 12403 strain. A representative experiment is shown in Fig. 1A using sera from the healthy adult population. Antibody titers were compared at given dilutions where the response was linear. Sera were ranked based on the IgG and IgA reactivity against the two complex antigenic mixtures (including serotype specific type III capsule), and the highest ones were selected for further testing by immunoblotting. This analysis confirmed a high antibody reactivity of the pre-selected sera against multiple GBS proteins, especially when compared to not selected, low-titer sera (Fig 1B). However, ELISA ranking of sera did not always correlated with immunoblot signals suggesting that anti-capsular antibodies were abundant and dominated the ELISA reactivities against total bacterial extracts. Thus the final selection of sera to be included in antibody-pools was based mainly on multiple immunogenic bands in immunoblotting experiments. This extensive antibody characterization approach has led to the unambiguous identification of anti-GBS hyperimmune sera.

The 97 cervical secretions were determined for IgA content, and same amount (2μg) was tested for anti-GBS reactivity by immunoblotting. Positively selected sera (as it is shown in Fig. 1C) were devided into colonized and noncolonized IgA pools and used separately in bacterial surface display experiments.

5 sera from both donor groups were selected and pooled for antigen identification by bacterial surface display. Selected sera included in the four pregnant women pools (PSAg10-IgG,-IgA, PSAg11-IgG, PSAg18-IgG and PSAg-sIgA) and one healthy adult (non-pregnant) pool (NSAg8-IgG,-IgA). IgG and IgA antibodies were purified from pooled sera by affinity chromatography and depleted of E. coli -reactive antibodies to avoid background in the bacterial surface display screen.

**Example 2: Generation of highly random, frame-selected, small-fragment, genomic DNA libraries of *Streptococcus agalactiae***

*Experimental procedures*

*Preparation of streptococcal genomic DNA.* 50 ml Todd-Hewitt Broth medium was inoculated with *S. agalactiae* ATCC 12403 bacteria from a frozen stab and grown with aeration and shaking for 18 h at 37°C. The culture was then harvested, centrifuged with 1,600x g for 15 min and the supernatant was removed. Bacterial pellets were washed 3 x with PBS and carefully re-suspended in 0.5 ml of Lysozyme solution (100 mg/ml). 0.1 ml of 10 mg/ml heat treated RNase A and 20 U of RNase T1 were added, mixed carefully and the solution was incubated for 1 h at 37°C. Following the addition of 0.2 ml of 20 % SDS solution and 0.1 ml of Proteinase K (10 mg/ml) the tube was incubated overnight at 55°C. 1/3 volume of saturated NaCl was then added and the solution was incubated for 20 min at 4°C. The extract was pelleted in a microfuge (13,000 rpm) and the supernatant transferred into a new tube. The solution was extracted with PhOH/$CHCl_3$/IAA (25:24:1) and with $CHCl_3$/IAA (24:1). DNA was precipitated at room temperature by adding 0.6x volume of Isopropanol, spooled from the solution with a sterile Pasteur pipette and transferred into tubes containing 80% ice-cold ethanol. DNA was recovered by centrifuging the precipitates with 10-12,000x g, then dried on air and dissolved in dd$H_2O$.

*Preparation of small genomic DNA fragments.* Genomic DNA fragments were mechanically sheared into fragments ranging in size between 150 and 300 bp using a cup-horn sonicator (Bandelin Sonoplus UV 2200 sonicator equipped with a BB5 cup horn, 10 sec. pulses at 100 % power output) or into fragments of size between 50 and 70 bp by mild DNase I treatment (Novagen). It was observed that sonication yielded a much tighter fragment size distribution when breaking the DNA into fragments of the 150-300 bp size range. However, despite extensive exposure of the DNA to ultrasonic wave-induced hydromechanical

shearing force, subsequent decrease in fragment size could not be efficiently and reproducibly achieved. Therefore, fragments of 50 to 70 bp in size were obtained by mild DNase I treatment using Novagen's shotgun cleavage kit. A 1:20 dilution of DNase I provided with the kit was prepared and the digestion was performed in the presence of $MnCl_2$ in a 60 µl volume at 20°C for 5 min to ensure double-stranded cleavage by the enzyme. Reactions were stopped with 2 µl of 0.5 M EDTA and the fragmentation efficiency was evaluated on a 2% TAE-agarose gel. This treatment resulted in total fragmentation of genomic DNA into near 50-70 bp fragments. Fragments were then blunt-ended twice using T4 DNA Polymerase in the presence of 100 µM each of dNTPs to ensure efficient flushing of the ends. Fragments were used immediately in ligation reactions or frozen at -20°C for subsequent use.

*Description of the vectors.* The vector pMAL4.31 was constructed on a pASK-IBA backbone {Skerra, A., 1994} with the beta-lactamase (*bla*) gene exchanged with the Kanamycin resistance gene. In addition the *bla* gene was cloned into the multiple cloning site. The sequence encoding mature beta-lactamase is preceded by the leader peptide sequence of *ompA* to allow efficient secretion across the cytoplasmic membrane. Furthermore a sequence encoding the first 12 amino acids (spacer sequence) of mature beta-lactamase follows the *ompA* leader peptide sequence to avoid fusion of sequences immediately after the leader peptidase cleavage site, since e.g. clusters of positive charged amino acids in this region would decrease or abolish translocation across the cytoplasmic membrane {Kajava, A. et al., 2000}. A *Sma*I restriction site serves for library insertion. An upstream FseI site and a downstream NotI site, which were used for recovery of the selected fragment, flank the *Sma*I site. The three restriction sites are inserted after the sequence encoding the 12 amino acid spacer sequence in such a way that the *bla* gene is transcribed in the -1 reading frame resulting in a stop codon 15 bp after the *Not*I site. A +1 bp insertion restores the *bla* ORF so that beta-lactamase protein is produced with a consequent gain of Ampicillin resistance.

The vector pMAL9.1 was constructed by cloning the *lamB* gene into the multiple cloning site of pEH1 {Hashemzadeh-Bonehi, L. et al., 1998}. Subsequently, a sequence was inserted in *lamB* after amino acid 154, containing the restriction sites *Fse*I, *Sma*I and *Not*I. The reading frame for this insertion was constructed in such a way that transfer of frame-selected DNA fragments excised by digestion with *Fse*I and *Not*I from plasmid pMAL4.31 yields a continuous reading frame of *lamB* and the respective insert.

The vector pHIE11 was constructed by cloning the *fhuA* gene into the multiple cloning site of pEH1. Thereafter, a sequence was inserted in *fhuA* after amino acid 405, containing the restriction site *Fse*I, *Xba*I and *Not*I. The reading frame for this insertion was chosen in a way that transfer of frame-selected DNA fragments excised by digestion with *Fse*I and *Not*I from plasmid pMAL4.31 yields a continuous reading frame of *fhuA* and the respective insert.

*Cloning and evaluation of the library for frame selection.* Genomic *S. agalactiae* DNA fragments were ligated into the *Sma*I site of the vector pMAL4.31. Recombinant DNA was electroporated into DH10B electrocompetent *E. coli* cells (GIBCO BRL) and transformants plated on LB-agar supplemented with Kanamycin (50 µg/ml) and Ampicillin (50 µg/ml). Plates were incubated over night at 37°C and colonies collected for large scale DNA extraction. A representative plate was stored and saved for collecting colonies for colony PCR analysis and large-scale sequencing. A simple colony PCR assay was used to initially determine the rough fragment size distribution as well as insertion efficiency. From sequencing data the precise fragment size was evaluated, junction intactness at the insertion site as well as the frame selection accuracy (*3n+1 rule*).

*Cloning and evaluation of the library for bacterial surface display.* Genomic DNA fragments were excised from the pMAL4.31 vector, containing the *S. agalactiae* library with the restriction enzymes *Fse*I and *Not*I. The entire population of fragments was then transferred into plasmids pMAL9.1 (LamB) or pHIE11 (FhuA), which have been digested with *Fse*I and *Not*I. Using these two restriction enzymes, which recognise an 8 bp GC rich sequence, the reading frame that was selected in the pMAL4.31 vector is maintained in each of the platform vectors. The plasmid library was then transformed into *E. coli* DH5alpha cells by

electroporation. Cells were plated onto large LB-agar plates supplemented with 50 µg/ml Kanamycin and grown over night at 37°C at a density yielding clearly visible single colonies. Cells were then scraped off the surface of these plates, washed with fresh LB medium and stored in aliquots for library screening at -80°C.

*Results*

*Libraries for frame selection.* Two libraries (LSAg-70 and LSAg-300) were generated in the pMAL4.31 vector with sizes of approximately 70 and 300 bp, respectively. For each library, ligation and subsequent transformation of approximately 1 µg of pMAL4.31 plasmid DNA and 50 ng of fragmented genomic *S. agalactiae* DNA yielded 4x $10^5$ to 2x $10^6$ clones after frame selection. To assess the randomness of the libraries, approximately 576 randomly chosen clones of LSAg-70 were sequenced. The bioinformatic analysis showed that of these clones only very few were present more than once. Furthermore, it was shown that approximately 80% of the clones fell in the size range between 25 and 100 bp with an average size of approximately 40 bp (Figure 2). Allmost all sequences followed the 3n+1 rule, showing that all clones were properly frame selected.

*Bacterial surface display libraries.* The display of peptides on the surface of *E. coli* required the transfer of the inserts from the LSAg-70 and LSAg-300 libraries from the frame selection vector pMAL4.31 to the display plasmids pMAL9.1 (LamB) or pHIE11 (FhuA). Genomic DNA fragments were excised by *Fse*I and *Not*I restriction and ligation of 5ng inserts with 0.1µg plasmid DNA and subsequent transformation into DH5alpha cells resulted in 2-5x $10^6$ clones. The clones were scraped off the LB plates and frozen without further amplification.

**Example 3: Identification of highly immunogenic peptide sequences from *S. agalactiae* using bacterial surface displayed genomic libraries and human serum**

*Experimental procedures*

*MACS screening.* Approximately 2.5x $10^8$ cells from a given library were grown in 5 ml LB-medium supplemented with 50 µg/ml Kanamycin for 2 h at 37°C. Expression was induced by the addition of 1 mM IPTG for 30 min. Cells were washed twice with fresh LB medium and approximately 2x $10^7$ cells re-suspended in 100 µl LB medium and transferred to an Eppendorf tube.

10 to 20 µg of biotinylated, human IgGs purified from serum was added to the cells and the suspension incubated overnight at 4°C with gentle shaking. 900 µl of LB medium was added, the suspension mixed and subsequently centrifuged for 10 min at 6,000 rpm at 4°C (For IgA screens, 10 µg of purified IgAs were used and these captured with biotinylated anti-human-IgG secondary antibodies). Cells were washed once with 1 ml LB and then re-suspended in 100 µl LB medium. 10 µl of MACS microbeads coupled to streptavidin (Miltenyi Biotech, Germany) were added and the incubation continued for 20 min at 4°C. Thereafter 900 µl of LB medium was added and the MACS microbead cell suspension was loaded onto the equilibrated MS column (Miltenyi Biotech, Germany) which was fixed to the magnet. (The MS columns were equilibrated by washing once with 1 ml 70% EtOH and twice with 2 ml LB medium.)

The column was then washed three times with 3 ml LB medium. After removal of the magnet, cells were eluted by washing with 2 ml LB medium. After washing the column with 3 ml LB medium, the 2 ml eluate was loaded a second time on the same column and the washing and elution process repeated. The loading, washing and elution process was performed a third time, resulting in a final eluate of 2 ml.

A second and third round of screening was performed as follows. The cells from the final eluate were collected by centrifugation and re-suspended in 1 ml LB medium supplemented with 50 µg/ml Kanamycin. The culture was incubated at 37°C for 90 min and then induced with 1 mM IPTG for 30 min.

Cells were subsequently collected, washed once with 1 ml LB medium and suspended in 10 µl LB medium. 10 to 20 µg of human, biotinylated IgGs were added again and the suspension incubated over night at 4°C with gentle shaking. All further steps were exactly the same as in the first selection round. Cells selected after two rounds of selection were plated onto LB-agar plates supplemented with 50 µg/ml Kanamycin and grown over night at 37°C.

*Evaluation of selected clones by sequencing and Western blot analysis.* Selected clones were grown overnight at 37°C in 3 ml LB medium supplemented with 50 µg/ml Kanamycin to prepare plasmid DNA using standard procedures. Sequencing was performed at MWG (Germany) or in collaboration with TIGR (U.S.A.).

For Western blot analysis approximately 10 to 20 µg of total cellular protein was separated by 10% SDS-PAGE and blotted onto HybondC membrane (Amersham Pharmacia Biotech, England). The LamB or FhuA fusion proteins were detected using human serum as the primary antibody at a dilution of approximately 1:3,000 to 1:5,000 and anti-human IgG or IgA antibodies coupled to HRP at a dilution of 1:5,000 as secondary antibodies. Detection was performed using the ECL detection kit (Amersham Pharmacia Biotech, England). Alternatively, rabbit anti-FhuA or rabbit anti-LamB polyclonal immune sera were used as primary antibodies in combination with the respective secondary antibodies coupled to HRP for the detection of the fusion proteins.

***Results***

*Screening of bacterial surface display libraries by magnetic activated cell sorting (MACS) using biotinylated Igs.* The libraries LSag-70 in pMAL9.1 and LSag-300 in pHIE11 were screened with pools of biotinylated, human IgGs and IgAs prepared from sera of healthy adults (NSag8-IgG,-IgA) or P10,11,18 (see Example 1: *Preparation of antibodies from human serum*). The selection procedure was performed as described under Experimental procedures. Figure 3A shows a representative example of a screen with the LSag-70 library and PSag11-IgGs. As can be seen from the colony count after the first selection cycle from MACS screening, the total number of cells recovered at the end is drastically reduced from $2x10^7$ cells to approximately $2x\ 10^4$ cells, but the selection without antibodies added showed a similar reduction in cell numbers (Figure 3A). Therefore a second and third round of selection was performed. At the end of round three, approximately $10^4$ cells was recovered with PSag11-IgGs, while only $2x\ 10^3$ cells were recovered when no IgGs from human serum were added, clearly showing that selection was dependent on *S. agalactiae* specific antibodies. To evaluate the performance of the screen, 26 selected clones were picked randomly and subjected to immunoblot analysis with screening IgG pool (Figure 3B). This analysis revealed that more than 80% of the selected clones showed reactivity with antibodies present in the relevant serum whereas the control strain expressing LamB without a *S. agalactiae* specific insert did not react with the same serum. In general, the rate of reactivity was observed to lie within the range of 35 to 90%. Colony PCR analysis showed that all selected clones contained an insert in the expected size range.

Subsequent sequencing of a larger number of randomly picked clones (600 to 1200 per screen) led to the identification of the gene and the corresponding peptide or protein sequence that was specifically recognized by the human serum antibodies used for screening. The frequency with which a specific clone is selected reflects at least in part the abundance and/or affinity of the specific antibodies in the serum used for selection and recognizing the epitope presented by this clone. In that regard it is striking that clones derived from some ORFs (e.g. gbs1087, gbs1306, gbs2018) were picked more than 100 times, indicating their highly immunogenic property. Table 1 summarizes the data obtained for all 13 performed screens. All clones that are presented in Table 1 have been verified by immunoblot analysis using whole cellular extracts from single clones to show the indicated reactivity with the pool of human serum used in the respective screen. As can be seen from Table 1, distinct regions of the identified ORF are identified as immunogenic, since variably sized fragments of the proteins are displayed on the surface

by the platform proteins.

It is further worth noticing that most of the genes identified by the bacterial surface display screen encode proteins that are either attached to the surface of *S. agalactiae* and/or are secreted. This is in accordance with the expected role of surface attached or secreted proteins in virulence of *S. agalactiae*.

**Example 4: Assessment of the reactivity of highly immunogenic peptide sequences with individual human sera.**

*Experimental procedures*

*Peptide synthesis*
Peptides were synthesized in small scale (4 mg resin; up to 288 in parallel) using standard F-moc chemistry on a Rink amide resin (PepChem, Tübingen, Germany) using a SyroII synthesizer (Multisyntech, Witten, Germany). After the sequence was assembled, peptides were elongated with Fmoc-epsilon-aminohexanoic acid (as a linker) and biotin (Sigma, St. Louis, MO; activated like a normal amino acid). Peptides were cleaved off the resin with 93%TFA, 5% triethylsilane, and 2% water for one hour. Peptides were dried under vacuum and freeze dried three times from acetonitrile/water (1:1). The presence of the correct mass was verified by mass spectrometry on a Reflex III MALDI-TOF (Bruker, Bremen Germany). The peptides were used without further purification.

*Enzyme linked immune assay (ELISA).*
Biotin-labeled peptides (at the N-terminus) were coated on Streptavidin ELISA plates (EXICON) at 10 μg/ml concentration according to the manufacturer's instructions. Highly specific Horse Radish Peroxidase (HRP)-conjugated anti-human IgG secondary antibodies (Southern Biotech) were used according to the manufacturers' recommendations (dilution: 1,000x). Sera were tested at two serum dilutions, 200X and 1,000X. Following manual coating, peptide plates were processed and analyzed by the Gemini 160 ELISA robot (TECAN) with a built-in ELISA reader (GENIOS, TECAN).

***Results***

Following the bioinformatic analysis of selected clones, corresponding peptides were designed and synthesized. In case of epitopes with more than 26 amino acid residues, overlapping peptides were made. All peptides were synthesized with a N-terminal biotin-tag and used as coating reagents on Streptavidin-coated ELISA plates.

The analysis was performed in two steps. First, peptides were selected based on their reactivity with the individual sera, which were included in the serum pools used for preparations of IgG and IgA screening reagents for bacterial surface display. A summary for serum reactivity of 58 peptides representing *S. agalactiae* epitopes from the genomic screen analysed with 22 human sera (from 13 patient and 9 healthy exposed high titer individuals) used for the antigen identification is shown in Table 2. The peptides were compared by the score calculated for each peptide based on the number of positive sera and the extent of reactivity. Peptides range from highly and widely reactive to weakly positive ones.

**Example 5: Gene distribution studies with highly immunogenic proteins identified from *S. agalactiae*.**

*Experimental procedures*

*Gene distribution of GBS antigens by PCR.* An ideal vaccine antigen would be an antigen that is present in all, or the vast majority of strains of the target organism to which the vaccine is directed. In order to

establish whether the genes encoding the identified *Streptococcus agalactiae* antigens occur ubiquitously in *S. agalactiae* strains, PCR was performed on a series of independent *S. agalactiae* isolates with primers specific for the gene of interest. *S. agalactiae* isolates were obtained covering the serotypes most frequently present in patients as shown in Figure 4A. Oligonucleotide sequences as primers were designed for all identified ORFs yielding products of approximately 1,000 bp, if possible covering all identified immunogenic epitopes. Genomic DNA of all *S. agalactiae* strains was prepared as described under Example 2. PCR was performed in a reaction volume of 25 µl using Taq polymerase (1U), 200 nM dNTPs, 10 pMol of each oligonucleotide and the kit according to the manufacturers instructions (Invitrogen, The Netherlands). As standard, 30 cycles (1x: 5min. 95°C, 30x: 30sec. 95°C, 30sec. 56°C, 30sec. 72°C, 1x 4min. 72°C) were performed, unless conditions had to be adapted for individual primer pairs.

*Results*

Identified genes encoding immunogenic proteins were tested by PCR for their presence in 46 different strains of *S. agalactiae* (Figure 4A). As an example, figure 4B shows the PCR reaction for GBS0061 with all indicated 46 strains. As clearly visible, the gene is present in all strains analysed. The PCR fragment from a type IA strain was sequenced and showed that all 657 bp were identical as compared to the *S. agalactiae* ATCC 12403 strain, indicating a high level of conservation between the two isolates.
From a total of 117 genes analysed, more than 100 were present in all or almost all strains tested, while only 5 genes were absent in more than 10% of the tested 46 strains (Table 3). In addition, only few genes (e.g. GBS0016, GBS1087, GBS1528 and GBS2018) showed variation in size but were present in all or most strain isolates. Sequencing of the generated PCR fragment from one strain and subsequent comparison to the type III strain ATCC 12403 confirmed the amplification of the correct DNA fragment and revealed a degree of sequence divergence as indicated in Table 3. Importantly, many of the identified antigens are well conserved in all strains in sequence and size and are therefore novel vaccine candidates to prevent infections by GBS.

**Example 6: Characterization of immune sera obtained from mice immunized with highly immunogenic proteins/peptides from *S. agalactiae* displayed on the surface of *E. coli*.**

*Experimental procedures*

*Generation of immune sera from mice*
*E. coli* clones harboring plasmids encoding the platform protein fused to a *S. agalactiae* peptide, were grown in LB medium supplemented with 50µg/ml Kanamycin at 37°C. Overnight cultures were diluted 1:10, grown until an $OD_{600}$ of 0.5 and induced with 0.2 mM IPTG for 2 hours. Pelleted bacterial cells were suspended in PBS buffer and disrupted by sonication on ice, generating a crude cell extract. According to the $OD_{600}$ measurement, an aliquot corresponding to $5x10^7$ cells was injected into NMRI mice i.v., followed by a boost after 2 weeks. Serum was taken 1 week after the second injection. Epitope specific antibody levels were measured by peptide ELISA.

*In vitro expression of antigens*
Expression of antigens by *in vitro* grown *S. agalactiae* serotype III was tested by immunoblotting. Different growth media and culture conditions were tested to detect the presence of antigens in total lysates and bacterial culture supernatants. Expression was considered confirmed when a specific band corresponding to the predicted molecular weight and electrophoretic mobility was detected.

*Cell surface staining*
Flow cytometric analysis was carried out as follows. Bacteria were grown under culture conditions, which resulted in expression of the antigen as shown by the immunoblot analysis. Cells were washed twice in Hanks Balanced Salt Solution (HBSS) and the cell density was adjusted to approximately 1 X $10^6$ CFU in 100µl HBSS, 0.5% BSA. After incubation for 30 to 60 min at 4°C with mouse antisera diluted 50 to

100-fold, unbound antibodies were washed away by centrifugation in excess HBSS, 0.5% BSA. Secondary goat anti-mouse antibody ($F(ab')_2$ fragment specific) labeled with fluorescein (FITC) was incubated with the cells at 4°C for 30 to 60 min. After washing, cells were fixed with 2% paraformaldehyde. Bound antibodies were detected using a Becton Dickinson FACScan flow cytometer and data further analyzed with the computer program CELLQuest. Negative control sera included mouse pre-immune serum and mouse polyclonal serum generated with lysates prepared from IPTG induced *E. coli* cells transformed with plasmids encoding the genes *lamB* or *fhuA* without *S. agalactiae* genomic insert.

*Bactericidal (killing) assay*

Murine macrophage cells (RAW246.7 or P388.D1) and bacteria were incubated and the loss of viable bacteria after 60 min was determined by colony counting. In brief, bacteria were washed twice in Hanks Balanced Salt Solution (HBSS) and the cell density was adjusted to approximately 1X $10^5$ CFU in 50µl HBSS. Bacteria were incubated with mouse sera (up to 25%) and guinea pig complement (up to 5%) in a total volume of 100µl for 60min at 4°C. Pre-opsonized bacteria were mixed with macrophages (murine cell line RAW264.7 or P388.D1; 2X $10^6$ cells per 100µl) at a 1:20 ratio and were incubated at 37°C on a rotating shaker at 500 rpm. An aliquot of each sample was diluted in sterile water and incubated for 5 min at room temperature to lyse macrophages. Serial dilutions were then plated onto Todd-Hewitt Broth agar plates. The plates were incubated overnight at 37°C, and the colonies were counted with the Countermat flash colony counter (IUL Instruments). Control sera included mouse pre-immune serum and mouse polyclonal serum generated with lysates prepared from IPTG induced *E. coli* transformed with plasmids harboring the genes *lamB* or *fhuA* without *S. agalactiae* genomic insert.

***Results***

*Immunogenicity in mice.* The presence of specific antibodies was determined by peptide ELISA and/or immunoblotting using the *E. coli* clone expressing the given epitope embedded in LamB or FhuA platform proteins, as it is exemplified in Fig. 5A and B, respectively, and summarized in Table 4. 31 novel GBS antigens represented by 43 different epitope regions were shown to be immunogenic in mice. Positive sera were then analysed by immunblotting using total bacterial lysates and culture supernatants prepared from *S. agalactiae* serotype III strain (data not shown). This analysis served as a first step to determine whether the antigenic protein were expressed, and if, under which growth conditions, in order to evaluate surface expression of the polypeptide by FACS analysis. It was anticipated based on literature data that not all proteins would be expressed under *in vitro* conditions.

*Cell surface staining of S. agalactiae.* Cell surface accessibility for several antigenic proteins was subsequently demonstrated by an assay based on flow cytometry. GBS cells were incubated with preimmune and polyclonal mouse sera raised against *S. agalactiae* lysate or *E. coli* clones harboring plasmids encoding the platform protein fused to a *S. agalactiae* peptide, followed by detection with fluorescently tagged secondary antibody. As shown in Fig. 6A, antisera raised against *S. agalactiae* lysate contains antibodies against surface components, demonstrated by a significant shift in fluorescence of the *S. agalactiae* serotype III cell population. Similar cell surface staining of *S. agalactiae* serotype III cells was observed with polyclonal sera raised against peptides of many of the GBS antigens identified (Fig. 6B ). In some instancies, a subpopulation of the bacteria was not stained, as indicated by the detection of two peaks in the histograms (Fig. 6B). This phenomenon may be a result of differential expression of the gene products during the growth of the bacterium, insufficient antibody levels or partial inhibition of antibody binding caused by other surface molecules or plasma proteins. Importantly, a well-known protective GBS antigen, Sip/gbs0031 is proved to be also positive in this assay.

*In vitro bactericidal activity.* Opsonophagocytic killing is the cornerstone of host defense against extracellular bacteria, such as *S. agalactiae*. Cell surface binding of antibodies to bacterial antigens are opsonizing and induce killing (bactericidal) by phagocytic cells (macrophages and neutrophil granulocytes) if the antibodies induced by the particular antigens can bind activated complement

components (C3bi). In Figure 7 data are presented on bactericidal activity measured by antigen-specific antibodies generated in mice with corresponding epitopes. According to these data, several of the novel GBS antigens gbs0012, gbs0016, gbs0428, gbs1306 and gbs2018 induce functional antibodies. Importantly, a well-known protective GBS antigen, Sip/gbs0031 is proved to be strongly positive in the very same assay.

These experiments confirmed the bioinformatic prediction that many of the proteins are exported due to their signal peptide sequence and in addition showed that they are present on the cell surface of *S. agalactiae* serotype III. They also confirm that these proteins are available for recognition by human antibodies with functional properties and make them valuable candidates for the development of a vaccine against GBS diseases.

**Table 1A: Immunogenic proteins identified by bacterial surface display.**

A, 300bp library of *S.agalactiae* ATCC 12403 in fhuA with IC8-IgA (826), B, 300bp library in fhuA with P10-IgA (768), C, 300bp library in fhuA with P10-IgG (711), D, 300bp library in fhuA with P11-IgG (640), E, 70bp library in lamB with IC8-IgA (1057), F, 70bp library in lamB with IC8-IgG (869), G, 70bp library in lamB with P10-IgA (904), H, 70bp library in lamB with P10-IgA-adsorbed (493), I, 70bp library in lamB with P10-IgG (910), J, 70bp library in lamB with P11-IgA (631), K, 70bp library in lamB with P11-IgG (926), L, 70bp library in lamB with P18-IgA (691), M, 70bp library in lamB with Sekret-IgA (628); *, prediction of antigenic sequences longer than 5 amino acids was performed with the program ANTIGENIC (Kolaskar and Tongaonkar, 1990).

| *S. agalactiae* antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| gbs0012 | weakly similar to beta-lactamase | 4-20,35-44,65-70,73-87,92-98,112-137,152-161,177-186,193-200,206-213,229-255,282-294,308-313,320-326,349-355,373-384,388-406,420-425 | B:13, C:6 | 115-199 | 1, 218 |
| gbs0016 | glucan-binding protein B | 5-24,35-41,44-70,73-89,103-109,127-143,155-161,185-190,192-207,212-219,246-262,304-336,372-382,384-393,398-407,412-418,438-444 | B:12, C:4, D:3, E:5, H:4, I:12, M:2 | 1-75, 76-161, 164-239 | 2, 219 |
| gbs0024 | phosphoribosylformylglycinamidine synthase | 4-10,16-58,60-71,77-92,100-126,132-146,149-164,166-172,190-209,214-220,223-229,241-256,297-312,314-319,337-343,351-359,378-387,398-418,421-428,430-437,440-448,462-471,510-519,525-536,552-559,561-568,573-582,596-602,608-630,637-649,651-665,681-702,714-732,739-745,757-778,790-805,807-815,821-829,836-842,846-873,880-903,908-914,916-923,931-940,943-948,956-970,975-986,996-1015,1031-1040,1051-1069,1072-1095,1114-1119,1130-1148,1150-1157,1169-1176,1229-1238 | F:4 | 802-812 | 3, 220 |
| gbs0031 | surface immunogenic protein | 5-12,14-26,35-47,52-67,72-78,83-98,121-141,152-159,163-183,186-207,209-257,264-277,282-299,301-309,312-318,324-339,358-368,372-378,387-397,425-431 | A:17, B:53, C:36, D:4 | 46-291 | 4, 221 |
| gbs0048 | Hypothetical protein | 29-38,44-64,70-76,78-87,94-100,102-112,119-134,140-149,163-173,178-186,188-194,207-234,247-262,269-290 | K:13 | 73-92 | 5, 222 |
| gbs0053 | aldehyde-alcohol | 10-28,36-63,77-87,103-119,127-136,141- | B:4 | 757-774 | 6, 223 |

| S. agalactiae antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| | dehydrogenase (adhE) | 169,171-183,195-200,207-232,236-246,251-265,268-283,287-297,314-322,335-343,354-363,384-390,405-411,419-436,443-455,467-473,480-513,518-529,550-557,565-585,602-608,616-625,632-660,665-677,685-701,726-736,738-747,752-761,785-796,801-813,838-853,866-871 | | | |
| gbs0061 | rplB ribosomal protein L2 | 31-38,61-66,74-81,90-115,123-145,154-167,169-179,182-193,200-206,238-244,267-272 | F:2, I:12 | 235-251 | 7, 224 |
| gbs0084 | DNA-directed RNA polymerase, alpha subunit (rpoA) | 19-25,38-54,56-64,66-72,74-92,94-100,116-129,143-149,156-183,204-232,253-266,269-275,294-307 | C:4, D:6 | 241-313 | 8, 225 |
| gbs0107 | conserved hypothetical protein | 5-34,50-56,60-65,74-85,89-97,108-119,159-165,181-199,209-225,230-240,245-251,257-262,274-282,300-305 | K:2 | 64-75 | 9, 226 |
| gbs0108 | deoxyuridine 5'-triphosphate nucleotidohydrolase | 5-13,16-21,27-42,45-52,58-66,74-87,108-114,119-131 | I:5 | 39-51 | 10, 227 |
| gbs0113 | ribose ABC transporter | 6-23,46-54,59-65,78-84,100-120,128-133,140-146,159-165,171-183,190-204,224-232,240-248,250-259,274-280,288-296,306-315 | F:4 | 267-274 | 11, 228 |
| gbs0123 | similar to argininosuccinate synthase | 5-12,15-24,26-36,42-65,68-80,82-104,111-116,125-144,159-167,184-189,209-218,235-243,254-265,269-283,287-300,306-316,318-336,338-352,374-392 | K:17 | 162-174 | 12, 229 |
| gbs0127 | rpmV 50S ribosomal protein L28 | 30-42,45-54 | F:11 | 25-37 | 13, 230 |
| gbs0144 | oligopeptide ABC transporter, substrate-binding | 10-30,53-59,86-95,116-130,132-147,169-189,195-201,212-221,247-256,258-265,278-283,291-298,310-316,329-339,341-352,360-367,388-396,398-411,416-432,443-452,460-466,506-512,515-521,542-548 | E:7 | 419-431 | 14, 231 |
| gbs0183 | membrane protein, putative | 4-27,30-53,60-67,70-90,92-151,159-185,189-195,198-210,215-239 | F:9 | 173-189 | 15, 232 |
| gbs0184 | oligopeptide ABC transporter, | 4-26,41-54,71-78,116-127,140-149,151-158,161-175,190-196,201-208,220-226,240- | E:6 | 174-188 | 16, 233 |

| S. agalactiae antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| | oligopeptide-binding | 252,266-281,298-305,308-318,321-329,344-353,372-378,384-405,418-426,429-442,457-463,494-505,514-522 | | | |
| gbs0235 | glycine betaine/carnitine/choline ABC transporter | 17-25,27-39,61-67,81-89,99-110,120-131,133-139,147-161,167-172,179-185,192-198,203-213,226-238,243-258,261-267,284-290,296-307,311-328,340-352,356-371 | G:8, H:15 | 239-256 | 17, 234 |
| gbs0255 | conserved hypothetical protein | 8-30,40-49,67-80,114-123,126-142,152-162,188-194 | E:2 | 57-70 | 18, 235 |
| gbs0260 | glycyl-tRNA synthetase (beta subunit) | 4-23,28-34,36-47,50-61,76-81,89-94,96-104,112-119,126-146,155-181,195-200,208-214,220-229,244-260,263-276,282-288,292-300,317-323,336-351,353-359,363-375,382-399,415-432,444-455,458-471,476-481,484-492,499-517,522-529,535-541,543-568,572-584,586-600,607-617,626-637,656-675 | F:3 | 282-297 | 19, 236 |
| gbs0268 | transketolase (tkt) | 6-24,30-35,38-45,63-91,134-140,146-160,167-188,214-220,226-234,244-250,260-270,286-301,316-329,340-371,429-446,448-459,474-481,485-491,512-526,537-544,550-565,573-583,596-613,621-630,652-658 | E:7 | 87-97 | 20, 237 |
| gbs0286 | NH3-dependent NAD+ synthetase | 8-20,26-48,56-67,76-86,94-109,115-121,123-129,143-160,178-186,191-198,201-208,221-236,238-244,260-268 | F:12, G:7, H:8 | 237-247 | 21, 238 |
| gbs0288 | similar to penicillin-binding protein 1A | 4-40,42-57,73-87,98-117,126-135,150-156,166-174,196-217,231-236,248-258,276-284,293-301,307-313,339-347,359-365,375-387,395-402,428-440,445-456,485-490,497-505,535-541,547-555,610-625,648-656,665-671 | D:5, K:3 | 448-528 | 22, 239 |
| gbs0343 | seryl-tRNA synthetase (serS) | 10-18,39-45,51-61,80-96,98-106,110-115,158-172,174-183,191-200,220-237,249-255,274-289,308-324,331-341,372-381,384-397,405-414 | I:3 | 322-338 | 23, 240 |
| gbs0411 | Hypothetical protein | 30-36,38-56,85-108,134-147,149-160,163-183,188-201,206-211,219-238,247-254 | I:11 | 5-13 | 24, 241 |
| gbs0428 | similar to fibrinogen binding protein, putative | 11-40,98-103,110-115,133-145,151-159,172-179,192-201,204-212,222-228,235-245,258-268,283-296,298-309,322-329,342-351,354- | A:7, B:2, C:31 | 1-148 | 25, 242 |

| S. agalactiae antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| | peptidoglycan linked protein (LPXTG motif) | 362,372-378,385-393,407-418,495-516 | | | |
| gbs0437 | glucose-6-phosphate isomerase (pgi) | 5-19,21-36,73-94,112-119,122-137,139-145,152-167,184-190,198-204,208-224,249-265,267-281,299-304,309-317,326-333,356-364,368-374,381-389,391-414,419-425,430-435 | I:26 | 113-140 | 26, 243 |
| gbs0460 | decarboxylase | 45-54,59-67,78-91 | I:7, K:11 | 15-23 | 27, 244 |
| gbs0465 | oxydoreductase | 11-22,33-47,52-80,88-112,124-129 | F:4 | 6-25 | 28, 245 |
| gbs0470 | similar to alpha protein, putative peptidoglycan linked protein (LPXTG motif) | 26-41,51-63,80-89,93-115,150-163,187-193,220-237,240-249,286-294,296-306,316-329,345-353,361-370,407-425,428-437,474-482,484-494,504-517,533-541,549-558,595-613,616-625,660-668,673-685,711-726,736-744,749-761,787-802,812-820,825-837,863-878,888-896,901-913,939-954,964-972,977-989,1003-1008,1016-1022,1028-1034,1041-1053,1059-1074,1101-1122 | B:4, C:2, D:8 | 420-511, 581-704 | 29, 246 |
| gbs0489 | acetyltransferase, GNAT family | 18-25,27-55,71-83,89-95,102-113,120-146,150-156,174-185 | E:32 | 159-175 | 30, 247 |
| gbs0492 | gbs0492 valyl-tRNA synthetase | 24-30,38-56,63-68,87-93,136-142,153-164,183-199,213-219,226-234,244-261,269-278,283-289,291-297,320-328,330-336,340-346,348-356,358-366,382-387,401-408,414-419,449-455,468-491,504-512,531-537,554-560,597-608,621-627,632-643,650-662,667-692,703-716,724-737,743-758,783-794,800-818,846-856 | A:3 | 806-884 | 31, 248 |
| gbs0538 | amino acid ABC transporter (ATP-binding protein) | 4-14,21-39,86-92,99-107,121-131,136-144,147-154,158-166,176-185,193-199,207-222,224-230 | G:1 | 117-136 | 32, 249 |
| gbs0539 | similar to phosphomannomutase | 65-76,85-97,103-109,115-121,125-146,163-169,196-205,212-219,228-237,241-247,254-262,269-288,294-303,305-313,328-367,395-401,405-412,418-429,437-447,481-488,506-513,519-524,530-541,546-557 | K:4 | 266-284 | 33, 250 |
| gbs0555 | beta-lactam resistance factor | 5-14,37-42,49-71,78-92,97-112,127-136,147-154,156-163,186-198,216-225,233-243,248- | E:3 | 194-223 | 34, 251 |

| S. agalactiae antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| | (fibA) | 253,295-307,323-332,359-366,368-374,380-398 | | | |
| gbs0579 | dipeptidase | 4-11,33-39,45-72,100-113,119-129,136-144,169-176,177-185,200-208,210-219,262-276,278-297,320-326,336-344,347-362,381-394,443-453 | I:4 | 438-454 | 35, 252 |
| gbs0580 | zinc ABC transporter, zinc-binding adhesion, lipoprotein | 4-29,31-52,55-61,95-110,138-158,162-171,179-187,202-229,239-248,251-256,262-267,269-285,304-310,351-360,362-368,381-388,415-428,435-440,448-458 | I:11 | 161-178 | 36, 253 |
| gbs0628 | cell wall surface anchor family protein (IPxTG) | 4-17,19-28,32-43,47-59,89-110,112-126,128-134,140-148,152-161,169-184,191-204,230-235,255-264,328-338,341-347,401-409,413-419,433-441,449-458,463-468,476-482,486-492,500-506,529-545 | I:9, H:1 | 305-381 | 37, 254 |
| gbs0632 | cell wall surface anchor family protein, putative (FPKTG motive) | 10-29,38-45,53-61,134-145,152-160,163-170,202-208,219-229,248-258,266-275,282-288,315-320,328-334,377-385,392-402,418-424,447-453,460-471,479-487,491-497,500-507,531-537,581-594,615-623,629-635,644-652,659-666,668-678,710-717,719-728,736-741,747-760,766-773,784-789,794-800,805-817,855-861,866-887 | H:3 | 698-715 | 38, 255 |
| gbs0634 | putative surface protein | 16-26,29-37,44-58,62-68,74-80,88-95,97-120,125-144,165-196 | H:1 | 58-72 | 39, 256 |
| gbs0667 | regulatory protein, putative, truncation | 14-21,23-46,49-60,63-74,78-92,96-103,117-129,134-161,169-211,217-231,239-248,252-281,292-299,313-343 | I:2 | 243-257 | 40, 257 |
| gbs0672 | transcriptional regulator (GntR family) | 11-27,46-52,67-72,76-84,91-112,116-153,160-175,187-196,202-211,213-220 | G:11 | 43-76 | 41, 258 |
| gbs0687 | Hypothetical protein | 5-29,37-56,78-86,108-118,152-161 | I:4 | 120-130 | 42, 259 |
| gbs0785 | Similar to penicillin binding protein 2B | 8-14,19-41,52-66,75-82,87-92,106-121,127-133,136-143,158-175,180-187,196-204,221-228,239-245,259-265,291-306,318-323,328-340,352-358,361-368,375-381,391-399,411-418,431-442,446-455,484-496,498-510,527-533,541-549,558-565,575-585,587-594,644-655,661-668,671-677 | K:3 | 184-196 | 43, 260 |

| *S. agalactiae* antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| gbs0811 | beta-glucosidase | 4-22,29-38,55-62,75-81,102-107,110-134,143-150,161-167,172-179,191-215,223-233,241-247,251-264,266-272,288-309,340-352,354-366,394-402,414-438 | L:13 | 198-218 | 44, 261 |
| gbs0828 | hypothetical protein | 24-44,49-70,80-91,105-118,128-136,140-154 | I:3 | 77-92 | 45, 262 |
| gbs0851 | hypothetical protein | 5-22,31-36,41-47,67-74,83-90,105-122,135-143,160-167 | B:2 | 118-129 | 46, 263 |
| gbs0865 | hypothetical protein | 4-25,33-73,81-93,96-106,114-120,122-128,130-172,179-208,210-241,251-283,296-301 | K:4 | 92-100 | 47, 264 |
| gbs0890 | exonuclease RexB (rexB) | 14-24,29-38,43-50,52-72,86-97,101-107,110-125,127-141,145-157,168-175,177-184,186-195,205-226,238-250,255-261,284-290,293-304,307-314,316-323,325-356,363-371,383-390,405-415,423-432,442-454,466-485,502-511,519-527,535-556,558-565,569-574,612-634,641-655,672-686,698-709,715-722,724-732,743-753,760-769,783-792,818-825,830-839,842-849,884-896,905-918,926-940,957-969,979-1007,1015-1021,1049-1057 | E:5 | 336-349 | 48, 265 |
| gbs0896 | similar to acetoin dehydrogenase | 6-16,26-31,33-39,62-73,75-85,87-100,113-123,127-152,157-164,168-181,191-198,208-214,219-226,233-254,259-266,286-329 | K:2 | 181-195 | 49, 266 |
| gbs0898 | acetoin dehydrogenase, thymine PPi dependent | 4-13,32-39,53-76,99-108,110-116,124-135,137-146,149-157,162-174,182-190,207-231,242-253,255-264,274-283,291-323,334-345,351-360,375-388,418-425,456-474,486-492,508-517,520-536,547-560,562-577 | B:13, F:2, I:2, J:2 | 31-45, 419-443 | 50, 267 |
| gbs0904 | phosphoglucomutase /phosphomannomutase family protein | 15-26,30-37,42-49,58-90,93-99,128-134,147-154,174-179,190-197,199-205,221-230,262-274,277-287,300-314,327-333,343-351,359-377,388-396,408-413,416-425,431-446 | I:3 | 246-256 | 51, 268 |
| gbs0918 | weakly similar to histidine triad protein, putative lipoprotein | 5-26,34-42,47-54,61-67,71-104,107-115,131-138,144-153,157-189,196-202,204-210,228-245,288-309,316-329,332-341,379-386,393-399,404-412,414-421,457-468,483-489,500-506,508-517,523-534,543-557,565-580,587-605,609-617,619-627,631-636,640-646,662-668,675-682,705-710,716-723,727-732,750- | B:5, C:11, D:36, E:3, K:3 | 14-138, 166-286, 372-503, 674-696, 754-859 | 52, 269 |

| *S. agalactiae* antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| | | 758,784-789,795-809,869-874 | | | |
| gbs0931 | pyruvate kinase | 5-17,32-38,40-47,80-89,113-119,125-137,140-154,157-163,170-177,185-199,213-225,228-236,242-248,277-290,292-305,323-333,347-353,364-370,385-394,399-406,423-433,441-451,462-474,477-487 | F:78 | 116-124 | 53, 270 |
| gbs0947 | similar to L-Lactate Dehydrogenase | 7-16,18-30,32-49,53-61,63-85,95-101,105-115,119-134,143-150,159-178,185-202,212-229,236-250,254-265,268-294 | K:28 | 63-72 | 54, 271 |
| gbs0948 | DNA gyrase, A subunit (gyrA) | 4-12,19-47,73-81,97-103,153-169,188-198,207-213,217-223,236-242,255-265,270-278,298-305,309-317,335-347,354-363,373-394,419-424,442-465,486-492,500-507,542-549,551-558,560-572,580-589,607-614,617-623,647-653,666-676,694-704,706-714,748-754,765-772,786-792,795-806 | I:4 | 358-370 | 55, 272 |
| gbs0969 | similar to unknown plasmid protein | 18-28,30-38,40-46,49-55,69-78,82-98,104-134,147-153,180-190,196-202,218-236,244-261,266-273,275-286,290-295,301-314,378-387,390-395,427-434 | E:3 | 290-305 | 56, 273 |
| gbs0971 | similar to putative plasmid replication protein | 4-13,20-31,39-51,54-61,69-84,87-105,117-124 | K:17 | 108-125 | 57, 274 |
| gbs0972 | Hypothetical protein | 24-34,43-54,56-66,68-79 | E:3 | 60-69 | 58, 275 |
| gbs0983 | similar to plasmid protein | 5-43,71-77,102-131,141-148,150-156,159-186,191-207,209-234,255-268,280-286,293-299,317-323,350-357,363-372,391-397,406-418,428-435,455-465,484-497,499-505,525-531,575-582,593-607,621-633,638-649,655-673,684-698,711-725,736-741,743-752,759-769,781-793,813-831,843-853,894-905,908-916,929-946,953-963,970-978,1001-1007,1011-1033 | D:11, E:2, F:2, J:10, K:10, L:46, M:3 | 165-178, 818-974 | 59, 276 |
| gbs0986 | surface antigen proteins, putative peptidoglycan bound | 16-44,63-86,98-108,185-191,222-237,261-274,282-294,335-345,349-362,374-384,409-420,424-430,440-447,453-460,465-473,475-504,522-534,538-551,554-560,567-582,598-607,611-619,627-640,643-653,655-661,669-680,684-690,701-707,715-731,744-750,756- | B:3, C:12, D:2, E:3, F:20, H:3, I:3, J:5, M:2 | 77-90, 144-212, 279-355, 434-536, 782-810, 875-902 | 60, 277 |

| S. agalactiae antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| | | 763,768-804,829-837,845-853,855-879,884-890,910-928 | | | |
| gbs0988 | similar to plasmid surface exclusion protein, putative peptidoglycan bound protein (LPXTG motif) | 4-22,29-41,45-51,53-66,70-77,86-95,98-104,106-124,129-135,142-151,153-161,169-176,228-251,284-299,331-337,339-370,380-387,393-398,406-411,423-433,440-452,461-469,488-498,501-516,523-530,532-559,562-567,570-602,612-628,630-645,649-659,666-672,677-696,714-723,727-747 | J:2 | 212-227 | 61, 278 |
| gbs0991 | ATP-dependent Clp protease, ATP-binding subunit ClpA | 4-9,17-31,35-41,56-61,66-75,81-87,90-124,133-138,149-163,173-192,213-219,221-262,265-275,277-282,292-298,301-307,333-346,353-363,371-378,419-430,435-448,456-469,551-570,583-599,603-612 | F:15 | 275-291 | 62, 279 |
| gbs0993 | similar to plasmid proteins | 28-34,53-58,72-81,100-128,145-154,159-168,172-189,217-225,227-249,256-263,299-309,322-330,361-379,381-388,392-401,404-417,425-436,440-446,451-464,469-487,502-511,543-551,559-564,595-601,606-612,615-626,633-642,644-650,664-670,674-684,692-701,715-723,726-734,749-756,763-771,781-787,810-843,860-869,882-889,907-917,931-936,941-948,951-958,964-971,976-993,1039-1049,1051-1065,1092-1121,1126-1132,1145-1151,1158-1173,1181-1192,1194-1208,1218-1223,1229-1243,1249-1254,1265-1279,1287-1297,1303-1320,1334-1341,1343-1358,1372-1382,1406-1417,1419-1425,1428-1434,1441-1448,1460-1473,1494-1504,1509-1514,1529-1550 | B:2, F:2, J:4, K:2, M:7 | 654-669, 1400-1483 | 63, 280 |
| gbs0995 | hypothetical protein | 10-16,20-25,58-65,97-109,118-132,134-146,148-155,186-195,226-233,244-262,275-284,295-310,317-322,330-339,345-351,366-375,392-403,408-415,423-430,435-444,446-457,467-479,486-499,503-510,525-537,540-585,602-612,614-623,625-634,639-645,650-669,700-707,717-724,727-739 | H:3, I:39, J:3, M:3 | 205-230, 733-754 | 64, 281 |
| gbs0997 | hypothetical protein | 5-22,37-43,72-81,105-113,128-133,148-160,188-194,204-230,238-245,251-257 | D:2, F:52 | 194-213 | 65, 282 |

| *S. agalactiae* antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| gbs0998 | hypothetical protein | 16-21,35-41,56-72,74-92,103-109 | I:2 | 62-68 | 66, 283 |
| gbs1001 | hypothetical protein | 4-15,17-82,90-104,107-159,163-170,188-221,234-245,252-265 | G:8 | 220-235 | 67, 284 |
| gbs1015 | hypothetical protein | 16-22,36-46,61-75,92-107,113-121,139-145,148-160 | K:17 | 30-42 | 68, 285 |
| gbs1035 | conserved hypothetical protein | 4-12,20-26,43-49,55-62,66-78,121-127,135-141,146-161,164-170,178-189,196-205,233-238,269-279,288-318,325-332,381-386,400-407 | B:3 | 328-346 | 69, 286 |
| gbs1041 | hypothetical protein | 5-12,31-49,57-63,69-79,89-97,99-114,116-127,134-142,147-154,160-173,185-193,199-204,211-222,229-236,243-249,256-274 | L:2 | 58-68 | 70, 287 |
| gbs1066 | hypothetical protein | 10-20,28-34,39-53,68-79,84-90,99-106 | K:2 | 73-79 | 71, 288 |
| gbs1087 | FbsA | 14-37,45-50,61-66,77-82,93-98,109-114,125-130,141-146,157-162,173-178,189-194,205-210,221-226,237-242,253-258,269-274,285-290,301-306,316-332,349-359,371-378,385-406 | A:7, B:2, C:4, E:277, G:523, J:25 | 34-307, 312-385 | 72, 289 |
| gbs1103 | ABC transporter (ATP-binding protein) | 4-10,17-38,50-85,93-99,109-116,128-185,189-197,199-210,223-256,263-287,289-312,327-337,371-386,389-394,406-419,424-432,438-450,458-463,475-502,507-513,519-526,535-542,550-567 | I:5 | 361-376 | 73, 290 |
| gbs1116 | xanthine permease (pbuX) | 10-39,42-93,100-144,155-176,178-224,230-244,246-255,273-282,292-301,308-325,332-351,356-361,368-379,386-393,400-421 | I:48 | 138-155 | 74, 291 |
| gbs1126 | similar to plasmid unknown protein | 5-11,17-34,40-45,50-55,72-80,101-123,145-151,164-172,182-187,189-195,208-218,220-241,243-252,255-270,325-331,365-371,391-398,402-418,422-428,430-435,443-452,463-469,476-484,486-494,503-509,529-553,560-565,570-590,608-614,619-627,654-661,744-750,772-780,784-790,806-816,836-853,876-885,912-918,926-933,961-975,980-987,996-1006,1016-1028,1043-1053,1057-1062 | E:2, K:3 | 994-1003, 1033-1056 | 75, 292 |
| gbs1143 | putative peptidoglycan linked protein (LPXTG) | 17-45,64-71,73-81,99-109,186-192,223-238,262-275,283-295,336-346,350-363,375-385,410-421,425-431,441-448,454-463,468-474,476-512,523-537,539-552,568-583,599- | C:3, D:2, F:15, J:3 | 274-350, 443-513 | 76, 293 |

| *S. agalactiae* antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| | | 608,612-620,628-641,644-654,656-662,670-681,685-695,702-708,716-723,725-735,757-764,769-798,800-806,808-816,826-840,846-854,856-862,874-881,885-902,907-928 | | | |
| gbs1145 | surface exclusion protein Sec10 | 4-22,29-41,45-51,53-61,70-76,85-92,99-104,111-122,134-140,142-154,163-174,224-232,255-265,273-279,283-297,330-335,337-348,356-367,373-385,391-396,421-431,442-455,475-485,493-505,526-538,544-561,587-599,605-620,622-651,662-670,675-681,687-692,697-712,714-735 | C:2 | 252-262 | 77, 294 |
| gbs1158 | Similar to oxidoreductase | 4-12,15-35,40-46,50-59,67-94,110-128,143-169,182-188,207-215,218-228,238-250 | K:2 | 74-90 | 78, 295 |
| gbs1165 | cysteine desulphurase (iscS-1) | 9-18,42-58,78-85,88-95,97-106,115-122,128-134,140-145,154-181,186-202,204-223,261-267,269-278,284-293,300-336,358-368 | F:5 | 12-29 | 79, 296 |
| gbs1195 | staphylokinase and streptokinase | 7-34,46-53,62-72,82-88,100-105,111-117,132-137,144-160,166-180,183-189,209-221,231-236,246-253,268-282,286-293,323-336,364-372,378-392,422-433 | B:3, C:2, D:2, G:3, H:8 | 388-405 | 80, 297 |
| gbs1209 | ATP-dependent DNA helicase PcrA | 21-27,34-50,72-77,80-95,164-177,192-198,202-220,226-236,239-247,270-279,285-292,315-320,327-334,348-355,364-371,388-397,453-476,488-497,534-545,556-576,582-588,601-607,609-616,642-662,674-681,687-697,709-715,721-727,741-755 | C:3, I:5 | 621-739 | 81, 298 |
| gbs1214 | conserved hypothetical protein | 4-14,16-77,79-109 | B:2 | 25-99 | 82, 299 |
| gbs1242 | CpsG, beta-1,4-galactosyltransferase | 4-9,17-23,30-37,44-55,65-72,77-93,102-121,123-132,146-153 | L:24 | 17-29 | 83, 300 |
| gbs1260 | ABC transporter, ATP-binding protein | 4-18,25-41,52-60,83-92,104-112,117-123,149-155,159-167,170-192,201-210,220-227,245-250 | I:17 | 124-137 | 84, 301 |
| gbs1270 | gbs1270 hyaluronate lyase | 8-25,50-55,89-95,138-143,148-153,159-169,173-179,223-238,262-268,288-295,297-308,325-335,403-409,411-417,432-446,463-475,492-501,524-530,542-548,561-574,576-593,604-609,612-622,637-654,665-672,678-685,720-725,731-739,762-767,777-783,820- | C:19, D:5, L:19 | 1-128, 252-341, 771-793, 1043-1058 | 85, 302 |

| *S. agalactiae* antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| | | 838,851-865,901-908,913-920,958-970,1000-1006,1009-1015,1020-1026,1043-1052,1055-1061 | | | |
| gbs1305 | hypothetical protein | 16-26,33-46 | I:2 | 64-76 | 86, 303 |
| gbs1306 | Laminin binding protein | 4-27,69-77,79-101,117-123,126-142,155-161,171-186,200-206,213-231,233-244,267-273,313-329,335-344,347-370,374-379,399-408,422-443,445-453,461-468,476-482,518-534,544-553,556-567,578-595,601-620,626-636,646-658,666-681,715-721,762-768,778-785,789-803,809-819 | A:6, B:7, C:17, D:72, E:8, F:91, G:2, H:4, I:26, J:3, K:14 | 22-108, 153-318, 391-527, 638-757 | 87, 304 |
| gbs1307 | Lmb, laminin-binding surface protein | 6-21,32-43,62-92,104-123,135-141,145-152,199-216,218-226,237-247,260-269,274-283,297-303 | A:2, D:3 | 1-72, 127-211 | 88, 305 |
| gbs1308 | C5a peptidase, authentic frameshift | 6-26,50-56,83-89,108-114,123-131,172-181,194-200,221-238,241-247,251-259,263-271,284-292,304-319,321-335,353-358,384-391,408-417,424-430,442-448,459-466,487-500,514-528,541-556,572-578,595-601,605-613,620-631,635-648,660-670,673-679,686-693,702-708,716-725,730-735,749-755,770-777,805-811,831-837,843-851,854-860,863-869,895-901,904-914,922-929,933-938,947-952,956-963,1000-1005,1008-1014,1021-1030,1097-1103,1120-1130,1132-1140 | B:4, C:15, D:70, E:18, F:26, G:5, H:4, J:2, K:40 | 1-213, 269-592, 992-1120 | 89, 306 |
| gbs1309 | hypothetical protein | 9-16,33-39,47-59,65-79,81-95,103-108,115-123,138-148,163-171,176-185,191-196,205-211,213-221,224-256,261-276,294-302,357-363,384-390 | E:2, F:4, H:2, J:2 | 95-111, 161-189 | 90, 307 |
| gbs1311 | transposase, C-terminal part | 21-27,35-45,70-76,92-105,129-143,145-155,161-166,170-191,204-211,214-231,234-246,249-255,259-275 | F:3 | 1-18 | 91, 308 |
| gbs1321 | hypothetical protein | 21-35,45-53,56-64,69-97 | F:7 | 1-16 | 92, 309 |
| gbs1352 | putative helicase and methylase | 25-33,41-47,61-68,86-101,106-114,116-129,134-142,144-156,163-176,181-190,228-251,255-261,276-292,295-305,334-357,368-380,395-410,424-429,454-460,469-482,510-516,518-527,531-546,558-570,579-606,628-636,638-645,651-656,668-674,691-698,717- | E:3, H:2, M:4 | 748-847, 1381-1391 | 93, 310 |

| S. agalactiae antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| | | 734,742-754,765-770,792-797,827-835,847-859,874-881,903-909,926-933,942-961,964-977,989-1004,1010-1028,1031-1047,1057-1075,1081-1095,1108-1117,1138-1144,1182-1189,1193-1206,1220-1229,1239-1246,1257-1267,1271-1279,1284-1301,1312-1320,1329-1335,1341-1347,1358-1371,1399-1404,1417-1426,1458-1463,1468-1476,1478-1485,1493-1506,1535-1541,1559-1574,1583-1590,1595-1601,1603-1611,1622-1628,1634-1644,1671-1685,1689-1696,1715-1720,1734-1746,1766-1775,1801-1806,1838-1844,1858-1871,1910-1917,1948-1955,1960-1974,2000-2015,2019-2036,2041-2063 | | | |
| gbs1356 | Putative peptidoglycan linked protein (LPXTG motif) - Agglutinin receptor | 5-12,18-24,27-53,56-63,96-113,119-124,131-136,157-163,203-209,215-223,233-246,264-273,311-316,380-389,393-399,425-433,445-450,457-462,464-470,475-482,507-513,527-535,542-548,550-565,591-602,607-613,627-642,644-664,673-712,714-732,739-764,769-782,812-818,826-838,848-854,860-871,892-906,930-938,940-954,957-973,990-998,1002-1021,1024-1033,1037-1042,1050-1060,1077-1083,1085-1092,1100-1129,1144-1161,1169-1175,1178-1189,1192-1198,1201-1207,1211-1221,1229-1239,1250-1270,1278-1292,1294-1300,1314-1335,1344-1352,1360-1374,1394-1405,1407-1414,1416-1424,1432-1452,1456-1462,1474-1497,1500-1510,1516-1522,1534-1542,1550-1559,1584-1603,1608-1627 | C:5, D:62, I:22 | 187-273, 306-441 | 94, 311 |
| gbs1376 | similar to ATP-dependent Clp proteinase (ATP-binding subunit), ClpL | 70-80,90-97,118-125,128-140,142-148,154-162,189-202,214-222,224-232,254-260,275-313,317-332,355-360,392-398,425-432,448-456,464-470,476-482,491-505,521-528,533-546,560-567,592-597,605-614,618-626,637-644,646-653,660-666,677-691 | K:4 | 207-227 | 95, 312 |
| gbs1377 | similar to homocysteine S- | 5-19,26-34,37-55,57-66,69-83,86-102,115-134,138-143,154-172,178-195,209-246,251- | M:2 | 256-266 | 96, 313 |

| S. agalactiae antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| | methyltransferase | 257,290-302,306-311 | | | |
| gbs1386 | hydroxy-3-methylglutaryl-coenzyme A synthase | 10-20,22-28,35-57,72-79,87-103,108-128,130-144,158-171,190-198,225-242,274-291,301-315,317-324,374-385 | G:2 | 353-365 | 97, 314 |
| gbs1390 | hypothetical protein | 4-9,17-30,34-54,59-66,73-94,118-130,135-150,158-171,189-198,219-239,269-275,283-301 | E:3, K:4 | 89-106, 176-193 | 98, 315 |
| gbs1391 | hypothetical protein | 14-20,22-74,77-86,89-99,104-109,126-135,154-165,181-195,197-212,216-224,264-275 | E:3 | 107-118 | 99, 316 |
| gbs1403 | similar to 5'-nucleotidase, putative peptidoglycan bound protein (LPXTN) | 4-18,21-38,63-72,101-109,156-162,165-179,183-192,195-210,212-218,230-239,241-256,278-290,299-311,313-322,332-341,348-366,386-401,420-426,435-450,455-460,468-479,491-498,510-518,532-538,545-552,557-563,567-573,586-595,599-609,620-626,628-636,652-657,665-681 | A:3, C:12, D:4, J:2 | 1-198 | 100, 317 |
| gbs1408 | Similar to ABC transporter (ATP-binding protein) | 4-10,16-38,51-68,73-79,94-115,120-125,132-178,201-208,216-223,238-266,269-295,297-304,337-342,347-356,374-401,403-422,440-447,478-504,510-516,519-530,537-544 | D:2, K:4 | 191-206 | 101, 318 |
| gbs1420 | similar to cell wall proteins, putative peptidoglycan linked protein (LPXTG motif) | 12-40,42-48,66-71,77-86,95-102,113-120,129-137,141-148,155-174,208-214,218-225,234-240,256-267,275-283,300-306,313-321,343-350,359-367,370-383,398-405,432-439,443-461,492-508,516-526,528-535 | C:3, D:4 | 370-478 | 102, 319 |
| gbs1429 | hypothetical protein | 6-14,20-37,56-62,90-95,97-113,118-125,140-145,161-170,183-202,237-244,275-284,286-305,309-316,333-359,373-401,405-412 | B:2, C:2 | 176-187 | 103, 320 |
| gbs1442 | hypothetical thiamine biosynthesis protein, ThiI | 33-44,50-55,59-80,86-101,129-139,147-153,157-163,171-176,189-201,203-224,239-245,257-262,281-287,290-297,304-320,322-331,334-350,372-390,396-401 | L:28 | 71-88, 353-372 | 104, 321 |
| gbs1452 | rplT 50S ribosomal protein L20 | 5-11,15-24,26-33,40-47,75-88,95-103,105-112 | E:2 | 17-30 | 105, 322 |
| gbs1464 | ferrichrome ABC transporter (permease) | 5-11,16-39,46-54,62-82,100-107,111-124,126-150,154-165,167-183,204-238,245-295,301-313,316-335 | F:4 | 8-16 | 106, 323 |

| S. agalactiae antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| gbs1470 | conserved hypothetical protein | 4-19,34-48,69-74,79-107,115-127,129-135,143-153,160-169,171-182 | I:4 | 142-153 | 107, 324 |
| gbs1528 | conserved hypothetical protein | 4-30,65-74,82-106,110-120,124-132,135-140,146-175,179-184,190-196,217-223,228-233,250-267,275-292,303-315,322-332 | I:7 | 174-186 | 108, 325 |
| gbs1529 | Putative peptidoglycan bound protein (LPXTG motif) | 9-16,29-41,47-57,68-84,87-109,113-119,162-180,186-193,195-201,203-208,218-230,234-243,265-271,281-292,305-312,323-332,341-347,349-363,368-374,383-390,396-410,434-440,446-452,455-464,466-473,515-522,529-542,565-570,589-600,602-613,618-623,637-644,1019-1027,1238-1244,1258-1264,1268-1276,1281-1292,1296-1302 | C:2 | 883-936 | 109, 326 |
| gbs1531 | UvrB excinuclease ABC chain B | 10-17,23-32,39-44,54-72,75-81,88-111,138-154,160-167,178-185,201-210,236-252,327-334,336-342,366-376,388-400,410-430,472-482,493-526,552-558,586-592,598-603,612-621,630-635,641-660 | M:2 | 384-393 | 110, 327 |
| gbs1533 | glutamine ABC transporter, glutamine-binding protein | 4-22,24-39,50-59,73-84,100-105,111-117,130-138,155-161,173-178,182-189,205-215,266-284,308-313,321-328,330-337,346-363,368-374,388-395,397-405,426-434,453-459,482-492,501-507,509-515,518-523,527-544,559-590,598-612,614-629,646-659,663-684,686-694,698-721 | I:4 | 445-461 | 111, 328 |
| gbs1536 | hypothetical protein | 14-22,27-33 | E:10 | 3-17 | 112, 329 |
| gbs1542 | oxidoreductase, aldo/keto reductase family | 29-41,66-73,81-87,90-108,140-146,150-159,165-184,186-196,216-226,230-238,247-253,261-269 | I:13 | 126-140 | 113, 330 |
| gbs1547 | small protein, SmpB | 5-12,16-25,27-33,36-45,60-68,83-88,103-126 | L:11 | 86-101 | 114, 331 |
| gbs1565 | hypothetical protein | 14-23,36-47,56-66,84-89,94-105,111-127,140-153,160-174,176-183,189-203,219-225,231-237,250-257 | F:2, J:2, K:8, L:21 | 194-227 | 115, 332 |
| gbs1586 | peptidyl-prolyl cis-trans isomerase, cyclophilin-type | 4-25,54-60,64-71,73-82,89-106,117-124,157-169,183-188,199-210,221-232,236-244,255-264 | E:3 | 58-98 | 116, 333 |
| gbs1591 | S-methylthioadenosine nucleosidase/S-adenosylhomocysteine | 13-19,26-36,41-53,55-71,77-84,86-108,114-135,157-172,177-183,187-194,208-213,218-226 | I:18, L:2 | 110-125, 156-170 | 117, 334 |

| *S. agalactiae* antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| | nucleosidase (pfs) | | | | |
| gbs1632 | similar to branched-chain amino acid ABC transporter, amino acid-binding protein | 5-24,63-69,77-85,94-112,120-137,140-146,152-159,166-172,179-187,193-199,206-212,222-228,234-240,244-252,257-264,270-289,298-309,316-328,337-348,363-375 | B:2, E:4, I:3 | 1-56, 340-352 | 118, 335 |
| gbs1638 | amino acid permease | 18-39,42-71,78-120,124-144,152-173,179-189,199-209,213-222,228-258,269-304,329-361,364-372,374-389,396-441 | E:8, G:9, H:9 | 313-327 | 119, 336 |
| gbs1662 | conserved hypothetical protein | 19-25,91-98,108-120,156-162,168-174,191-204,211-216,232-266,272-278,286-308,316-321,327-333,344-355,358-364,384-391,395-428,464-476,487-495,497-511,544-561,563-573,575-582,588-594 | E:3, H:2 | 10-25, 322-338 | 120, 337 |
| gbs1666 | SWI/SNF family helicase | 14-26,32-49,51-57,59-72,80-91,102-112,119-125,147-161,164-173,175-183,188-213,217-222,246-254,260-276,282-303,308-318,321-328,333-350,352-359,371-378,392-401,407-414,416-443,448-463,471-484,490-497,501-514,519-527,539-551,557-570,578-590,592-598,600-610,618-629,633-647,654-667,676-689,702-709,718-726,728-737,741-760,764-780,786-795,808-826,836-842,845-852,865-874,881-887,931-945,949-957,968-974,979-986,1003-1009,1023-1029 | F:4 | 90-103 | 121, 338 |
| gbs1673 | conserved hypothetical protein | 11-16,37-56,60-66,69-77,80-88,93-106,117-139,166-171 | E:2 | 72-90 | 122, 339 |
| gbs1695 | dihydroxyacetone kinase family protein | 59-84,123-133,145-150,161-167,178-189 | I:8 | 115-128 | 123, 340 |
| gbs1754 | excinuclease ABC, A subunit (uvrA) | 15-33,39-46,52-64,74-87,108-124,127-144,150-156,173-179,184-194,201-208,219-236,243-269,272-295,302-309,343-349,356-361,370-379,405-411,414-423,430-451,457-464,466-475,477-483,496-502,507-522,541-548,557-563,571-577,579-585,590-605,626-642,650-662,671-691,704-710,751-769,775-781,786-791,794-829,851-858,868-878,884-904,913-919,931-939 | I:2 | 132-142 | 124, 341 |
| gbs1760 | Similar to A/G- | 33-58,64-71,74-80,83-88,96-120,122- | K:8 | 97-115, 199- | 125, 342 |

| S. agalactiae antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| | specific adenine glycosylase | 139,146-157,167-177,207-213,220-225,236-242,264-279,300-305,326-336,340-347,350-360 | | 211 | |
| gbs1777 | glycerol uptake facilitator protein, putative | 4-26,43-57,70-99,102-117,121-133,142-148,151-168,170-183,192-220,235-249,258-279 | E:4 | 30-41 | 126, 343 |
| gbs1783 | polyprenyl synthetase family protein | 34-42,48-58,70-94,110-130,154-160,164-172,178-183,195-203,211-222,229-250,256-261,274-284,286-292,312-323 | I:3 | 222-233 | 127, 344 |
| gbs1784 | ABC transporter, ATP-binding protein CydC | 4-9,15-36,38-45,49-74,78-88,100-112,136-191,211-220,226-233,239-246,254-274,287-307,316-322,342-353,356-366,373-378,384-393,405-431,449-457,459-468,487-511,515-524,529-541,544-552,562-568,571-576 | C:2, D:2 | 208-280 | 128, 345 |
| gbs1790 | hypothetical protein | 10-27,31-37,39-54,71-108,124-143 | A:23, C:6 | 2-107 | 129, 346 |
| gbs1805 | Similar to secreted unknown protein | 16-27,38-57,64-70,90-102,104-113,116-137,160-166 | A:197, C:2 | 1-80 | 130, 347 |
| gbs1816 | HD domain protein | 13-21,31-36,56-67,127-136,153-171,173-180,184-200,214-222,225-231,239-263,267-273 | F:8 | 135-159 | 131, 348 |
| gbs1821 | Similar to 23S ribosomal RNA methyltransferase | 12-27,31-51,68-74,77-87,94-101,108-114,117-123,127-134,138-168,173-196,201-207,212-217,227-237,247-257,264-280 | K:5 | 205-223 | 132, 349 |
| gbs1823 | triad family protein | 17-22,25-54,70-76,92-100 | G:6, H:3 | 98-110 | 133, 350 |
| gbs1834 | two-component sensor histidine kinase | 7-29,40-50,60-67,87-96,105-111,119-164,172-199,206-212,220-227,237-259,272-279,282-293,295-309,313-319,321-328,345-363,376-386 | E:3, F:6 | 159-176 | 134, 351 |
| gbs1842 | transcriptional antiterminator, BglG family | 4-19,24-30,36-43,50-68,71-89,93-106,141-152,154-172,179-197,199-215,229-239,246-252,255-263,281-298,319-325,329-356,358-368,374-390,397-409,420-429,432-444,450-456,459-475,483-494,496-502,520-528,532-556 | I:19 | 362-377 | 135, 352 |
| gbs1850 | hypothetical transaldolase | 18-25,40-62,77-85,91-97,105-116,123-133,139-184,189-197 | G:2 | 122-140 | 136, 353 |
| gbs1869 | phosphoglycerate kinase | 4-49,52-58,62-70,79-105,109-133,142-150,163-168,206-214,220-228,233-240,243- | L:9 | 643-658 | 137, 354 |

| S. agalactiae antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| | | 254,274-281,303-311,327-338,357-373,378-396,403-413,420-436,441-453,461-467,475-481,484-498,506-512,514-521,523-529,562-579,589-595,598-603,615-648,714-722,728-742,749-758,777-792,795-807 | | | |
| gbs1875 | alkyl hydroperoxide reductase (large subunit) and NADH dehydrogenase | 8-27,37-48,51-56,72-79,87-106,120-138,140-147,167-176,187-197,205-216,222-229,234-239,243-249,277-288,292-315,334-343,347-353,363-391,398-404,430-447,461-467,478-492,498-507 | F:3 | 456-470 | 138, 355 |
| gbs1879 | endopeptidase O (pepO) | 5-12,18-24,59-69,80-93,95-109,119-125,130-137,139-147,158-163,168-176,182-202,206-215,222-239,241-249,267-277,291-298,311-318,321-327,338-344,348-355,373-386,393-406,411-417,434-443,446-465,473-484,514-521,532-553,584-594 | I:26 | 221-237 | 139, 356 |
| gbs1893 | 2-keto-3-deoxygluconate kinase | 4-14,27-34,50-58,63-72,79-106,109-114,121-142,146-154,161-167,169-175,178-201,223-238,249-254,259-264,278-292,294-312,319-330 | F:8, K:9 | 167-191 | 140, 357 |
| gbs1899 | N-acetylmuramoyl-L-alanine amidase, family 4 protein | 7-28,36-42,50-61,63-80,122-152,161-174,176-191 | B:2, C:2, E:3 | 140-190 | 141, 358 |
| gbs1907 | citrate carrier protein, CCS family | 20-57,59-65,70-78,86-102,119-133,142-161,163-173,177-188,192-202,204-220,222-236,240-253,279-319,326-331,337-383,390-399,406-412,420-427,431-438 | I:2 | 381-395 | 142, 359 |
| gbs1924 | similar to pneumococcal histidine triad protein B precursor (C-terminal part) | 13-18,28-34,37-43,50-59,75-81,83-97,105-121,139-147,200-206,209-227,231-247,260-271,318-327,366-381,388-394,399-406 | K:3 | 182-201 | 143, 360 |
| gbs1925 | similar to pneumococcal histidine triad protein B precursor (N-terminal part) | 6-29,37-43,51-56,70-77,82-102,110-119,127-143,178-190,201-209,216-243,261-269,281-292,305-313,327-339,341-354,356-373,391-397,423-429,438-445,450-478 | A:2, B:5, C:12, D:57 | 21-314 | 144, 361 |
| gbs1962 | conserved hypothetical protein | 4-12,15-21,32-41,59-76,80-89,96-104 | E:3 | 90-103 | 145, 362 |

| S. *agalactiae* antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| gbs2008 | similar to C5A peptidase, putative peptidoglycan linked protein (LPXTG motif) | 9-28,30-41,44-54,69-74,77-82,90-97,104-123,125-135,149-155,164-173,177-184,217-226,230-235,238-244,258-272,282-297,300-305,309-315,317-322,327-336,348-362,368-374,380-387,400-411,414-424,451-458,460-466,483-494,497-503,506-511,521-528,540-553,569-587,598-606,628-642,661-681,688-700,718-733,740-749,752-764,769-783,823-834,848-854,862-872,878-884,886-898,915-920,938-951,954-961,963-972,982-989,996-1003,1010-1016,1021-1032,1038-1044,1047-1057,1060-1070,1079-1088,1094-1102,1117-1127,1129-1135,1142-1153,1158-1204,1212-1229,1234-1263,1269-1277,1308-1313,1327-1338,1344-1376,1400-1415,1436-1443,1448-1458,1497-1504,1511-1522,1544-1566 | A:253, B:2, C:3, D:6, H:2 | 3-82, 509-576 | 146, 363 |
| gbs2018 | putative peptidoglycan linked protein (LPXTG motif) | 8-36,40-64,71-79,88-94,102-109,118-127,138-148,151-159,163-174,192-198,200-206,220-233,268-273,290-301,304-309,316-323,331-349,378-391,414-420,427-437,455-475,494-510,541-547,549-555,616-640 | A:132, B:6, C:13, D63, E:15, H:2, J:9, K:13 | 1-60, 55-139, 212-308, 386-458, 458-624 | 147, 364 |
| gbs2029 | hypothetical protein | 16-31,35-42,70-77,91-101,120-130,132-140,143-153,185-190,195-202,215-222,228-238,241-251,257-264,268-277,288-302,312-324,326-333,341-348,364-382,415-429,438-454,458-466,491-499,501-521 | G:8 | 273-281 | 148, 365 |
| gbs2042 | hypothetical protein | 8-14,32-57,74-149,155-177,179-212,221-266,271-296,304-324,329-346,349-359,368-401,413-419,426-454,465-478,493-510 | L:11 | 466-490 | 149, 366 |
| gbs2054 | DNA mismatch repair protein HexA | 22-28,33-51,64-89,96-119,126-132,138-146,152-159,161-169,172-179,193-198,205-211,221-231,235-254,273-280,297-303,312-320,328-346,351-373,378-384,391-398,448-454,460-468,470-481,516-558,574-593,597-602,613-623,626-646,649-656,668-673,675-683,696-708,715-722,724-739,745-751,759-777,780-804,816-822 | E:8 | 102-113 | 150, 367 |
| gbs2058 | hypothetical protein | 12-28,41-91,98-107,112-120,125-131,151-193,215-221,240-250,263-280 | L:3 | 128-138 | 151, 368 |

| *S. agalactiae* antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| gbs2060 | aspartyl-tRNA synthetase (aspS) | 16-24,32-38,46-62,68-81,90-105,127-133,144-150,160-166,178-184,186-202,210-219,232-240,252-258,264-273,293-324,337-344,349-357,360-369,385-398,410-416,419-427,441-449,458-476,508-515,523-539,544-549,562-569,571-579 | I:3, L:12 | 96-109, 127-139 | 152, 369 |
| gbs2075 | hypothetical protein | 19-25,28-34,56-61,85-97,110-116 | M:2 | 39-53 | 153, 370 |
| gbs2106 | protein of unknown function/lipoprotein, putative | 4-37,41-50,62-72,91-97,99-109,114-125,136-141,149-158,160-166,201-215 | A:5, B:6, C:4, D:14, E:11, I:8, K:23 | 27-225 | 154, 371 |
| gbs2118 | similar to inosine monophosphate dehydrogenase | 15-31,44-51,96-105,122-130,149-157,162-168,178-183,185-192,198-204,206-213,221-234,239-245,248-255,257-266,289-335,349-357,415-422,425-441,448-454,462-468 | K:17 | 463-481 | 155, 372 |
| gbs2131 | ABC transporter, permease protein, putative | 5-31,39-55,63-72,76-99,106-155,160-177,179-199,207-217,223-240,245-255,261-267,294-316,321-343,354-378,382-452,477-488,529-536,555-569,584-591,593-612,620-627,632-640,647-654,671-680,698-704,723-730,732-750,769-775,781-788,822-852 | I:2 | 505-525 | 156, 373 |
| | | | | | |
| ARF0112 | Hypothetical protein | none | F:6 | 3-18 | 157, 374 |
| ARF0147 | Hypothetical protein | 4-14 | E:3, I:3 | 12-24 | 158, 375 |
| ARF0532 | Hypothetical protein | 4-11,22-30 | F:10 | 12-25 | 159, 376 |
| ARF0534 | Hypothetical protein | 5-12 | E:2, G:2 | 4-18 | 160, 377 |
| ARF0557 | Hypothetical protein | 4-28 | E:2, G:6, H:4 | 7-14 | 161, 378 |
| ARF0862 | Hypothetical protein | 6-16 | G:7, H:4 | 8-16 | 162, 379 |
| ARF0891 | Hypothetical protein | 4-15,18-33 | K:6 | 24-36 | 163, 380 |
| ARF0895 | Hypothetical protein | 4-10,16-21 | I :21 | 20-31 | 164, 381 |
| ARF0943 | Hypothetical protein | none | C:2, K:9 | 6-19 | 165, 382 |
| ARF0973 | Hypothetical protein | 11-18 | D:2, G:3, H:8, I:2, K:2 | 3-10 | 166, 383 |
| ARF0999 | Hypothetical protein | 13-24 | B:4, K:3 | 3-15 | 167, 384 |
| ARF1010 | Hypothetical protein | 15-27 | K:2 | 7-16 | 168, 385 |
| ARF1230 | Hypothetical protein | 11-16 | K:11 | 1-15 | 169, 386 |
| ARF1503 | Hypothetical protein | 4-16 | E:13 | 9-21 | 170, 387 |
| ARF1556 | Hypothetical protein | 4-24,40-48,54-67 | F:2 | 22-39 | 171, 388 |

| *S. agalactiae* antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| ARF1585 | Hypothetical protein | 6-30,34-55,62-68,78-106 | I:5, J:4 | 68-74 | 172, 389 |
| ARF1588 | Hypothetical protein | none | I:2 | 3-14 | 173, 390 |
| ARF1735 | Hypothetical protein | 9-19 | I:13 | 6-21 | 174, 391 |
| ARF1809 | Hypothetical protein | 4-17 | H:2, L:17 | 1-9 | 175, 392 |
| ARF1826 | Hypothetical protein | 5-30 | I:6 | 1-8 | 176, 393 |
| ARF1882 | Hypothetical protein | 4-16,23-46,51-56 | K:23 | 45-55 | 177, 394 |
| ARF1996 | Hypothetical protein | none | F:3 | 7-16 | 178, 395 |
| CRF0123 | Hypothetical protein | none | F:32 | 2-14 | 179, 396 |
| CRF0180 | Hypothetical protein | 4-36,43-65 | E:6, G:6, H:12 | 50-62 | 180, 397 |
| CRF0208 | Hypothetical protein | 10-30 | I:2 | 14-21 | 181, 398 |
| CRF0258 | Hypothetical protein | 9-17 | I:2 | 1-10 | 182, 399 |
| CRF0285 | Hypothetical protein | 4-12 | F:2 | 3-16 | 183, 400 |
| CRF0311 | Hypothetical protein | 4-15 | H:4 | 5-23 | 184, 401 |
| CRF0446 | Hypothetical protein | none | L:20 | 10-21 | 185, 402 |
| CRF0455 | Hypothetical protein | none | F:5 | 6-16 | 186, 403 |
| CRF0491 | Hypothetical protein | 4-29,31-38 | G:4 | 2-14 | 187, 404 |
| CRF0520 | Hypothetical protein | 4-35 | H:4 | 33-42 | 188, 405 |
| CRF0530 | Hypothetical protein | none | G:13, H:8, K:3 | 2-17 | 189, 406 |
| CRF0570 | Hypothetical protein | 9-18,30-35 | I:2 | 15-33 | 190, 407 |
| CRF0649 | Hypothetical protein | 4-9 | G:8, H:6 | 6-12 | 191, 408 |
| CRF0853 | Hypothetical protein | none | I:6 | 3-17 | 192, 409 |
| CRF0955 | Hypothetical protein | 12-21,37-44,52-61,72-80 | E:7, L:44 | 38-48 | 193, 410 |
| CRF0983.1 | Hypothetical protein | 4-10,29-44,54-61,69-78 | K:59 | 13-27 | 194, 411 |
| CRF0983.2 | Hypothetical protein | 13-23,36-53 | L:33 | 2-15 | 195, 412 |
| CRF1083 | Hypothetical protein | 4-25,28-46,56-72,81-99,120-132,134-142,154-160 | F:18 | 129-141 | 196, 413 |
| CRF1095 | Hypothetical protein | 4-15,24-33,35-41,64-86 | L:15 | 21-33 | 197, 414 |
| CRF1212.1 | Hypothetical protein | 9-15 | I:5 | 4-13 | 198, 415 |
| CRF1212.2 | Hypothetical protein | 4-11,13-19,34-48 | L:30 | 15-32 | 199, 416 |
| CRF1290 | Hypothetical protein | 4-21 | I:7 | 11-31 | 200, 417 |
| CRF1383 | Hypothetical protein | 23-57 | K:13 | 38-50 | 201, 418 |
| CRF1416 | Hypothetical protein | 4-32 | E:16, J:7 | 3-13 | 202, 419 |
| CRF1500 | Hypothetical protein | 4-10,13-25,32-42,56-68,72-84 | E:16 | 26-38 | 203, 420 |
| CRF1513 | Hypothetical protein | 4-20,31-48,52-58,65-71,80-93,99-108,114-123 | I:2 | 37-49 | 204, 421 |

| S. agalactiae antigenic protein | Putative function (by homology) | predicted immunogenic aa** | No. of selected clones per ORF and screen | Location of identified immunogenic region (aa) | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|---|
| CRF1518 | Hypothetical protein | 6-12,14-20 | F:28 | 3-25 | 205, 422 |
| CRF1663 | Hypothetical protein | 14-25,27-38 | F:10 | 5-14 | 206, 423 |
| CRF1667 | Hypothetical protein | 4-41,57-105,109-118,123-136,144-152 | G:4 | 86-99 | 207, 424 |
| CRF1832 | Hypothetical protein | None | E:5, L:8 | 6-19 | 208, 425 |
| CRF1866 | Hypothetical protein | none | G:3, H: 18 | 2-19 | 209, 426 |
| CRF1892 | Hypothetical protein | 14-47 | L:11 | 1-14 | 210, 427 |
| CRF1942 | Hypothetical protein | 4-21,29-44 | F:14 | 2-18 | 211, 428 |
| CRF1992 | Hypothetical protein | 23-29 | K:10 | 10-28 | 212, 429 |
| CRF2047 | Hypothetical protein | 6-16,22-36 | K:9 | 11-22 | 213, 430 |
| CRF2050 | Hypothetical protein | 4-19,30-44 | I:2 | 18-27 | 214, 431 |
| CRF2096 | Hypothetical protein | 5-15,37-45,58-65 | G:2 | 38-47 | 215, 432 |
| CRF2113 | Hypothetical protein | 4-15,23-34 | I:5 | 4-15 | 216, 433 |
| NRF1311 | transposase, C-terminal part | 30-36,44-54,79-85,101-114,138-152,154-164,170-175,179-200,213-220,223-240,243-255,258-264,268-284 | F:3 | 10-28 | 217, 434 |

**Table 1B: Immunogenic proteins identified by amino acid sequence identity with peptides identified by bacterial surface display.** Antigenic peptides, which have been identified by bacterial surface display possess identical counterparts in the listed proteins from *S. agalactiae*. The peptides have been shown to react with multiple human sera (see table 2). Sera directed against these peptides can therefore recognize multiple proteins.

| S. agalactiae antigenic protein (new) | Identical region | Peptide sequence | Peptide name | Protein identified by BSD | Immunogenic region (aa) | Sequence ID (DNA, protein) |
|---|---|---|---|---|---|---|
| gbs0384 | 210 – 226<br>738 -753 | MEYKGNFSQKTINRFKS<br>QTQRSGKINTDFMRQL | SGO0995.1<br>SGO0995.2 | gbs0995<br>gbs0995 | 210 – 226<br>738 -753 | 435, 449 |
| gbs0393 | 326 – 344<br>326 – 348<br>338 – 354<br>371 – 392<br>801 – 809<br>877 – 901 | VKTIGYGKLTGKVNHHYVA<br>VKTIGYGKLTGKVNHHYVANKDG<br>VNHHYVANKDGSVTAFV<br>AAVNQNIVFRVLTKDGRPIFEK<br>TVIKKGTNL<br>VTHTTEKSKPVEPQKATPKAPAKGL | SGO0986.2<br>SGO1143.1<br>SGO0986.3<br>SGO1143.2<br>SGO0986.4<br>SGO0986.5 | gbs0986<br>gbs1143<br>gbs0986<br>gbs1143<br>gbs0986<br>gbs0986 | 326 – 344<br>327 - 349<br>338 – 354<br>372 - 393<br>801 – 809<br>877 - 901 | 436, 450 |
| gbs0396 | 893 - 906 | RQELLTPTQLSKLQ | SGO0983.1 | gbs0983 | 893 - 906 | 437, 451 |
| gbs0407 | 51 - 69 | VRYDKLEALVAYHGAKSAS | SGO0972.1 | gbs0972 | 51 - 69 | 438, 452 |
| gbs0408 | 110 - 125 | HQPNRIYLTDKLVPYI | SGO0971.1 | gbs0971 | 110 - 125 | 439, 453 |
| gbs0410 | 291 - 305 | QSIKQHDKEKLRTVL | SGO0969.1 | gbs0969 | 291 - 305 | 440, 454 |
| gbs0714 | 210 - 226<br>738 -753 | MEYKGNFSQKTINRFKS<br>QTQRSGKINTDFMRQL | SGO0995.1<br>SGO0995.2 | gbs0995<br>gbs0995 | 210 - 226<br>738 -753 | 441, 455 |
| gbs0723 | 326 – 344<br>326 – 348<br>338 – 354<br>371 – 392 | VKTIGYGKLTGKVNHHYVA<br>VKTIGYGKLTGKVNHHYVANKDG<br>VNHHYVANKDGSVTAFV<br>AAVNQNIVFRVLTKDGRPIFEK | SGO0986.2<br>SGO1143.1<br>SGO0986.3<br>SGO1143.2 | gbs0986<br>gbs1143<br>gbs0986<br>gbs1143 | 326 – 344<br>327 - 349<br>338 – 354<br>372 - 393 | 442, 456 |

| | | | | | | |
|---|---|---|---|---|---|---|
| | 801 – 809<br>877 – 901 | TVIKKGTNL<br>VTHTTEKSKPVEPQKATPKAPAKGL | SGO0986.4<br>SGO0986.5 | gbs0986<br>gbs0986 | 801 – 809<br>877 - 901 | |
| gbs0726 | 893 - 906 | RQELLTPTQLSKLQ | SGO0983.1 | gbs0983 | 893 - 906 | 443, 457 |
| gbs0737 | 551 - 69 | VRYDKLEALVAYHGAKSAS | SGO0972.1 | gbs0972 | 51 - 69 | 444, 458 |
| gbs0738 | 110 - 125 | HQPNRIYLTDKLVPYI | SGO0971.1 | gbs0971 | 110 - 125 | 445, 459 |
| gbs0740 | 291 - 305 | QSIKQHDKEKLRTVL | SGO0969.1 | gbs0969 | 291 - 305 | 446, 460 |
| gbs0897 | 32 - 44 | EGDVLLHIMSDKT | SGO0898.1 | gbs0898 | 32 - 44 | 447, 461 |
| gbs0966 | 399 -410 | PGLTVEEKFVTF | SGO0144.1 | gbs0144 | 420 - 431 | 448, 462 |

**Table 2. Epitope serology with human sera**

| Peptides | positivity | aa from | aa to | Seq ID |
|---|---|---|---|---|
| gbs0012.1 | ++ | 120 | 143 | 218 |
| gbs0012.2 | + | 138 | 161 | 218 |
| gbs0012.3 | + | 156 | 179 | 218 |
| gbs0016.2 | +++ | 110 | 129 | 219 |
| gbs0016.3 | + | 168 | 184 | 219 |
| gbs0048.1 | + | 74 | 90 | 222 |
| gbs0053.1 | +++ | 759 | 773 | 223 |
| gbs0061.1 | +++ | 237 | 260 | 224 |
| gbs0084.1 | + | 265 | 284 | 225 |
| gbs0107.1 | ++ | 65 | 74 | 226 |
| gbs0108.1 | ++ | 41 | 50 | 227 |
| gbs0123.1 | + | 163 | 174 | 229 |
| gbs0127.1 | ++ | 26 | 37 | 230 |
| gbs0183.1 | + | 174 | 189 | 232 |
| gbs0235.1 | ++ | 240 | 256 | 234 |
| gbs0260.1 | + | 285 | 297 | 236 |
| gbs0286.1 | + | 238 | 247 | 238 |
| gbs0288.1 | + | 491 | 519 | 239 |
| gbs0437.1 | ++ | 114 | 140 | 243 |
| gbs0539.1 | + | 267 | 284 | 250 |
| gbs0579.1 | + | 439 | 453 | 252 |
| gbs0580.1 | ++ | 162 | 178 | 253 |
| gbs0628.1 | ++ | 347 | 364 | 254 |
| gbs0632.1 | +++ | 699 | 715 | 255 |
| gbs0634.1 | + | 60 | 71 | 256 |
| gbs0667.1 | ++ | 244 | 257 | 257 |
| gbs0672.1 | + | 44 | 63 | 258 |
| gbs0672.2 | + | 57 | 76 | 258 |
| gbs0785.1 | + | 185 | 196 | 260 |
| gbs0851.1 | + | 119 | 129 | 263 |
| gbs0896.1 | ++ | 182 | 195 | 266 |
| gbs0898.1 | ++ | 32 | 44 | 267 |
| gbs0898.2 | + | 424 | 442 | 267 |
| gbs0904.1 | + | 247 | 256 | 268 |
| gbs0918.1 | ++ | 678 | 694 | 269 |
| gbs0918.2 | + | 785 | 805 | 269 |
| gbs0918.4 | + | 55 | 77 | 269 |
| gbs0918.5 | +++ | 72 | 94 | 269 |
| gbs0995.1 | + | 210 | 226 | 281 |
| gbs1087.3 | + | 37 | 59 | 289 |
| gbs1165.1 | + | 13 | 29 | 296 |
| gbs1816.1 | + | 136 | 159 | 348 |
| gbs1821.1 | + | 205 | 222 | 349 |
| gbs1823.1 | + | 99 | 110 | 350 |
| gbs1834.1 | + | 160 | 176 | 351 |
| gbs1875.1 | + | 457 | 470 | 355 |
| gbs1879.1 | + | 221 | 237 | 356 |
| gbs1893.1 | + | 167 | 190 | 357 |
| gbs1925.1 | + | 96 | 120 | 361 |
| gbs2018.3 | +++ | 399 | 417 | 364 |
| gbs2018.4 | +++ | 503 | 519 | 364 |
| gbs2018.5 | +++ | 544 | 563 | 364 |
| gbs2106.2 | + | 46 | 68 | 371 |
| gbs2106.7 | + | 159 | 183 | 371 |
| gbs2106.8 | + | 184 | 198 | 371 |
| gbs2118.1 | ++ | 463 | 481 | 372 |

**Table 3: Gene distribution in *S. agalactiae* strains.**

| ORF | Common name | Gene distribution (present of 50) | Amino acid substitutions (in serotype IA strain)* | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|
| gbs0012 | weakly similar to beta-lactamase | 44/44 | n.d. | 1, 218 |
| gbs0016 | glucan-binding protein B (S.mutans) | 40/44 | 0/224 | 2, 219 |
| gbs0024 | Phosphoribosylformylglycinamidine | 46/46 | 10/228 | 3, 220 |
| gbs0031 | surface immunogenic protein | 46/46 | 1/225 | 4, 221 |
| gbs0048 | Unknown | 30/46 | 0/61 | 5, 222 |
| gbs0053 | aldehyde-alcohol dehydrogenase (adhE) | 45/45 | 0/224 | 6, 223 |
| gbs0061 | rplB ribosomal protein L2 | 46/46 | 0/218 | 7, 224 |
| gbs0084 | DNA-directed RNA polymerase, alpha subunit (rpoA) | 45/45 | 0/207 | 8, 225 |
| gbs0107 | conserved hypothetical protein | 46/46 | 0/235 | 9, 226 |
| gbs0108 | deoxyuridine 5'-triphosphate nucleotidohydrolase | 44/44 | 0/125 | 10, 227 |
| gbs0113 | ribose ABC transporter | 44/45 | 0/227 | 11, 228 |
| gbs0123 | similar to argininosuccinate synthase | 44/44 | 0/184 | 12, 229 |
| gbs0127 | rpmV 50S ribosomal protein L28 | 46/46 | 0/40 | 13, 230 |
| gbs0144 | oligopeptide ABC transporter, substrate-binding | 45/45 | 0/282 | 14, 231 |
| gbs0183 | membrane protein, putative | 44/44 | 0/223 | 15, 232 |
| gbs0184 | oligopeptide ABC transporter, oligopeptide-binding | 46/46 | 1/203 | 16, 233 |
| gbs0235 | glycine betaine/carnitine/choline ABC transporter | 46/46 | 0/219 | 17, 234 |
| gbs0255 | conserved hypothetical protein | 46/46 | 0/180 | 18, 235 |
| gbs0260 | glycyl-tRNA synthetase (beta subunit | 46/46 | 0/209 | 19, 236 |
| gbs0268 | transketolase (tkt) | 46/46 | 0/208 | 20, 237 |
| gbs0286 | NH3-dependent NAD+ synthetase | 45/45 | 0/191 | 21, 238 |
| gbs0288 | similar to penicillin-binding protein 1A | 45/45 | 0/212 | 22, 239 |
| gbs0343 | seryl-tRNA synthetase (serS) | 46/46 | 0/228 | 23, 240 |
| gbs0428 | similar to fibrinogen binding protein, putative peptidoglycan linked protein (LPXTG motif) | 45/46 | 1/126 | 25, 242 |
| gbs0437 | glucose-6-phosphate isomerase (pgi) | 45/45 | 0/232 | 26, 243 |
| gbs0460 | decarboxylase | 46/46 | 1/81 | 27, 244 |
| gbs0465 | oxydoreductase | 46/46 | 0/126 | 28, 245 |
| gbs0489 | acetyltransferase, GNAT family | 45/45 | 3/144 | 30, 247 |
| gbs0492 | gbs0492 valyl-tRNA synthetase | 44/44 | 3/125 | 31, 248 |
| gbs0538 | amino acid ABC transporter (ATP-binding protein) | 46/46 | 0/214 | 32, 249 |

| ORF | Common name | Gene distribution (present of 50) | Amino acid substitutions (in serotype IA strain)* | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|
| gbs0539 | similar to phosphomannomutase | 46/46 | 0/244 | 33, 250 |
| gbs0555 | beta-lactam resistance factor (fibA) | 46/46 | 0/218 | 34, 251 |
| gbs0579 | dipeptidase | 46/46 | 0/218 | 35, 252 |
| gbs0580 | zinc ABC transporter, zinc-binding adhesion liprot | 45/45 | 2/235 | 36, 253 |
| gbs0628 | cell wall surface anchor family protein - (IPxTG) | 42/44 | 0/219 | 37, 254 |
| gbs0632 | cell wall surface anchor family protein, putative (FPKTG motive) | 44/45 | 0/238 | 38, 255 |
| gbs0667 | regulatory protein, putative, truncation | 44/44 | 0/229 | 40, 257 |
| gbs0672 | transcriptional regulator (GntR family) | 43/43 | 0/203 | 41, 258 |
| gbs0687 | unknown proteins | 45/45 | 0/149 | 42, 259 |
| gbs0785 | Similar to penicillin binding protein 2B | 45/45 | 0/218 | 43, 260 |
| gbs0828 | unknown proteins | 46/46 | 1/120 | 45, 262 |
| gbs0851 | hypothetical protein | 46/46 | 0/140 | 46, 263 |
| gbs0865 | gbs0865 Unknown | 44/44 | 0/241 | 47, 264 |
| gbs0890 | exonuclease RexB (rexB) | 46/46 | 0/232 | 48, 265 |
| gbs0896 | similar to acetoin dehydrogenase | 46/46 | 0/239 | 49, 266 |
| gbs0898 | acetoin dehydrogenase, thymine PPi dependent | 45/45 | 0/180 | 50, 267 |
| gbs0904 | phosphoglucomutase/phosphomannomutase family prote | 46/46 | 0/169 | 51, 268 |
| gbs0918 | weakly similar to histidine triad protein, putative lipoprotein | 45/45 | 1/209 | 52, 269 |
| gbs0931 | pyruvate kinase | 46/46 | 0/185 | 53, 270 |
| gbs0947 | similar to L-Lactate Dehydrogenase | 46/46 | 0/233 | 54, 271 |
| gbs0948 | DNA gyrase, A subunit (gyrA) | 44/44 | 0/172 | 55, 272 |
| gbs1035 | conserved hypothetical protein | 46/46 | 0/210 | 69, 286 |
| gbs1066 | gbs1066 Unknown | 17/46 | 2/92 | 71, 288 |
| gbs1087 | highly repetitive peptidoglycan bound protein (LPXTG motif) | 42/45 | n.d. | 72, 289 |
| gbs1103 | ABC transporter (ATP-binding protein) | 46/46 | 1/165 | 73, 290 |
| gbs1116 | xanthine permease (pbuX) | 45/45 | 1/170 | 74, 291 |
| gbs1158 | Similar to oxidoreductase | 44/44 | 1/170 | 78, 295 |
| gbs1165 | cysteine desulphurase (iscS-1) | 43/43 | 0/148# | 79, 296 |
| gbs1195 | staphylokinase and streptokinase | 45/45 | 60/142 | 80, 297 |
| gbs1209 | ATP-dependent DNA helicase PcrA | 43/44 | 1/94# | 81, 298 |
| gbs1214 | conserved hypothetical protein | 43/46 | 0/97 | 82, 299 |
| gbs1260 | ABC transporter, ATP-binding protein | 44/46 | 1/198 | 84, 301 |

| ORF | Common name | Gene distribution (present of 50) | Amino acid substitutions (in serotype IA strain)* | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|
| gbs1306 | Laminin binding protein (Spellerberg,B et al 1999) | 45/46 | 0/215 | 87, 304 |
| gbs1307 | lmb laminin-binding surface protein | 45/45 | n.d. | 88, 305 |
| gbs1308 | C5a peptidase, authentic frameshift | 46/46 | 0/205 | 89, 306 |
| gbs1309 | hypothetical protein | 44/46 | 0/214 | 90, 307 |
| gbs1356 | Putative peptidoglycan linked protein (LPXTG motif) - Agglutinin receptor | 20/46 | 50/211# | 94, 311 |
| gbs1376 | similar to ATP-dependent Clp proteinase (ATP-binding subunit), ClpL | 45/45 | 0/197 | 95, 312 |
| gbs1377 | similar to homocysteine S-methyltransferase | 45/45 | 0/55 | 96, 313 |
| gbs1386 | -hydroxy-3-methylglutaryl-coenzyme A synthase | 44/44 | 0/219 | 97, 314 |
| gbs1390 | gbs1390 Unknown | 43/43 | 0/198 | 98, 315 |
| gbs1391 | gbs1391 Unknown | 44/44 | 0/214 | 99, 316 |
| gbs1403 | similar to 5'-nucleotidase, putative peptidoglycan bound protein (LPXTN) | 45/45 | 3/189 | 100, 317 |
| gbs1408 | Similar to ABC transporter (ATP-binding protein) | 45/45 | 0/205 | 101, 318 |
| gbs1429 | unknown proteins | 46/46 | 1/193 | 103, 320 |
| gbs1452 | rplT 50S ribosomal protein L20 | 46/46 | 0/101 | 105, 322 |
| gbs1464 | ferrichrome ABC transporter (permease | 44/44 | 2/232 | 106, 323 |
| gbs1470 | conserved hypothetical protein | 46/46 | 2/164 | 107, 324 |
| gbs1528 | conserved hypothetical protein | 45/45 | 0/213 | 108, 325 |
| gbs1531 | UvrB excinuclease ABC chain B | 45/45 | 0/108 | 110, 327 |
| gbs1533 | glutamine ABC transporter, glutamine-binding prote | 44/44 | 0/166 | 111, 328 |
| gbs1542 | oxidoreductase, aldo/keto reductase family | 45/45 | 1/219 | 113, 330 |
| gbs1565 | hypothetical protein | 43/43 | 1/218 | 115, 332 |
| gbs1586 | peptidyl-prolyl cis-trans isomerase, cyclophilin-type | 45/45 | 1/227 | 116, 333 |
| gbs1591 | 5-methylthioadenosine nucleosidase/S-adenosylhomoc | 45/45 | 0/203 | 117, 334 |
| gbs1632 | similar to branched-chain amino acid ABC transporter, amino acid-binding protein | 45/45 | 0/223 | 118, 335 |
| gbs1638 | amino acid permease | 45/45 | 0/100 | 119, 336 |
| gbs1662 | conserved hypothetical protein | 45/45 | 0/213 | 120, 337 |
| gbs1666 | SWI/SNF family helicase | 45/45 | 0/200 | 121, 338 |
| gbs1673 | conserved hypothetical protein | 45/45 | 0/147 | 122, 339 |
| gbs1695 | dihydroxyacetone kinase family protein | 43/43 | 1/165 | 123, 340 |

| ORF | Common name | Gene distribution (present of 50) | Amino acid substitutions (in serotype IA strain)* | Seq. ID (DNA, Prot.) |
|---|---|---|---|---|
| gbs1754 | excinuclease ABC, A subunit (uvrA) | 43/43 | 0/224 | 124, 341 |
| gbs1760 | Similar to A/G-specific adenine glycosylase | 46/46 | 0/181 | 125, 342 |
| gbs1777 | glycerol uptake facilitator protein, putative | 43/43 | 0/199 | 126, 343 |
| gbs1783 | polyprenyl synthetase family protein | 45/45 | 0/217 | 127, 344 |
| gbs1784 | ABC transporter, ATP-binding protein CydC | 45/45 | 1/220 | 128, 345 |
| gbs1790 | unknown proteins | 41/43 | 3/75# | 129, 346 |
| gbs1805 | Similar to secreted unknown proteins | 45/45 | 0/66 | 130, 347 |
| gbs1816 | HD domain protein | 43/43 | 1/176 | 131, 348 |
| gbs1821 | Similar to 23S ribosomal RNA methyltransferase | 43/43 | 2/155# | 132, 349 |
| gbs1834 | two-component sensor histidine kinase | 44/44 | 0/213 | 134, 351 |
| gbs1842 | transcriptional antiterminator, BglG family | 43/43 | 0/208 | 135, 352 |
| gbs1850 | hypothetical transaldolase | 44/44 | 0/194 | 136, 353 |
| gbs1875 | alkyl hydroperoxide reductase (large subunit) and NADH dehydrogenase | 46/46 | 0/192 | 138, 355 |
| gbs1879 | endopeptidase O (pepO) | 43/43 | 0/135 | 139, 356 |
| gbs1893 | 2-keto-3-deoxygluconate kinase | 36/46 | 0/228 | 140, 357 |
| gbs1899 | N-acetylmuramoyl-L-alanine amidase, family 4 prote | 43/43 | 0/149 | 141, 358 |
| gbs1907 | citrate carrier protein, CCS family | 43/43 | 0/219 | 142, 359 |
| gbs1925 | similar to pneumococcal histidine triad protein B precursor (N-terminal part) | 43/43 | 0/103 | 144, 361 |
| gbs1962 | conserved hypothetical protein | 28/46 | 0/136 | 145, 362 |
| gbs2008 | similar to C5A peptidase, putative peptidoglycan linked protein (LPXTG motif) | 43/43 | n.d. | 146, 363 |
| gbs2018 | putative peptidoglycan linked protein (LPXTG motif) | 43/45 | 0/104 | 147, 364 |
| gbs2029 | unknown proteins | 44/44 | 1/238 | 148, 365 |
| gbs2054 | DNA mismatch repair protein HexA | 46/46 | 0/206 | 150, 367 |
| gbs2060 | aspartyl-tRNA synthetase (aspS) | 46/46 | 2/211 | 152, 369 |
| gbs2106 | protein of unknown function/lipoprotein, putative | 44/44 | 0/160 | 154, 371 |
| gbs2118 | similar to inosine monophosphate dehydrogenase | 43/43 | 0/113 | 155, 372 |
| gbs2131 | ABC transporter, permease protein, putative | 45/45 | 0/237 | 156, 373 |

Table 4. Immunogenicity of epitopes in mice

| ORF | aa from | aa to | IB | Peptide ELISA | Seq ID |
|---|---|---|---|---|---|
| gbs0016 | 110 | 129 | + | | 219 |
| | 168 | 184 | + | | |
| gbs0986 | 877 | 901 | + | | 277 |
| | 333 | 354 | + | | |
| | 326 | 344 | + | | |
| | 801 | 809 | + | | |
| gbs1805 | 1 | 54 | | +++++ | 347 |
| gbs2018 | 544 | 563 | ++ | +++++ | 364 |
| | 31 | 51 | + | +++ | |
| | 107 | 119 | + | | |
| | 399 | 417 | ++ | ++++ | |
| | 503 | 519 | + | ++++ | |
| gbs0012 | 120 | 198 | ++ | + | 218 |
| gbs0016 | 20 | 35 | + | ++ | 219 |
| gbs0031 | 118 | 201 | | ++++ | 221 |
| gbs0428 | 48 | 132 | + | +++++ | 242 |
| gbs0538 | 118 | 136 | + | ++++ | 249 |
| gbs0580 | 162 | 178 | + | + | 253 |
| gbs0628 | 347 | 364 | + | +++++ | 254 |
| gbs0632 | 699 | 715 | + | +++++ | 255 |
| gbs0672 | 50 | 76 | | + | 258 |
| gbs0918 | 785 | 819 | + | +++++ | 269 |
| | 44 | 128 | ++ | | |
| gbs0971 | 90 | 128 | | +++++ | 274 |
| gbs1087 | 314 | 384 | + | | 289 |
| gbs1143 | 327 | 349 | | +++ | 293 |
| gbs1306 | 242 | 314 | ++ | ++++ | 304 |
| | 405 | 478 | ++ | | |
| | 23 | 100 | + | | |
| gbs1307 | 129 | 210 | ++ | | 305 |
| gbs1309 | 162 | 188 | | ++ | 307 |
| gbs1352 | 750 | 772 | ++ | +++++ | 310 |
| gbs1632 | 1 | 56 | | ++ | 335 |
| gbs1662 | 322 | 337 | + | +++++ | 337 |
| gbs1673 | 72 | 90 | + | +++++ | 339 |
| gbs1784 | 374 | 395 | | + | 345 |
| gbs1816 | 136 | 159 | + | ++++ | 348 |
| gbs1899 | 141 | 164 | + | | 358 |
| gbs1925 | 96 | 157 | ++ | + | 361 |
| gbs2008 | 1 | 82 | | + | 363 |
| gbs2018 | 489 | 556 | + | +++++ | 364 |
| gbs2106 | 159 | 183 | | ++ | 371 |
| | 49 | 133 | + | +++++ | |

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Claims:

1. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence, which is selected from the group consisting of:
   a) a nucleic acid molecule having at least 70% sequence identity to a nucleic acid molecule selected from Seq ID No 14, 90, 157-216,
   b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
   c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
   d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b), or c)
   e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid molecule defined in a), b), c) or d).

2. The isolated nucleic acid molecule according to claim 1, wherein the sequence identity is at least 80%, preferably at least 95%, especially 100%.

3. An isolated nucleic acid molecule encoding a hyperimmune serum reactive antigen or a fragment thereof comprising a nucleic acid sequence selected from the group consisting of
   a) a nucleic acid molecule having at least 96% sequence identity to a nucleic acid molecule selected from Seq ID No 1, 3, 5-13, 15, 18-25, 27-31, 33-36, 39-68, 70-85, 92-100, 103-126, 128-145, 147, 149-156, 217, 435-448,
   b) a nucleic acid molecule which is complementary to the nucleic acid molecule of a),
   c) a nucleic acid molecule comprising at least 15 sequential bases of the nucleic acid molecule of a) or b)
   d) a nucleic acid molecule which anneals under stringent hybridisation conditions to the nucleic acid molecule of a), b) or c),
   e) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

4. An isolated nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of
   a) a nucleic acid molecule selected from Seq ID No 32, 86, 91, 101, 127,
   b) a nucleic acid molecule which is complementary to the nucleic acid of a),
   c) a nucleic acid molecule which, but for the degeneracy of the genetic code, would hybridise to the nucleic acid defined in a), b), c) or d).

5. The nucleic acid molecule according to any one of the claims 1, 2, 3 or 4, wherein the nucleic acid is DNA.

6. The nucleic acid molecule according to any one of the claims 1,2, 3, 4, or 5 wherein the nucleic acid is RNA.

7. An isolated nucleic acid molecule according to any one of claims 1 to 5, wherein the nucleic acid molecule is isolated from a genomic DNA, especially from a *S. agalactiae* genomic DNA.

8. A vector comprising a nucleic acid molecule according to any one of claims 1 to 7.

9. A vector according to claim 8, wherein the vector is adapted for recombinant expression of the hyperimmune serum reactive antigens or fragment thereof encoded by the nucleic acid molecule according to any one of claims 1 to 7.

10. A host cell comprising the vector according to claim 8 or 9.

11. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 1, 2, 5, 6 or 7 and fragments thereof, wherein the amino acid sequence is selected from the group consisting of Seq ID No 231, 307, 374-433.

12. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 3, 5, 6, or 7 and fragments thereof, wherein the amino acid sueqnece is selected from the group consisting of Seq ID No 218, 220, 222-230, 232, 235-242, 244-248, 250-253, 256-285, 287-302, 309-317, 320-343, 345-362, 364, 366-373, 434, 449-462.

13. A hyperimmune serum-reactive antigen comprising an amino acid sequence being encoded by a nucleic acid molecule according to any one of the claims 4, 5, 6, or 7 and fragments thereof, wherein the amino acid sequence is selected from the group consisting of Seq ID No 249, 303, 308, 318, 344.

14. Fragments of hyperimmune serum-reactive antigens selected from the group consisting of peptides comprising amino acid sequences of column "predicted immunogenic aa" and "location of identified immunogenic region" of Table 1A, **especially peptides comprising amino acid** 4-20, 35-44, 65-70, 73-87, 92-98, 112-137, 152-161, 177-186, 193-200, 206-213, 229-255, 282-294, 308-313, 320-326, 349-355, 373-384, 388-406, 420-425 and 115-199 of Seq ID No 218; 5-24, 35-41, 44-70, 73-89, 103-109, 127-143, 155-161, 185-190, 192-207, 212-219, 246-262, 304-336, 372-382, 384-393, 398-407, 412-418, 438-444, 1-75, 76-161 and 164-239 of Seq ID No 219; 4-10, 16-58, 60-71, 77-92, 100-126, 132-146, 149-164, 166-172, 190-209, 214-220, 223-229, 241-256, 297-312, 314-319, 337-343, 351-359, 378-387, 398-418, 421-428, 430-437, 440-448, 462-471, 510-519, 525-536, 552-559, 561-568, 573-582, 596-602, 608-630, 637-649, 651-665, 681-702, 714-732, 739-745, 757-778, 790-805, 807-815, 821-829, 836-842, 846-873, 880-903, 908-914, 916-923, 931-940, 943-948, 956-970, 975-986, 996-1015, 1031-1040, 1051-1069, 1072-1095, 1114-1119, 1130-1148, 1150-1157, 1169-1176, 1229-1238 and 802-812 of Seq ID No 220; 5-12, 14-26, 35-47, 52-67, 72-78, 83-98, 121-141, 152-159, 163-183, 186-207, 209-257, 264-277, 282-299, 301-309, 312-318, 324-339, 358-368, 372-378, 387-397, 425-431 and 46-291 of Seq ID No 221; 29-38, 44-64, 70-76, 78-87, 94-100, 102-112, 119-134, 140-149, 163-173, 178-186, 188-194, 207-234, 247-262, 269-290 and 73-92 of Seq ID No 222; 10-28, 36-63, 77-87, 103-119, 127-136, 141-169, 171-183, 195-200, 207-232, 236-246, 251-265, 268-283, 287-297, 314-322, 335-343, 354-363, 384-390, 405-411, 419-436, 443-455, 467-473, 480-513, 518-529, 550-557, 565-585, 602-608, 616-625, 632-660, 665-677, 685-701, 726-736, 738-747, 752-761, 785-796, 801-813, 838-853, 866-871 and 757-774 of Seq ID No 223; 31-38, 61-66, 74-81, 90-115, 123-145, 154-167, 169-179, 182-193, 200-206, 238-244, 267-272 and 235-251 of Seq ID No 224; 19-25, 38-54, 56-64, 66-72, 74-92, 94-100, 116-129, 143-149, 156-183, 204-232, 253-266, 269-275, 294-307 and 241-313 of Seq ID No 225; 5-34, 50-56, 60-65, 74-85, 89-97, 108-119, 159-165, 181-199, 209-225, 230-240, 245-251, 257-262, 274-282, 300-305 and 64-75 of Seq ID No 226; 5-13, 16-21, 27-42, 45-52, 58-66, 74-87, 108-114, 119-131 and 39-51 of Seq ID No 227; 6-23, 46-54, 59-65, 78-84, 100-120, 128-133, 140-146, 159-165, 171-183, 190-204, 224-232, 240-248, 250-259, 274-280, 288-296, 306-315 and 267-274 of Seq ID No 228; 5-12, 15-24, 26-36, 42-65, 68-80, 82-104, 111-116, 125-144, 159-167, 184-189, 209-218, 235-243, 254-265, 269-283, 287-300, 306-316, 318-336, 338-352, 374-392 and 162-174 of Seq ID No 229; 30-42, 45-54 and 25-37 of Seq ID No 230; 10-30, 53-59, 86-95, 116-130, 132-147, 169-189, 195-201, 212-221, 247-256, 258-265, 278-283, 291-298, 310-316, 329-339, 341-352, 360-367, 388-396, 398-411, 416-432, 443-452, 460-466, 506-512, 515-521, 542-548 and 419-431 of Seq ID No 231; 4-27, 30-53, 60-67, 70-90, 92-151, 159-185, 189-195, 198-210, 215-239 and 173-189 of Seq ID No 232; 4-26, 41-54, 71-78, 116-127, 140-149, 151-158, 161-175, 190-196, 201-208, 220-226, 240-252, 266-281, 298-305, 308-318, 321-329, 344-353, 372-378, 384-405, 418-426, 429-442, 457-463, 494-505, 514-522 and 174-188

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4-40, 42-57, 73-87, 98-117, 126-135, 150-156, 166-174, 196-217, 231-236, 248-258, 276-284, 293-301, 307-313, 339-347, 359-365, 375-387, 395-402, 428-440, 445-456, 485-490, 497-505, 535-541, 547-555, 610-625, 648-656, 665-671 and 448-528 of Seq ID No 239; 10-18, 39-45, 51-61, 80-96, 98-106, 110-115, 158-172, 174-183, 191-200, 220-237, 249-255, 274-289, 308-324, 331-341, 372-381, 384-397, 405-414 and 322-338 of Seq ID No 240; 30-36, 38-56, 85-108, 134-147, 149-160, 163-183, 188-201, 206-211, 219-238, 247-254 and 5-13 of Seq ID No 241; 11-40, 98-103, 110-115, 133-145, 151-159, 172-179, 192-201, 204-212, 222-228, 235-245, 258-268, 283-296, 298-309, 322-329, 342-351, 354-362, 372-378, 385-393, 407-418, 495-516 and 1-148 of Seq ID No 242; 5-19, 21-36, 73-94, 112-119, 122-137, 139-145, 152-167, 184-190, 198-204, 208-224, 249-265, 267-281, 299-304, 309-317, 326-333, 356-364, 368-374, 381-389, 391-414, 419-425, 430-435 and 113-140 of Seq ID No 243; 45-54, 59-67, 78-91 and 15-23 of Seq ID No 244; 11-22, 33-47, 52-80, 88-112, 124-129 and 6-25 of Seq ID No 245; 26-41, 51-63, 80-89, 93-115, 150-163, 187-193, 220-237, 240-249, 286-294, 296-306, 316-329, 345-353, 361-370, 407-425, 428-437, 474-482, 484-494, 504-517, 533-541, 549-558, 595-613, 616-625, 660-668, 673-685, 711-726, 736-744, 749-761, 787-802, 812-820, 825-837, 863-878, 888-896, 901-913, 939-954, 964-972, 977-989, 1003-1008, 1016-1022, 1028-1034, 1041-1053, 1059-1074, 1101-1122, 420-511 and 581-704 of Seq ID No 246; 18-25, 27-55, 71-83, 89-95, 102-113, 120-146, 150-156, 174-185 and 159-175 of Seq ID No 247; 24-30, 38-56, 63-68, 87-93, 136-142, 153-164, 183-199, 213-219, 226-234, 244-261, 269-278, 283-289, 291-297, 320-328, 330-336, 340-346, 348-356, 358-366, 382-387, 401-408, 414-419, 449-455, 468-491, 504-512, 531-537, 554-560, 597-608, 621-627, 632-643, 650-662, 667-692, 703-716, 724-737, 743-758, 783-794, 800-818, 846-856 and 806-884 of Seq ID No 248; 4-14, 21-39, 86-92, 99-107, 121-131, 136-144, 147-154, 158-166, 176-185, 193-199, 207-222, 224-230 and 117-136 of Seq ID No 249; 65-76, 85-97, 103-109, 115-121, 125-146, 163-169, 196-205, 212-219, 228-237, 241-247, 254-262, 269-288, 294-303, 305-313, 328-367, 395-401, 405-412, 418-429, 437-447, 481-488, 506-513, 519-524, 530-541, 546-557 and 266-284 of Seq ID No 250; 5-14, 37-42, 49-71, 78-92, 97-112, 127-136, 147-154, 156-163, 186-198, 216-225, 233-243, 248-253, 295-307, 323-332, 359-366, 368-374, 380-398 and 194-223 of Seq ID No 251; 4-11, 33-39, 45-72, 100-113, 119-129, 136-144, 169-175, 177-185, 200-208, 210-219, 262-276, 278-297, 320-326, 336-344, 347-362, 381-394, 443-453 and 438-454 of Seq ID No 252; 4-29, 31-52, 55-61, 95-110, 138-158, 162-171, 179-187, 202-229, 239-248, 251-256, 262-267, 269-285, 304-310, 351-360, 362-368, 381-388, 415-428, 435-440, 448-458 and 161-178 of Seq ID No 253; 4-17, 19-28, 32-43, 47-59, 89-110, 112-126, 128-134, 140-148, 152-161, 169-184, 191-204, 230-235, 255-264, 328-338, 341-347, 401-409, 413-419, 433-441, 449-458, 463-468, 476-482, 486-492, 500-506, 529-545 and 305-381 of Seq ID No 254; 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4-13, 32-39, 53-76, 99-108, 110-116, 124-135, 137-146, 149-157, 162-174, 182-190, 207-231, 242-253, 255-264, 274-283, 291-323, 334-345, 351-360, 375-388, 418-425, 456-474, 486-492, 508-517, 520-536, 547-560, 562-577, 31-45 and 419-443 of Seq ID No 267; 15-26, 30-37, 42-49, 58-90, 93-99, 128-134, 147-154, 174-179, 190-197, 199-205, 221-230, 262-274, 277-287, 300-314, 327-333, 343-351, 359-377, 388-396, 408-413, 416-425, 431-446 and 246-256 of Seq ID No 268; 5-26, 34-42, 47-54, 61-67, 71-104, 107-115, 131-138, 144-153, 157-189, 196-202, 204-210, 228-245, 288-309, 316-329, 332-341, 379-386, 393-399, 404-412, 414-421, 457-468, 483-489, 500-506, 508-517, 523-534, 543-557, 565-580, 587-605, 609-617, 619-627, 631-636, 640-646, 662-668, 675-682, 705-710, 716-723, 727-732, 750-758, 784-789, 795-809, 869-874, 14-138, 166-286, 372-503, 674-696 and 754-859 of Seq ID No 269; 5-17, 32-38, 40-47, 80-89, 113-119, 125-137, 140-154, 157-163, 170-177, 185-199, 213-225, 228-236, 242-248, 277-290, 292-305, 323-333, 347-353, 364-370, 385-394, 399-406, 423-433, 441-451, 462-474, 477-487 and 116-124 of Seq ID No 270; 7-16, 18-30, 32-49, 53-61, 63-85, 95-101, 105-115, 119-134, 143-150, 159-178, 185-202, 212-229, 236-250, 254-265, 268-294 and 63-72 of Seq ID No 271; 4-12, 19-47, 73-81, 97-103, 153-169, 188-198, 207-213, 217-223, 236-242, 255-265, 270-278, 298-305, 309-317, 335-347, 354-363, 373-394, 419-424, 442-465, 486-492, 500-507, 542-549, 551-558, 560-572, 580-589, 607-614, 617-623, 647-653, 666-676, 694-704, 706-714, 748-754, 765-772, 786-792, 795-806 and 358-370 of Seq ID No 272; 18-28, 30-38, 40-46, 49-55, 69-78, 82-98, 104-134, 147-153, 180-190, 196-202, 218-236, 244-261, 266-273, 275-286, 290-295, 301-314, 378-387, 390-395, 427-434 and 290-305 of Seq ID No 273; 4-13, 20-31, 39-51, 54-61, 69-84, 87-105, 117-124 and 108-125 of Seq ID No 274; 24-34, 43-54, 56-66, 68-79 and 50-69 of Seq ID No 275; 5-43, 71-77, 102-131, 141-148, 150-156, 159-186, 191-207, 209-234, 255-268, 280-286, 293-299, 317-323, 350-357, 363-372, 391-397, 406-418, 428-435, 455-465, 484-497, 499-505, 525-531, 575-582, 593-607, 621-633, 638-649, 655-673, 684-698, 711-725, 736-741, 743-752, 759-769, 781-793, 813-831, 843-853, 894-905, 908-916, 929-946, 953-963, 970-978, 1001-1007, 1011-1033, 165-178 and 818-974 of Seq ID No 276; 16-44, 63-86, 98-108, 185-191, 222-237, 261-274, 282-294, 335-345, 349-362, 374-384, 409-420, 424-430, 440-447, 453-460, 465-473, 475-504, 522-534, 538-551, 554-560, 567-582, 598-607, 611-619, 627-640, 643-653, 655-661, 669-680, 684-690, 701-707, 715-731, 744-750, 756-763, 768-804, 829-837, 845-853, 855-879, 884-890, 910-928, 77-90, 144-212, 279-355, 434-536, 782-810 and 875-902 of Seq ID No 277; 4-22, 29-41, 45-51, 53-66, 70-77, 86-95, 98-104, 106-124, 129-135, 142-151, 153-161, 169-176, 228-251, 284-299, 331-337, 339-370, 380-387, 393-398, 406-411, 423-433, 440-452, 461-469, 488-498, 501-516, 523-530, 532-559, 562-567, 570-602, 612-628, 630-645, 649-659, 666-672, 677-696, 714-723, 727-747 and 212-227 of Seq ID No 278; 4-9, 17-31, 35-41, 56-61, 66-75, 81-87, 90-124, 133-138, 149-163, 173-192, 213-219, 221-262, 265-275, 277-282, 292-298, 301-307, 333-346, 353-363, 371-378, 419-430, 435-448, 456-469, 551-570, 583-599, 603-612 and 275-291 of Seq ID No 279; 28-34, 53-58, 72-81, 100-128, 145-154, 159-168, 172-189, 217-225, 227-249, 256-263, 299-309, 322-330, 361-379, 381-388, 392-401, 404-417, 425-436, 440-446, 451-464, 469-487, 502-511, 543-551, 559-564, 595-601, 606-612, 615-626, 633-642, 644-650, 664-670, 674-684, 692-701, 715-723, 726-734, 749-756, 763-771, 781-787, 810-843, 860-869, 882-889, 907-917, 931-936, 941-948, 951-958, 964-971, 976-993, 1039-1049, 1051-1065, 1092-1121, 1126-1132, 1145-1151, 1158-1173, 1181-1192, 1194-1208, 1218-1223, 1229-1243, 1249-1254, 1265-1279, 1287-1297, 1303-1320, 1334-1341, 1343-1358, 1372-1382, 1406-1417, 1419-1425, 1428-1434, 1441-1448, 1460-1473, 1494-1504, 1509-1514, 1529-1550, 654-669 and 1400-1483 of Seq ID No 280; 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152, 161-174, 176-191 and 140-190 of Seq ID No 358; 20-57, 59-65, 70-78, 86-102, 119-133, 142-161, 163-173, 177-188, 192-202, 204-220, 222-236, 240-253, 279-319, 326-331, 337-383, 390-399, 406-412, 420-427, 431-438 and 381-395 of Seq ID No 359; 13-18, 28-34, 37-43, 50-59, 75-81, 83-97, 105-121, 139-147, 200-206, 209-227, 231-247, 260-271, 318-327, 366-381, 388-394, 399-406 and 182-201 of Seq ID No 360; 6-29, 37-43, 51-56, 70-77, 82-102, 110-119, 127-143, 178-190, 201-209, 216-243, 261-269, 281-292, 305-313, 327-339, 341-354, 356-373, 391-397, 423-429, 438-445, 450-478 and 21-314 of Seq ID No 361; 4-12, 15-21, 32-41, 59-76, 80-89, 96-104 and 90-103 of Seq ID No 362; 9-28, 30-41, 44-54, 69-74, 77-82, 90-97, 104-123, 125-135, 149-155, 164-173, 177-184, 217-226, 230-235, 238-244, 258-272, 282-297, 300-305, 309-315, 317-322, 327-336, 348-362, 368-374, 380-387, 400-411, 414-424, 451-458, 460-466, 483-494, 497-503, 506-511, 521-528, 540-553, 569-587, 598-606, 628-642, 661-681, 688-700, 718-733, 740-749, 752-764, 769-783, 823-834, 848-854, 862-872, 878-884, 886-898, 915-920, 938-951, 954-961, 963-972, 982-989, 996-1003, 1010-1016, 1021-1032, 1038-1044, 1047-1057, 1060-1070, 1079-1088, 1094-1102, 1117-1127, 1129-1135, 1142-1153, 1158-1204, 1212-1229, 1234-1263, 1269-1277, 1308-1313, 1327-1338, 1344-1376, 1400-1415, 1436-1443, 1448-1458, 1497-1504, 1511-1522, 1544-1566, 3-82 and 509-576 of Seq ID No 363; 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15. A process for producing a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof according to any one of the claims 11 to 14 comprising expressing the nucleic acid molecule according to any one of claims 1 to 7.

16. A process for producing a cell, which expresses a *S. agalactiae* hyperimmune serum reactive antigen or a fragment thereof according to any one of the claims 11 to 14 comprising transforming or transfecting a suitable host cell with the vector according to claim 8 or claim 9.

17. A pharmaceutical composition, especially a vaccine, comprising a hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of claims 11 to 14 or a nucleic acid molecule according to any one of claims 1 to 7.

18. A pharmaceutical composition, especially a vaccine, according to claim 17, characterized in that it further comprises an immunostimulatory substance, preferably selected from the group comprising polycationic polymers, especially polycationic peptides, immunostimulatory deoxynucleotides (ODNs), peptides containing at least two LysLeuLys motifs, neuroactive compounds, especially human growth hormone, alumn, Freund's complete or incomplete adjuvants or combinations thereof.

19. Use of a nucleic acid molecule according to any one of claims 1 to 7 or a hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 for the manufacture of a pharmaceutical preparation, especially for the manufacture of a vaccine against *S. agalactiae* infection.

20. An antibody, or at least an effective part thereof, which binds at least to a selective part of the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14.

21. An antibody according to claim 20, wherein the antibody is a monoclonal antibody.

22. An antibody according to claim 20 or 21, wherein said effective part comprises Fab fragments.

23. An antibody according to any one of claims 20.to 22, wherein the antibody is a chimeric antibody.

24. An antibody according to any one of claims 20 to 23, wherein the antibody is a humanized antibody.

25. A hybridoma cell line, which produces an antibody according to any one of claims 20 to 24.

26. A method for producing an antibody according to claim 20, characterized by the following steps:
    - initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of the claims 11 to 14, to said animal,
    - removing an antibody containing body fluid from said animal, and
    - producing the antibody by subjecting said antibody containing body fluid to further purification steps.

27. Method for producing an antibody according to claim 21, characterized by the following steps:
    - initiating an immune response in a non-human animal by administrating an hyperimmune serum-reactive antigen or a fragment thereof, as defined in any one of the claims 12 to 15, to said animal,
    - removing the spleen or spleen cells from said animal,
    - producing hybridoma cells of said spleen or spleen cells,
    - selecting and cloning hybridoma cells specific for said hyperimmune serum-reactive antigens or a fragment thereof,
    - producing the antibody by cultivation of said cloned hybridoma cells and optionally further purification steps.

28. Use of the antibodies according to any one of claims 20 to 24 for the preparation of a medicament for treating or preventing *S. agalactiae* infections.

29. An antagonist, which binds to the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14.

30. A method for identifying an antagonist capable of binding to the hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 comprising:
   a) contacting an isolated or immobilized hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 with a candidate antagonist under conditions to permit binding of said candidate antagonist to said hyperimmune serum-reactive antigen or fragment, in the presence of a component capable of providing a detectable signal in response to the binding of the candidate antagonist to said hyperimmune serum reactive antigen or fragment thereof; and
   b) detecting the presence or absence of a signal generated in response to the binding of the antagonist to the hyperimmune serum reactive antigen or the fragment thereof.

31. A method for identifying an antagonist capable of reducing or inhibiting the interaction activity of a hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 to its interaction partner comprising:
   a) providing a hyperimmune serum reactive antigen or a hyperimmune fragment thereof according to any one of claims 11-14,
   b) providing an interaction partner to said hyperimmune serum reactive antigen or a fragment thereof, especially an antibody according to any one of the claims 20 to 24,
   c) allowing interaction of said hyperimmune serum reactive antigen or fragment thereof to said interaction partner to form a interaction complex,
   d) providing a candidate antagonist,
   e) allowing a competition reaction to occur between the candidate antagonist and the interaction complex,
   f) determining whether the candidate antagonist inhibits or reduces the interaction activities of the hyperimmune serum reactive antigen or the fragment thereof with the interaction partner.

32. Use of any of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14 for the isolation and/or purification and/or identification of an interaction partner of said hyperimmune serum reactive antigen or fragment thereof.

33. A process for *in vitro* diagnosing a disease related to expression of the hyperimmune serum-reactive antigen or a fragment thereof according to any one of claims 11 to 14 comprising determining the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen and fragment according to any one of claims 1 to 7 or the presence of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11-14.

34. A process for *in vitro* diagnosis of a bacterial infection, especially a *S. agalactiae* infection, comprising analysing for the presence of a nucleic acid sequence encoding said hyperimmune serum reactive antigen and fragment according to any one of claims 1 to 7 or the presence of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14.

35. Use of the hyperimmune serum reactive antigen or fragment thereof according to any one of claims 11 to 14 for the generation of a peptide binding to said hyperimmune serum reactive antigen or fragment thereof, wherein the peptide is selected from the group comprising anticalines.

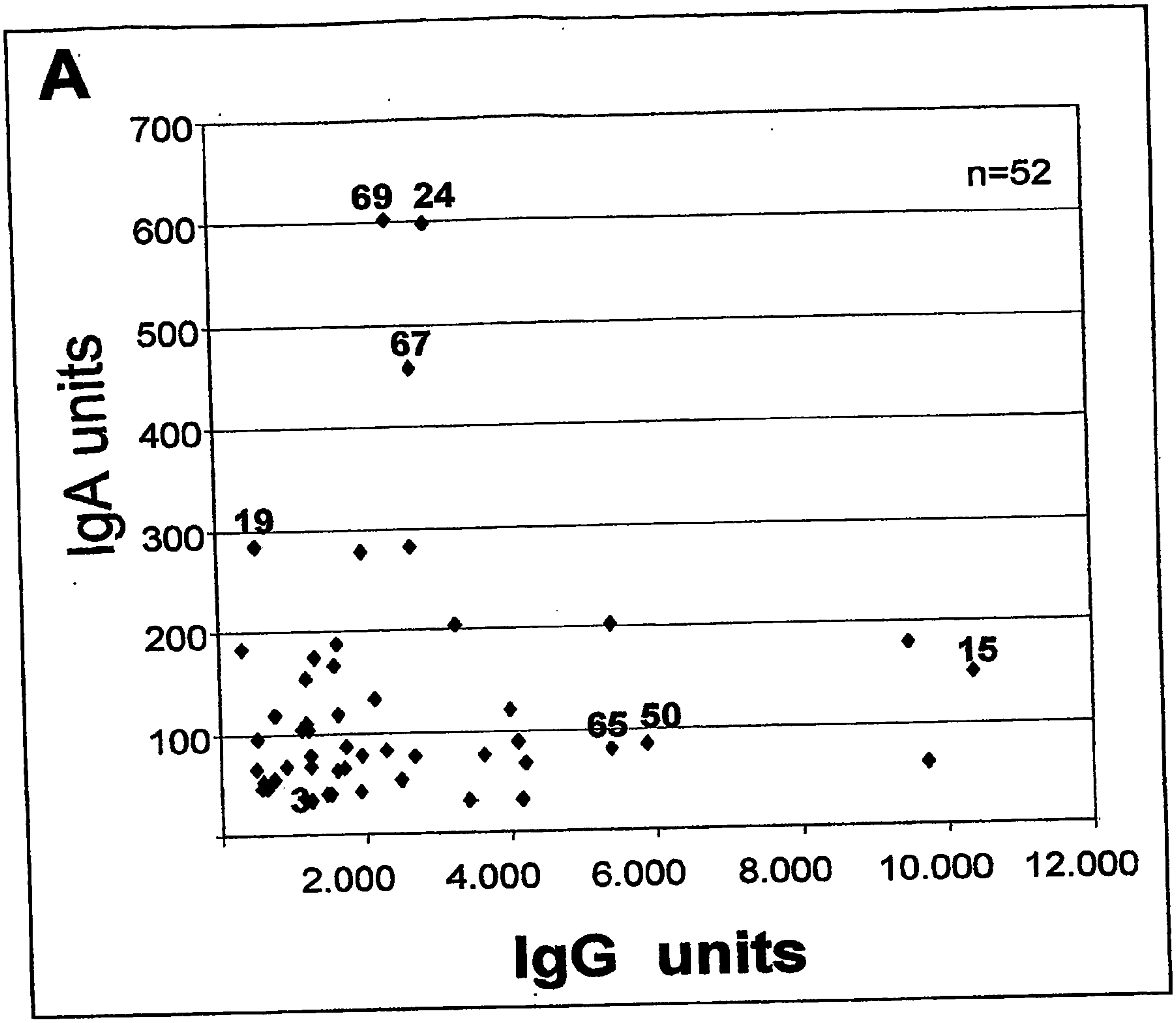
36. Use of the hyperimmune serum-reactive antigen or fragment thereof according to any one of claims 11 to 14 for the manufacture of a functional nucleic acid, wherein the functional nucleic acid is selected from the group comprising aptamers and spiegelmers.

37. Use of a nucleic acid molecule according to any one of claims 11 to 14 for the manufacture of a functional ribonucleic acid, wherein the functional ribonucleic acid is selected from the group comprising ribozymes, antisense nucleic acids and siRNA.

Summary:

The present invention discloses isolated nucleic acid molecules encoding a hyperimmune serum reactive antigen or a fragment thereof as well as hyperimmune serum reactive antigens or fragments thereof from *S. agalactiae*, methods for isolating such antigens and specific uses thereof.

[no Fig. on front page]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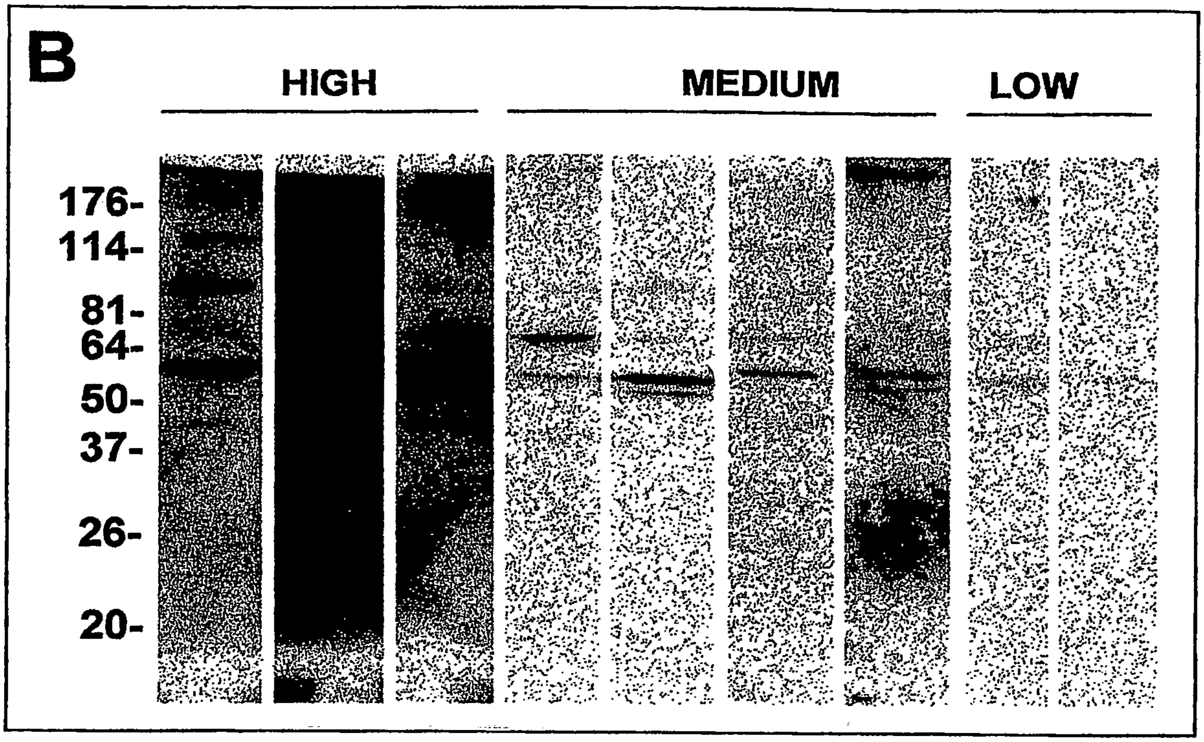
12.000
IgG units

Fig. 1



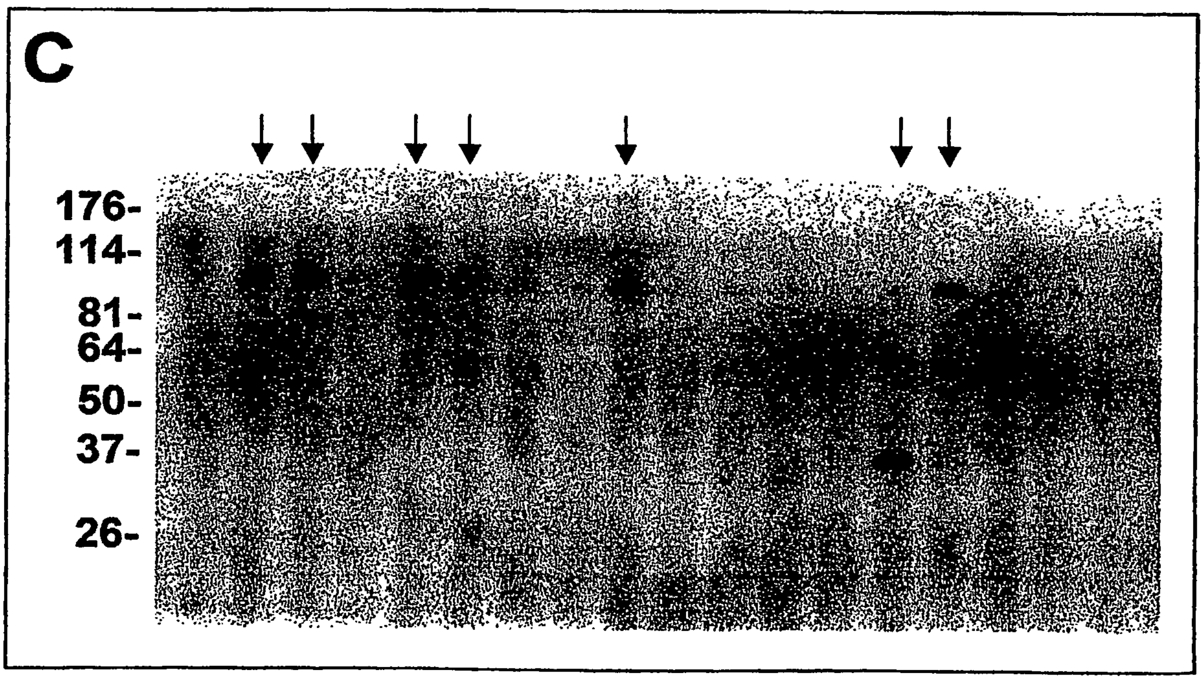
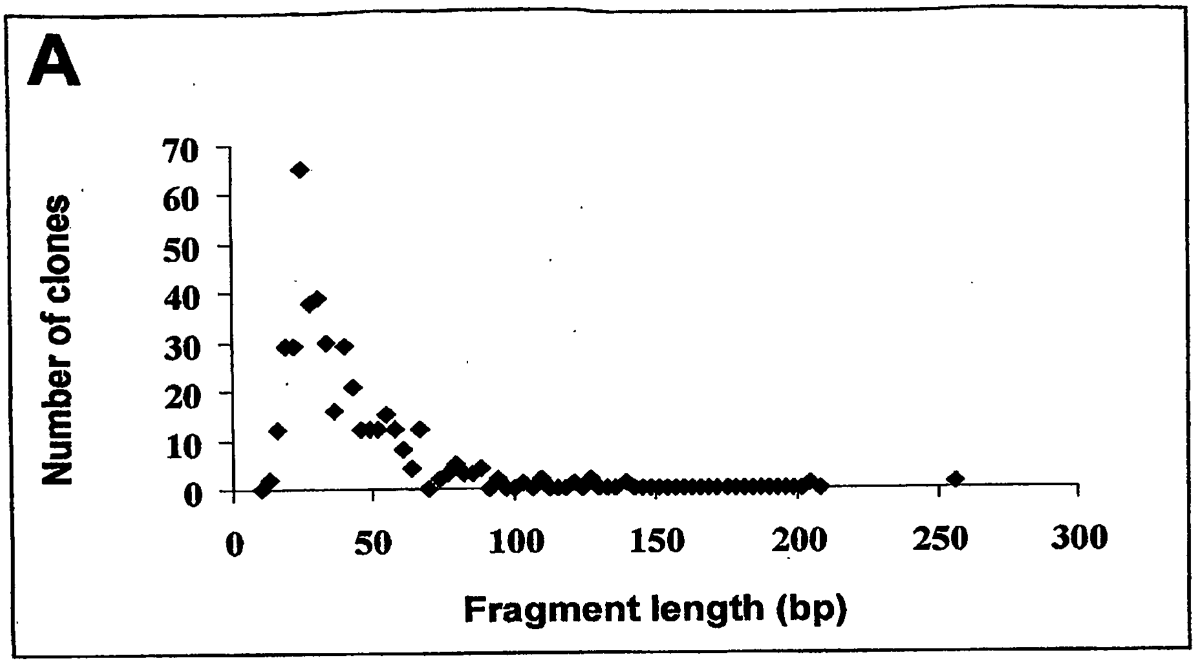
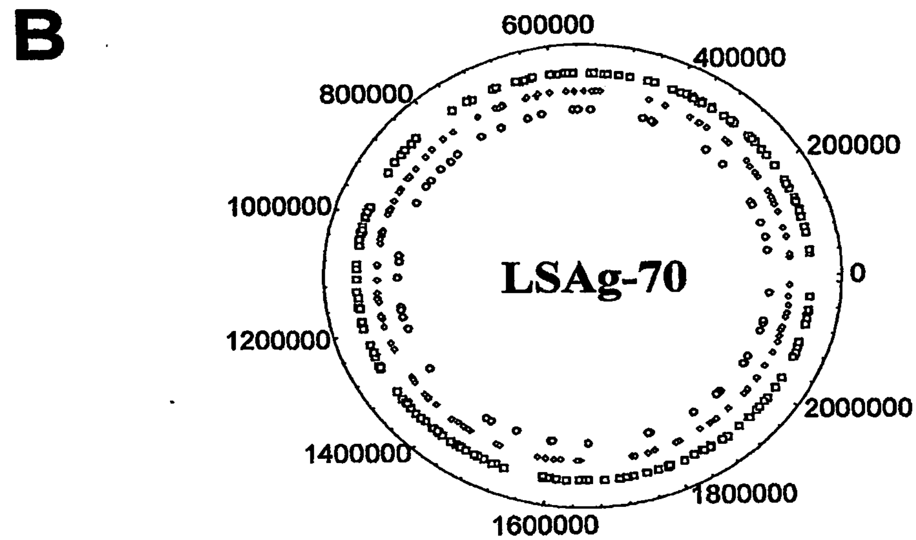




Fig. 1

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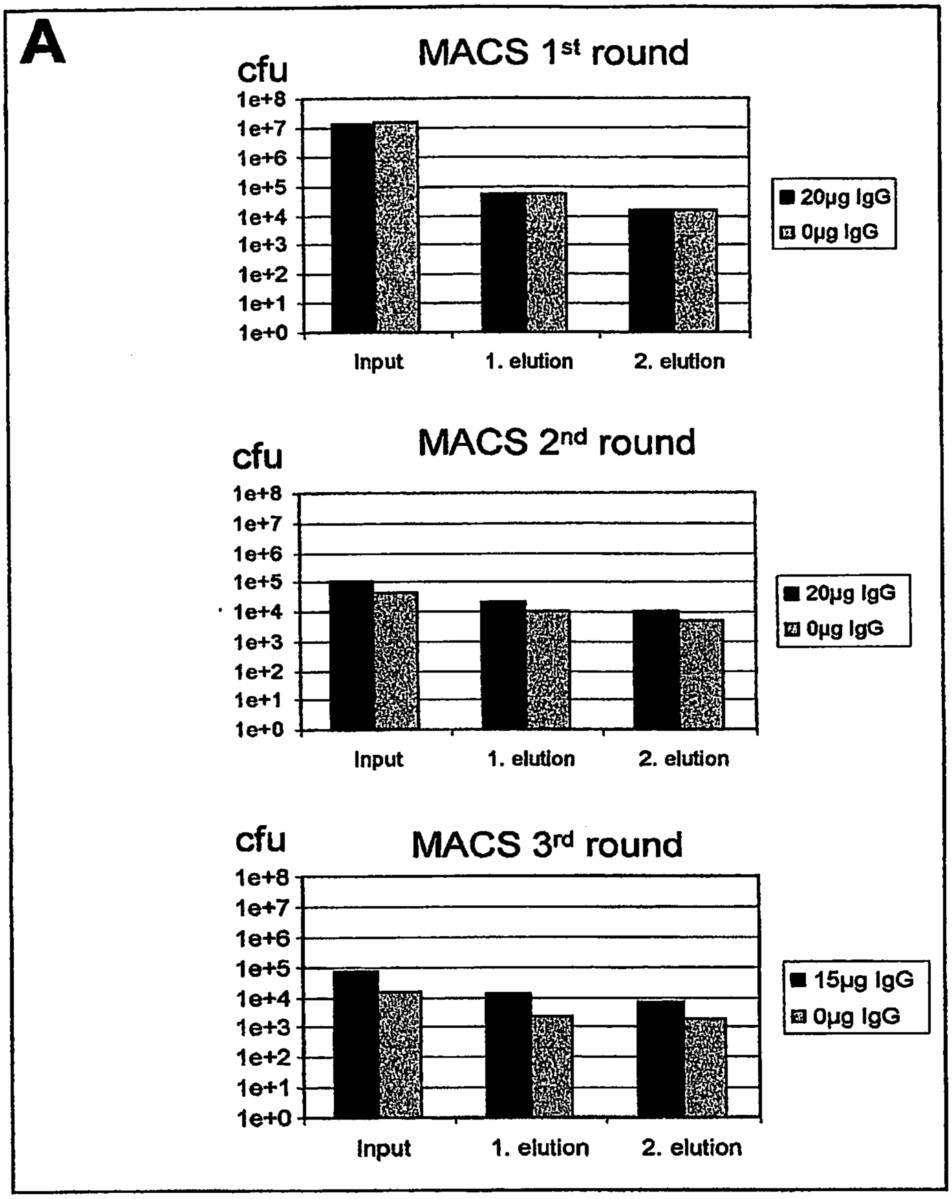
| **ORF** (+/+, +/-) | 333 | (71.8 %) |
| **non-ORF** (+/+, +/-) | 36 | (7.8 %) |
| **chimeric** | 53 | (11.4 %) |
| **non-blastable** | 42 | (9.0 %) |

Fig. 2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1e+3
1e+2
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1e+0
Input
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2. elution
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0µg IgG
MACS 2nd round
cfu
1e+8
1e+7
1e+6
1e+5
1e+4
1e+3
1e+2
1e+1
1e+0
Input
1. elution
2. elution
20µg IgG
0µg IgG
MACS 3rd round
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1e+7
1e+6
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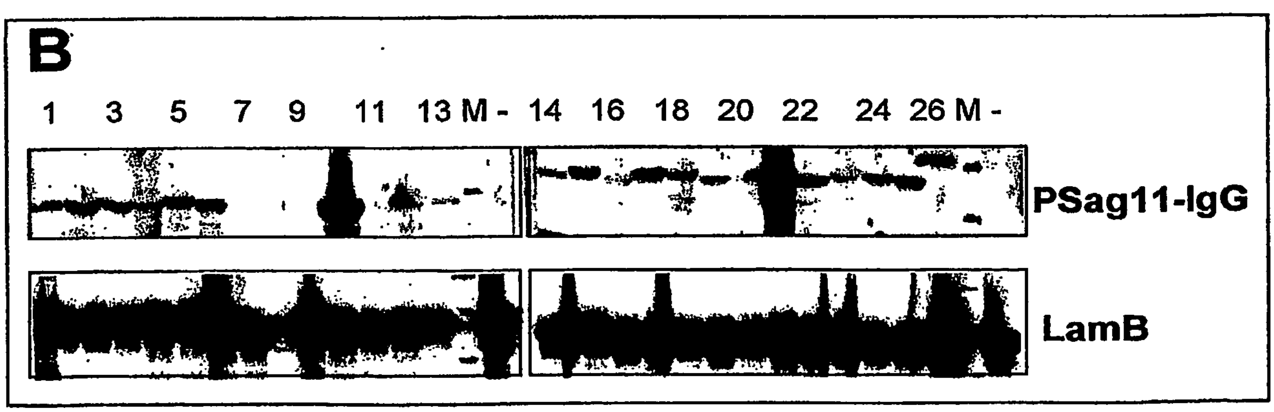
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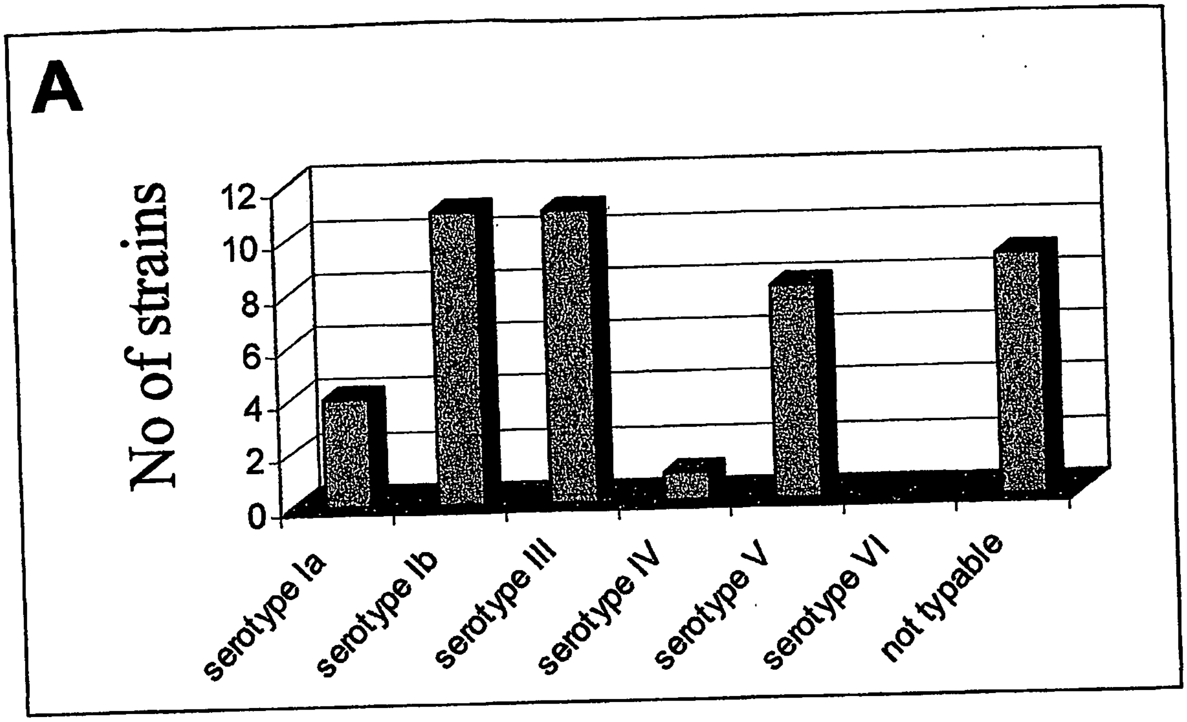
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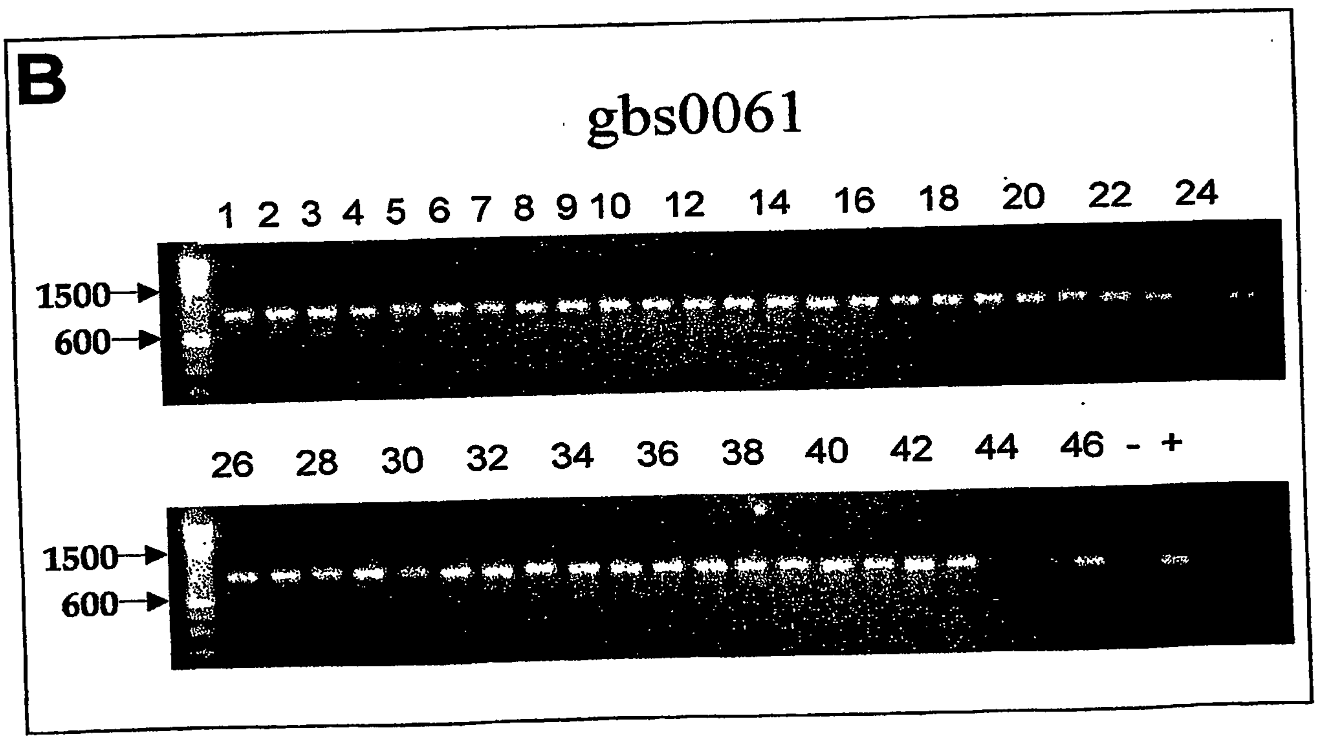
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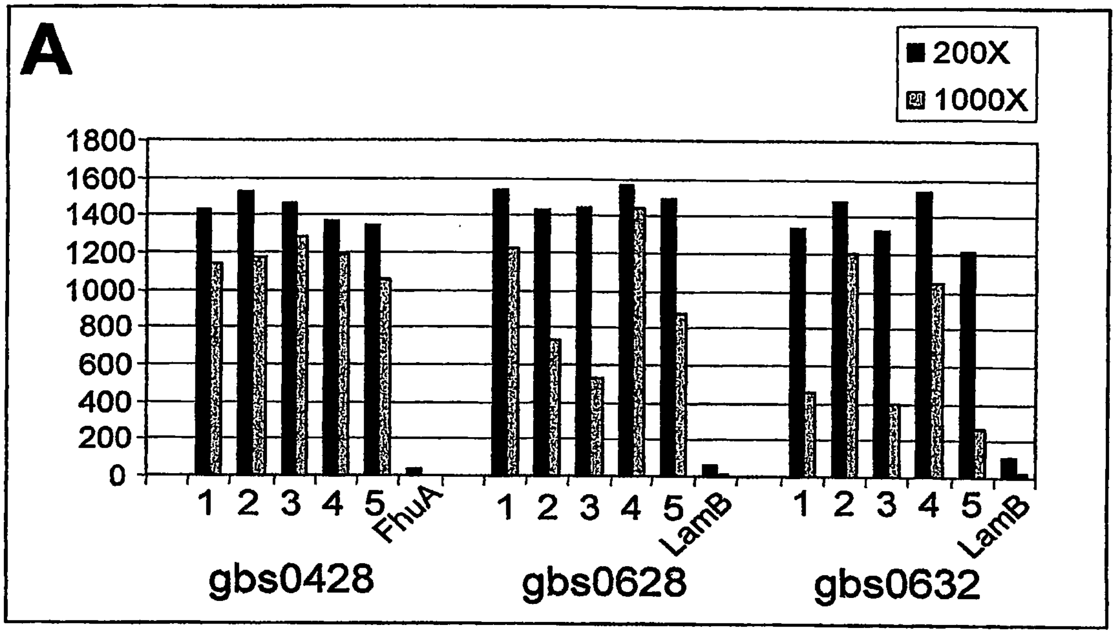
Fig. 4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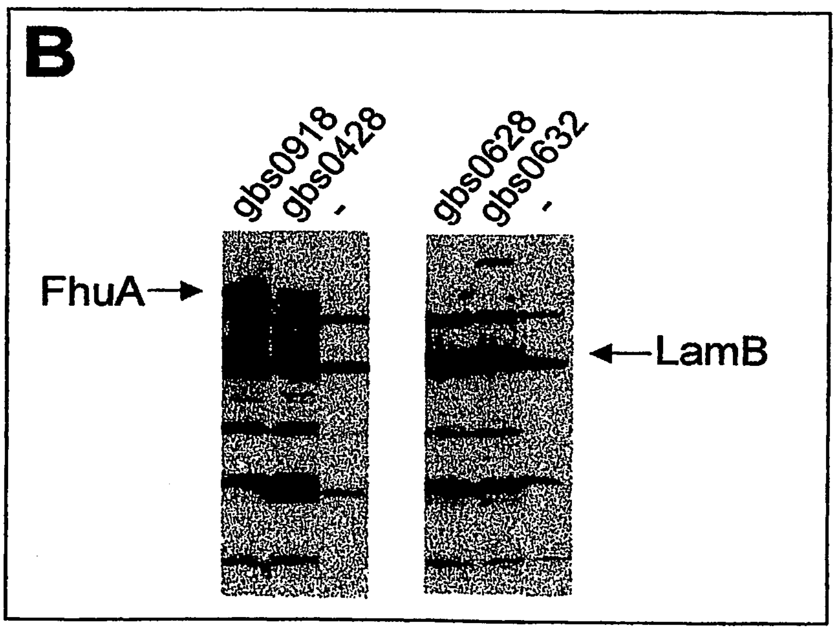
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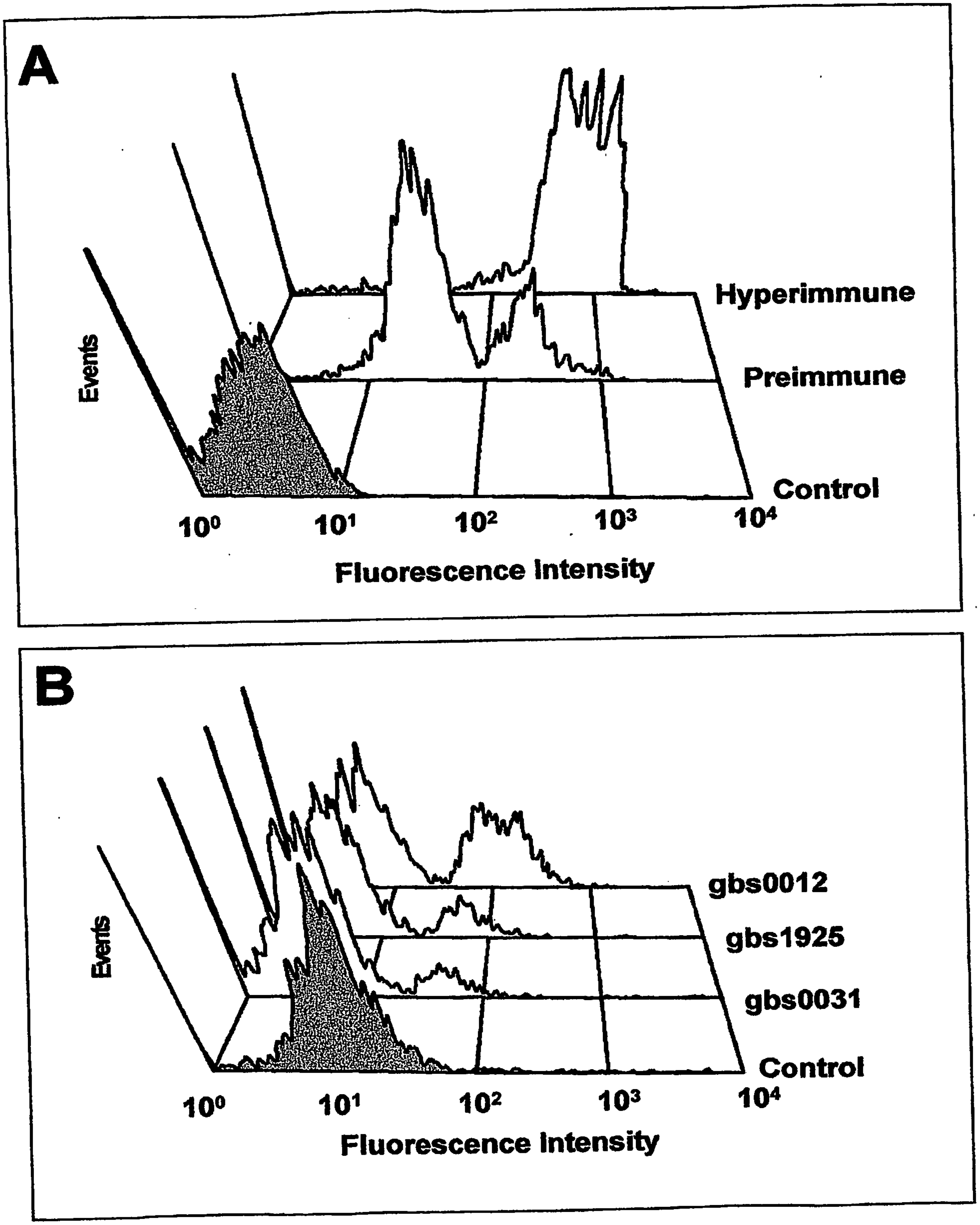
Fig. 5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Fluorescence Intensity

Fig. 6

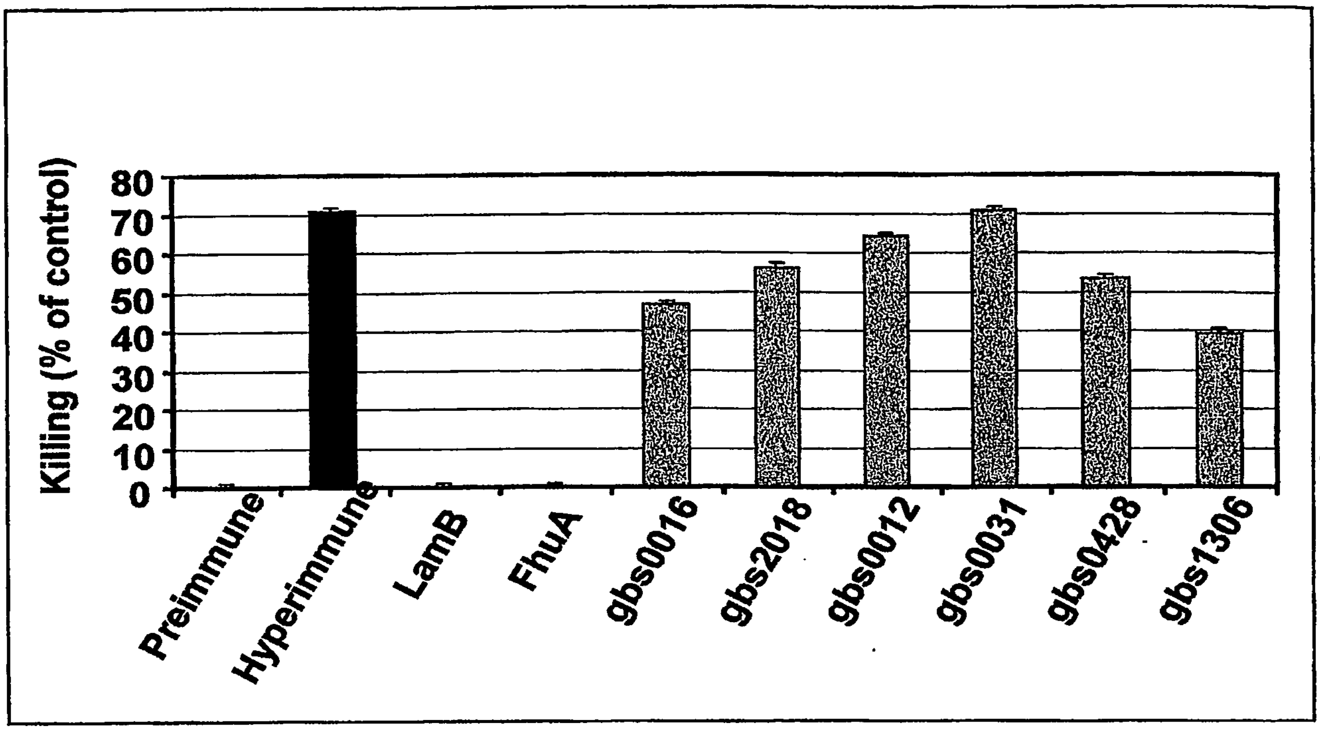
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Fig. 7

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<212> DNA

<213> Streptococcus agalactiae

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<210> 3

<211> 3726

<212> DNA

<213> Streptococcus agalactiae

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<213> Streptococcus agalactiae

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<210> 5
<211> 903
<212> DNA
<213> Streptococcus agalactiae

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<210> 6

<211> 2643

<212> DNA

<213> Streptococcus agalactiae

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<211> 834

<212> DNA

<213> Streptococcus agalactiae

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gcaggacgta acaacaacgg acgtattact gttcgtcacc aaggtggtgg acacaaacgt 180

cattaccgtt tgattgactt caaacgtaat aaagatggtg ttgaagcagt tgttaaaaca 240

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gaagcagata tcaaagttgg taacgcactt ccacttgcta acattccagt cggtacagtt 420

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gttggtcgta aagcaccatc tactccatgg ggtaaacctg cacttggact taaaactcgt 780

aataagaaag ctaaatcaga caaacttatt gttcgtcgtc gtaaccaaaa ataa 834

<210> 8

<211> 939

<212> DNA

<213> Streptococcus agalactiae

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<210> 9
<211> 927
<212> DNA
<213> Streptococcus agalactiae

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agtatggttt atgacaacta taaagctaca gcaggtaaga aagagcttta tattgtaaaa 840
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<210> 10
<211> 447
<212> DNA

<213> Streptococcus agalactiae

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gaacctggtg aaattacatt ggtcccgacc ggtattaaag cacacatgca accaggggag 180
gtcctgtacc tttatgatcg ttcatcgaat ccacgtaaaa aagggattgt cctaataaat 240
tcagttggtg ttattgatgg tgactactat aataaccaag tcaatgaagg acatattttt 300
gcacagatgc aaaatattac tgatcaggct gttattttag aagaagggga acggattgtt 360
caggctgttt ttgccccatt cttattggca gatgacgatc aggctacagg aatgcgtaca 420
ggtggttttg gtagtactgg aaaataa 447

<210> 11

<211> 969

<212> DNA

<213> Streptococcus agalactiae

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<210> 12

<211> 1191

<212> DNA

<213> Streptococcus agalactiae

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gatcttgatt ttattcacga taaggcttta acaataggtg ccatagaatc ttatatttta 180

gatgttaaag atgagttcgc tgagcatttt gtgttaccag ctttacaggc acatgcgatg 240

tatgaacaaa aatacccgct tgtttcagcg cttagtcgtc caattattgc tcaaaaatta 300

gttgaaatgg cacatcaaac aggtgcgacc acaattgccc atggatgtac aggtaaagga 360

aatgaccaag tgcgttttga agttgcaatt gcagcactag atcctgaatt aaaagtaatt 420

gcccctgttc gtgagtggaa gtggcatcgt gaagaggaaa ttacttttgc aaaagctaac 480

ggcgtaccta ttccagcaga tttagataac ccttattcta tagaccaaaa tttatgggga 540

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caaaatggga agcctatagc tataaacaat caagaaatga cactagcaga tttgatttta 720

tcgctaaatg aaattgcagg aaaacatggt attggacgca ttgatcatgt tgaaaatcgt 780

ttagtcggta tcaaatcacg tgaaatttat gaatgtcctg cggcaatggt actgttagct 840

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aacttagcaa cttatacagc tgctgataac tttgatcaag atgcagcagt tggttttatc 1140

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<210> 13

<211> 189

<212> DNA

<213> Streptococcus agalactiae

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gcgatgaacc aaacaaaacg tactgttaaa ccaaaccttc aaaaagttac tgttcttatc 120

gacggtaaac caaaaaaagt ttgggtttca gctcgtgcgc ttaaatctgg taaagtagaa 180

cgcgtttaa 189

<210> 14

<211> 1656

<212> DNA

<213> Streptococcus agalactiae

<400> 14

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gttgcgactc ttgctgcatg tggaagtaaa tcagcttccc aggattctaa tggagcgatt 120

aattgggcta ttccaacaga aatcaataca ctagatttat ctaaagttac agacacttac 180

tcaaatctag ctattggtaa ctctagtagt aatttccttc gcttagataa ggatggaaag 240

acgagaccag atttggctac taaagttgat gtttcaaaag atggtttaac ttatacagct 300

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gaagggcatg tgcttaatgc cgataaaatc aacgaaggac aagagaaaga cttgaataag 480

ctaggtgtta aggcagaagg cgatgacaaa gttgttatta ctttatctag tccgtctcca 540

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gacgctgctt ataacaaggc aatttccgaa gatgccttaa aaccagaaga atcagcaaag 1500

gactataaag aagcagagaa aattctattt gagcaaggcg cttataaccc actctacttc 1560

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ttgtcaatag actttacaca tgcttataaa aaataa 1656

<210> 15

<211> 729

<212> DNA

<213> Streptococcus agalactiae

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acattttata cacaagctta taaaccaggt ggcgatttaa tattttggtt tttaaatcca 240

gcaacaattg cttttgcagt tcctctctat aagaaaaatg acgttgttaa aaaatattgg 300

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acaacagcaa ttgctcttcc aataacagca gcaattggag ggaacacagc tgtgacagca 480

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ttgctataa 729

<210> 16

<211> 1629

<212> DNA

<213> Streptococcus agalactiae

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gatgaattgg ttgtttctat gggggcaaag cttcctcatg aattcgatcc aaaggaccgt 180

tatggaatcc ataatgaagg taatattact catagtaccc tattgaaacg ttctcctgaa 240

ctagatataa aaggagagct tgctaaaaaa tataaaatct ctaaggatgg cttaacgtgg 300

tcgttcgact taaatgatga ttttaaattc tccaatggtg agcctgttac tgctgacgat 360

gttaagttta cttatgatat gttgaaagca gatggaaaag cttgggattt gacctttatt 420

aagaatgttg aagtagttgg gaaaaaccag gtaaatattc atttgactga ggcgcattcg 480

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agtcttaacc atacttatat tggtgataaa cgtatcaatg taggtaaaca aggtgtccat 1560
agtcatggtc atgattggtc attattgact aacattgctg aatggacttg ggatgaatct 1620
gctaagtaa 1629

<210> 17

<211> 1146

<212> DNA

<213> Streptococcus agalactiae

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agtggatcag gtaaaacaac attaatgcgt atggttaacc atatgttaaa accaacaaat 180
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<210> 18

<211> 708

<212> DNA

<213> Streptococcus agalactiae

<400> 18

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caaccgcaaa cgaataatac accagttact ccaggggtta acaatactgt tccgactcca     660
ggaactggta ctgcacctgc tactaatggg acgggtgttg ctcagtaa                 708
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<210> 19

<211> 2040

<212> DNA

<213> Streptococcus agalactiae

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<210> 20
<211> 1986
<212> DNA
<213> Streptococcus agalactiae

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<210> 21

<211> 822

<212> DNA

<213> Streptococcus agalactiae

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<210> 22

<211> 2238

<212> DNA

<213> Streptococcus agalactiae

<400> 22
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<210> 23
<211> 1278
<212> DNA
<213> Streptococcus agalactiae

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<210> 24

<211> 801

<212> DNA

<213> Streptococcus agalactiae

<400> 24
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ttgccagcct tagctaagga acagattgcg ccacaactac tgtgggcacg ccgtacaagt 180
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<210> 25

<211> 1566

<212> DNA

<213> Streptococcus agalactiae

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gagatgtccc aacctaaaac aaccattaca gctccaacag ctaacacttc tacaaatgta 180
gaaagtagta ctgataaggc attatcaaaa gttactacga tggagacaag ttcagaaatg 240
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ccatatgaag cgtttggtgg agatggcatg ttaacgcgtt taatccttaa atcttctgaa 540
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<210> 26

<211> 1350

<212> DNA

<213> Streptococcus agalactiae

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<210> 27

<211> 318

<212> DNA

<213> Streptococcus agalactiae

<400> 27
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agatataatg atgatatttt atttggtgag gtttgggcaa aagaggatca tttaacagat 120
aaaacacgtt ctattattac tatatctgcc ttaattagcg gaggaaatct tgaacagtta 180
gagcatcatc ttcaatttgc caaacaaaac ggagttacta aagaagaaat tgctgacatt 240
atcactcacc ttgcttttta tgttggatgg ccaaaagctt ggtcagcctt taataaagct 300
aaggaaattt ggatataa 318

<210> 28

<211> 471

<212> DNA

<213> Streptococcus agalactiae

<400> 28
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aactttttag aaaaagactt agaaaatatc ttaaaaaatg gtcatgttaa acctgctgtc 120
aatcaaatct tagctcacat cggaaataca cctttcgact tgattgatta ctgtcaaagt 180
aaaggtattc aagttgaagc ttattcacca attgcacatg gacaagcatt gaaatctgat 240

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ggtattcaaa aaatggctga aaaatatggg gttagtgttg ctcaattatg tattcaatat     300
ttactacaat taaacctgat cgttttacca aaggcttcta gtaaagaaca tttacagtct     360
aatctagact ttgactttgt aattagtgac gaagatatgt cgatattaaa atcacttatg     420
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<210> 29

<211> 3381

<212> DNA

<213> Streptococcus agalactiae

<400> 29

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gattctacag ctttaagaaa taggatagat gaagtaataa ataatgcaaa tgatcctaag     540
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<210> 30

<211> 570

<212> DNA

<213> Streptococcus agalactiae

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gaggttgcct atccagcagg gctcagccca atagcatctt tagaagatga gtatgattat 180

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<210> 31

<211> 2655

<212> DNA

<213> Streptococcus agalactiae

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<210> 32

<211> 735

<212> DNA

<213> Streptococcus agalactiae

<400> 32
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ttaaaaggca ttgacttgga tattcatcaa ggagaagtgg tggttattat tggcccttct 120

ggctctggta agtcaacatt tttaagaaca atgaatctct tggaagtacc aacaaaggga 180

acagtgactt ttgaagggat tgatataaca gacaaaaaga atgatatttt taaaatgcgc 240

gaaaaaatgg gcatggtttt tcaacagttc aatctatttc ccaatatgac tgtactagaa 300

aatattactt tatcacctat taagacaaag ggactttcta agcttgatgc tcagacaaaa 360

gcatacgagc tacttgaaaa agttggactc aaagagaagg ctaatgctta tccagctagc 420

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ggttttgcac gtgaagtagc ggatcgtgtc atttttatgg atgcaggcat tattgttgag 660

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agtaaagtat tataa 735

<210> 33

<211> 1695

<212> DNA

<213> Streptococcus agalactiae

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acattagaat ttggaacggc gggattgaga ggtaaacttg gagcaggaac caatcgtatg 180

aatacttata tggtggggaa agcagcacaa gcattagcta atacgattat tgatcatggc 240

cctgaagcta ttgcacgtgg aattgcagtt agttatgatg tccgttatca atctaaggaa 300

tttgcagaat taacttgttc cattatggca gcaaatggta ttaagtctta tatttataaa 360

gggattcgcc caacaccaat gtgctcatat gctattcgtg ctctaggatg tgtttcgggt 420

gtgatggtta ctgctagtca taatcctcaa gcttataatg gttataaggc atattggaaa 480

gaaggatctc agattttaga tgatattgct gatcaaattg ccaatcatat ggatgctata 540

accgattatc agcaaattag gcaaataccc tttgaagagg ctctggcaag tggtttggca 600

agttatattg atgagagtat tgaagaagca tataaaaaag aagtgcttgg tttaaccatt 660

aatgatacta acattgataa gtcagtccga gtagtttata ctcctttaaa tggcgtagga 720
aatttacctg tgcgcgaagt tttaagacgc cgtggttttg aaaatgttta tgtggtacct 780
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aatagtacta aataa 1695

<210> 34
<211> 1212
<212> DNA
<213> Streptococcus agalactiae

<400> 34
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ggcttttttg acggtgaaac ccaaattgcc agcgctagta ttctcatcaa atcacttcct 180
cttggcttct ccatgctata tattccgcgt ggaccaatca tggattactc caatctagat 240
attgtaacta aggtccttaa ggaccttaaa gcttttggca aaaaacaaag agctctcttt 300
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cccgatgaaa aagaagggtt aatcgccatt gatcatttac agcgtgcagg tgctgattgg 420
actggtcgga caacagattt agctcatact atccaaccac gttttcaggc aaacctatat 480
gctaatcaat ttggacttga taaaatgtct aaaaaaactc gtcaagctat tcgaacttcc 540
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<210> 35

<211> 1398

<212> DNA

<213> Streptococcus agalactiae

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gctagaacgg aagactctgt taatggcgat ttcacaccca aaaaattaaa ggtaatgaca 120
tctaaagatc aaccgcgtca ttacaaatca gttttatcaa attttgaagt agatttacca 180
gataacccac ttccttatac ttcagtaccg gacgcattgg gaaaagatgg tatatggggt 240
gaagccggta ttaacagtaa aaatgtagcg atgagtgcta cagaaactat tacaacgaat 300
tcccgcgttt tgggtgcaga tcctttggtt tcagatggta taggggaaga ggatatactc 360
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ttttcaatgg gagattaa 1398

<210> 36
<211> 1521
<212> DNA
<213> Streptococcus agalactiae

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gttcaagtta aacaagtttg ggctgatagt aaacttaaag tggtaacaac tttttaccca 120
gtttatgagt ttacaaaaaa tgtcgttggt gataaagctg atgtatctat gttaattaaa 180
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gaggaaatgg aaaactggcc aacatacttc ccagctaaaa tgtctggacg tgaagttgcc 1500
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<210> 37
<211> 1665
<212> DNA
<213> Streptococcus agalactiae

<400> 37
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actgttgaac cagtagctca gtttgcgact ggaatgagta ttgtaagagc tgcagaagtg 120
tcacaagaac gcccagcgaa aacaacagta aatatctata aattacaagc tgatagttat 180
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cctgataaag aaatcgagtt tacagtatca caaacatctt ataatacaaa accaactgac 1500

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atccctaata ctggtggtat tggtacggct atctttgtcg ctatcggtgc tgcggtgatg 1620

gcttttgctg ttaaggggat gaagcgtcgt acaaaagata actaa 1665

<210> 38

<211> 2673

<212> DNA

<213> Streptococcus agalactiae

<400> 38

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gtaattgtta aaaaaacggg agacaatgct acaccattag gcaaagcgac ttttgtgtta 180

aaaaatgaca atgataagtc agaaacaagt cacgaaacgg tagagggttc tggagaagca 240

acctttgaaa acataaaacc tggagactac acattaagag aagaaacagc accaattggt 300

tataaaaaaa ctgataaaac ctggaaagtt aaagttgcag ataacggagc aacaataatc 360

gagggtatgg atgcagataa agcagagaaa cgaaaagaag ttttgaatgc ccaatatcca 420

aaatcagcta tttatgagga tacaaaagaa aattacccat tagttaatgt agagggttcc 480

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tataaaattg aattaactgt tgagggtaaa accactgttg aaacgaaaga acttaatcaa 660

ccactagatg tcgttgtgct attagataat tcaaatagta tgaataatga aagagccaat 720

aattctcaaa gagcattaaa agctggggaa gcagttgaaa agctgattga taaaattaca 780

tcaaataaag acaatagagt agctcttgtg acatatgcct caaccatttt tgatggtact 840

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<210> 39

<211> 606

<212> DNA

<213> Streptococcus agalactiae

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<210> 40
<211> 1059
<212> DNA
<213> Streptococcus agalactiae

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<210> 41
<211> 672
<212> DNA
<213> Streptococcus agalactiae

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ttgaaagctt aa 672

<210> 42

<211> 567

<212> DNA

<213> Streptococcus agalactiae

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gaagaagcca aaaagattgc atttaaagat gctaatatag aggaatcaga agtcagtaat 420

cttaagatca aagaagaaat tgaaaatgga aaatcagttt atgatattga ctttgtggac 480

ctgaaaaata aaaatgaagt tgattatcaa attgatgcag aaactggaaa aatcattgaa 540

cgttctagag atcatatgaa tgattaa 567

<210> 43

<211> 2043

<212> DNA

<213> Streptococcus agalactiae

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taa 2043

<210> 44

<211> 1428

<212> DNA

<213> Streptococcus agalactiae

<400> 44

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ttaggcgatt tcaccgccaa acctactcca gacaatttga agctagaagc aattgatttt 180

tatcataact ataaaaatga tataaaactg tttgcagaga tgggctttaa agtttttaga 240

acctctattg cctggtctcg aatttttcca aatggtgatg atagtgctcc aaacgaagct 300

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<210> 45

<211> 486

<212> DNA

<213> Streptococcus agalactiae

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aactaa 486

<210> 46

<211> 546

<212> DNA

<213> Streptococcus agalactiae

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aatgcctatt ctttggaaaa tgtctcagat attgttaatg aagctcaggc tttgtataaa 360

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gcatcgcatc aagataatac agacttaaaa aacttttatg ctgagttaga tgatatgtat 480

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<210> 47

<211> 921

<212> DNA

<213> Streptococcus agalactiae

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<210> 48

<211> 3234

<212> DNA

<213> Streptococcus agalactiae

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<210> 49

<211> 999

<212> DNA

<213> Streptococcus agalactiae

<400> 49

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<210> 50

<211> 1758

<212> DNA

<213> Streptococcus agalactiae

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<212> DNA
<213> Streptococcus agalactiae

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<210> 52
<211> 2634
<212> DNA
<213> Streptococcus agalactiae

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<211> 1503

<212> DNA

<213> Streptococcus agalactiae

<400> 53

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<210> 54
<211> 990
<212> DNA
<213> Streptococcus agalactiae

<400> 54

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<210> 55

<211> 2460

<212> DNA

<213> Streptococcus agalactiae

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cataagaaat cagcacgtat tactggtgat gttatgggta aataccatcc acatggtgat 240

tcatctattt acgaagcaat ggtgcgtatg gcacaatggt ggtcatatcg tcatatgctc 300

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<210> 56

<211> 1329

<212> DNA

<213> Streptococcus agalactiae

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<211> 384
<212> DNA
<213> Streptococcus agalactiae

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<210> 58
<211> 279
<212> DNA
<213> Streptococcus agalactiae

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<210> 59
<211> 3150
<212> DNA

<213> Streptococcus agalactiae

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<210> 60
<211> 2802
<212> DNA
<213> Streptococcus agalactiae

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<210> 61

<211> 2262

<212> DNA

<213> Streptococcus agalactiae

<400> 61
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gaaaccgcaa aaacgcctca agttacagaa agtcaagtta atagcgcaaa agttactgcc 180
gatcaagcaa taagtgatgt taataaccaa caaattgtag ttgatgaggc tcaaaagcag 240
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<210> 62

<211> 1920

<212> DNA

<213> Streptococcus agalactiae

<400> 62
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<210> 63

<211> 4731

<212> DNA

<213> Streptococcus agalactiae

<400> 63
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<210> 64
<211> 2367
<212> DNA
<213> Streptococcus agalactiae

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agaagcggaa aaatcaatac agacttcatg cgacaattga cagcttctct taatcgttca 2280
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<210> 65
<211> 801
<212> DNA
<213> Streptococcus agalactiae

<400> 65
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aatatatcaa gttcacctga agaaaaaaat gatggcttag gaacggccta tcaaacgcaa 180
aatgaagatt tgaaatctaa aagttttgat ggtcaacatc aagtcatagt ggttaatgaa 240
aaagcacaat ttacggcaga agagttgagc atgagaaatg gttcatggga aaaatacgat 300
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aagaaaacaa atcatcatgt tcgttatcga gtgaccccac ttttcaaaaa tgtggagtta 660
gtagctcgtg gcgtacgtat agaagcacaa agtattgaag atgagaccat ctcatttgat 720
gtctatattt ttaatgggca accaggatat gacattgatt atttgacggg atcatctgaa 780

aaaataatga ttacaaaatg a 801

<210> 66

<211> 348

<212> DNA

<213> Streptococcus agalactiae

<400> 66
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atttcggaag aatatgagta tccgtctttt aatgaattta tgcttgctca attgcaacgg 120

attgtcgaaa atggtggtct tgatttatat gataataaat ttgcggaaac cttggcagtt 180

attaaagaac aacaagcaca aatattggat cagctcctaa aaaacgaaat caagttactg 240

gcttatcatg caaagcaaga tatagtggaa gagctaacaa ccgactggtt acgatttatg 300

gatgatgttg atgcgctggc tgcggaaaga ggagcaggag gacgttga 348

<210> 67

<211> 843

<212> DNA

<213> Streptococcus agalactiae

<400> 67
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atttgtggtt taaattggct catcaaaata gtattcaaag gacaatttta tcttttctca 120

gctgtctttt gtggcttgtt gacctactat atgccacaag atattcaatt atttacagtg 180

agagttttag agctaatcat catgctaaaa gtgataatag atgttaccca tacagctctt 240

tcaagagatt ttaaacggat gaaaacgcct cttttttttag gagtgatgta cgtcttcttt 300

ctagctggta acagttatat taaagcacat cttttgacag aagttatggt taatcatctt 360

atttcgtttt ggcttatcag cctgtttttt gccactcttg taatagttat tcagcccaga 420

ttatttaagc attatctgtt aaaaaaagtc attgataagg aatacttggg tatccgaaaa 480

ttcacagact ctcttcctcc agaaatcaat ttgtacaagg atgcggacga agaagatgcg 540

gacaaacgga tgcgactgat caaccagaat gtcatcaaac acccctatca agaagttgtt 600

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gaaaaagaaa ctgaacgtac ttttatagac gatgatacca tctattatcc catttttacg 720

gttcaccctt tcagaaattt ggaagggaaa tcagattttt atcacatact aatgaaactt 780

aaactcagtc gaaaagcggc ctttacaaaa aatggtgagc gattattaat tagagatttt 840

taa 843

<210> 68

<211> 495

<212> DNA

<213> Streptococcus agalactiae

<400> 68
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cctttcactg acttaggaga atttgattct attcagatga agttcaaaca acctgttaga 120

aatctggtaa ataagtactc tggtaaacct tataatctta gttggcaaaa taagattgaa 180

cagatgagag tgctatatat taaatatcag aaaagcttga agctagaaga tgaagaacaa 240

gaggttcata accgagttaa aaataaaaag tctaaaaaat atgttcatga aatcgttaca 300

acatatttga agttaggatt caggtttaaa gaaattgaag caagggtatc cctattcaat 360

actcgtcttc gtcggaactg gaaaagaagc gactatgtga caactgataa ccctgaattc 420

tatttgaaga aggatctaca gaatggttat tgttctccaa attcatttct tcctcggagt 480

atgaaaataa actaa 495

<210> 69

<211> 1272

<212> DNA

<213> Streptococcus agalactiae

<400> 69
atgaacgaaa tcaaatgccc tcattgtgga acagcttttg ccatcaacga gtctgaatac 60

catcaattac tagaacaaat tcgtggagat gcttttgaca aagaagtaag tgaacggttg 120

gaaaaagaac gtctaatatt aggggagcaa gcaaaaaatc aattacagga agttgttgta 180

gaaaaagaca aggagatagc taaacttcag tacaaagtca aacaatttct tatagaaaaa 240

gacaatcttc tcaaagacaa tgagtaccaa ctcgctgagc aattaaatca aaaagacatg 300

atgcttcgcg accttgaaaa ccaaatcgat agactacgtt tagagcatga aaatagcttg 360

caagaggcgc taacaaaagt cgaacgagaa agagatgcaa tacaaaatca gttgcacatt 420

caagaaaaag aaaaagattt agctttagct tcagtaaaaa gtgattatga agtacaacta 480

aaggcagcca atgaacaagt agaattctat aaaaacttca aagctcaaca gtctactaaa 540

gcagtaggag aaagtttaga acattatgct gaaacagaat ttaataaagt gcgacatttg 600

gcctttccta atgcttattt tgagaaggac aatacattat caagtcgtgg ctcaaagggg 660

gactttatct atcgagaaaa ggatgaaaat gaccttgagt ttttaagtat catgtttgaa 720

atgaaaaatg agtctgatga tactatcaag aagcataaaa atgaagattt tttcaaagaa 780

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gatgtttctg tcaagaaatt aacaagaaaa aatccaacaa tgaaagcaaa attcgatgct 1260
ctaaaagact aa 1272

<210> 70

<211> 843

<212> DNA

<213> Streptococcus agalactiae

<400> 70
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aatattatca actatctcaa aaagaatagt ttaacttctc tatctgttcg caatatggcc 120
gtagtatcaa aatgtaaaaa tcctactttc tttatagaaa attataaaca gctagacctt 180
aaaaaacttc gacaagaatt caaaaaattt ccagttctat cgattttgga ttctaactat 240
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tgtcagtctg ttaaaaagat tatcaaggag actaacaatc aatttgttat cgtaagtggt 420
ttagcgcgtg gcattgatac agcagcacat gttagtgctt taaaaaatgg cggcagtagt 480
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gccgaagcta agatgagatc tggaagttta attacctgtg aaagagcatt agaagaggga 720
cgagaagttt ttgccattcc cggaaatatt atcgatggca aatcagatgg atgccaccat 780
cttatccaag aaggagctaa atgcattatt tcaggaaaag atatcctttc tgaatatcag 840
tag 843

<210> 71

<211> 357

<212> DNA

<213> Streptococcus agalactiae

<400> 71
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gataatgctg agaatagtaa aaggctctta caaaaattga aaaacgacgt catggagtta 120
caaatagagt tactagaatc attaaaactc ggtgatgcct atttaacaga atcagaagaa 180
ttagaagaga ataatgactt tattctaacg gtaaatagtg aaacactaag tttatcctat 240
gacaatagga taaacttagt ttctaaagag attatggatt atgaaaatgc attagataag 300
ttgtattatg aaaaacagag tttgatgcaa aaaagtaatg aaagaaaagg aggttaa 357

<210> 72
<211> 1233
<212> DNA
<213> Streptococcus agalactiae

<400> 72
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gtgctaggat caactattat tttaggatca agtcctgtat ctgctatgga tagtgttgga 120
aatcaaagtc agggcaatgt tttagagcgt cgtcaacgtg atgcagaaaa cagaagccaa 180
ggcaatgttc tagagcgtcg tcaacgcgat gcagaaaaca gaagccaagg taatgttcta 240
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agtcgctgcg gtttgagacg caatgaaaat taa 1233

<210> 73

<211> 1722

<212> DNA

<213> Streptococcus agalactiae

<400> 73
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attattgtat cacagagaat taatagtata caaaatgcag atagaatctt actccttgat 1620

aaggggaaac aagttggttt tgataatcat caatctttat tagctcataa caaagtttat 1680
aagtccattt accattcaca aaattttaag gaggaggagt aa 1722

<210> 74
<211> 1275
<212> DNA
<213> Streptococcus agalactiae

<400> 74
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aaaaaattaa tatga 1275

<210> 75
<211> 3237
<212> DNA

<213> Streptococcus agalactiae

<400> 75
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gctatagata ttgtggccgt tgcgagctca ctaggactta acttgaaaca aggttcaggt 120
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<210> 76

<211> 2799

<212> DNA

<213> Streptococcus agalactiae

<400> 76
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<210> 77

<211> 2232

<212> DNA

<213> Streptococcus agalactiae

<400> 77
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gttattaatt aa 2232

<210> 78

<211> 762

<212> DNA

<213> Streptococcus agalactiae

<400> 78

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ttaaaatgct ttggagaaaa gttttcagag ggttactttt atccacttca aatggatatt 180
acaagtagag aatcggttga caaagcttta gaaagtctgc ctaaaaattt gcaatcaatt 240
gatttgttgg ttaataatgc aggtttagca cttggattgg ataaatcata tgaagctgat 300
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caattttctc tcaacttgcg tgccgattta gctggaacta aaatcagagt tactaaccta 540
gaacccggtt tatgtgaagg gacagaattt tcaactgtac gtttcaaagg agatcataaa 600
agagttgaaa aactttatga aggtgcgcat gcaattcaag cagaggatat tgctaatacc 660

gtgtcatggg ttgctagcca accagaacac attaatatta atcgcataga aataatgcca 720

gtcagtcaaa cttatggacc tcaacctgtt tatcgtgatt aa 762

<210> 79

<211> 1116

<212> DNA

<213> Streptococcus agalactiae

<400> 79

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gcaaatcaac ttttacgtga atgtcgacaa attattgctg aatatctaaa tgttaattca 180

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ttagctaaaa ccttaagaaa aattatagga gattaa 1116

<210> 80

<211> 1344

<212> DNA

<213> Streptococcus agalactiae

<400> 80

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gtagaaaacc caaatcctca cattattgta aatgttacag gtactgatca aaacggaaat 180
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ccacaagcag cttgttatcc aaacaaacaa tttgcttgcg aaaatactga ctctaaatac 1320
aactatagct atttagaaaa atag 1344

<210> 81

<211> 2280

<212> DNA

<213> Streptococcus agalactiae

<400> 81
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ggaccgcttt tgattatggc aggagctggc tctggaaaaa cacgtgttct gactcatcgt 120
attgcttatt taatagatga aaaatatgtt aatccttgga atattttagc gattactttt 180
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<210> 82

<211> 393

<212> DNA

<213> Streptococcus agalactiae

<400> 82
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tctactatat tcaacttacc tgtaccaggt agtattattg gattaatatt actattccta 120

gcgttaaaat acaaaatcat caggctcagg catattgatg ccgtggggaa ttttctatta 180

gcaaatatga ccattttatt tttaccacca gcagttggac tgatggagca ctttcaagac 240

ataaaaccct atctttttgg gatagctatc attatcttag gagcgctatt tctcaatatt 300

ctaactattg gactggtatc ccaatggatc aaaaagagat atgaaggaga ttatccagaa 360

attggaggta aaaatggcaa ctttaacgaa taa 393

<210> 83

<211> 474

<212> DNA

<213> Streptococcus agalactiae

<400> 83
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gatagattaa aagggacagg tgctattgat caagaagtgt tcattcaaac gggttactca 120

gactttgaac ctcagaattg tcagtggtca aaatttctct catatgatga tatgaactct 180

tacatgaaag aagctgagat tgttatcaca catggcggtc cagcgacgtt tatgtcagtt 240

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aatgatcatc aaatacaatt ttttaaaaaa attgcccacc tgtatccctt ggcttggatt 360

gaagatgtag atggacttgc ggaagtgttg aaaaggaata tagctacaga aaaatatcag 420

ggaaataatg atatgttttg tcataaatta gaaaaaatta taggtgaaat atga 474

<210> 84

<211> 762

<212> DNA

<213> Streptococcus agalactiae

<400> 84
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gaaatgaaaa cgatattaga ccatgttaat ttgagtattt atgaacatga cttcattaca 120

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gcagcgcttg atcctagaac aagtgtttcg cttatgggct tgactgatga gtttatcaaa 600

caagattcgt tgactgcctt aatgattaca catcatatgg aagatgctct caaatatgga 660

aatcgtatat tagtaatgaa agatggcaag attgtcagag atttaaatca ggcacaaaaa 720

aacaagatgg ctatagctga ctattatcaa ttatttgatt aa 762

<210> 85

<211> 3219

<212> DNA

<213> Streptococcus agalactiae

<400> 85
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caaataagag atactcaaac taataatatt gaagttctcc agactgaaag taccactgtc 180

aaagagacta gcaccacaac cacacaacaa gatctgtcta accccacagc ttcaaccgca 240

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gagctggtga aaaacggaga ttttaatcaa actaaccctg tatctggaag ctggtcacat 360

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<212> DNA
<213> Streptococcus agalactiae

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ttagactgct ttgaatacat tgagaatttt tataacaatt acaacccaca tacggctaat 180
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<210> 87
<211> 2469
<212> DNA
<213> Streptococcus agalactiae

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<211> 921

<212> DNA

<213> Streptococcus agalactiae

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<210> 89

<211> 3453

<212> DNA

<213> Streptococcus agalactiae

<400> 89

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<210> 90

<211> 1212

<212> DNA

<213> Streptococcus agalactiae

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<210> 91
<211> 837
<212> DNA
<213> Streptococcus agalactiae

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<211> 315
<212> DNA
<213> Streptococcus agalactiae

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<210> 93

<211> 6201

<212> DNA

<213> Streptococcus agalactiae

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<211> 2109

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<213> Streptococcus agalactiae

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<210> 98

<211> 915

<212> DNA

<213> Streptococcus agalactiae

<400> 98

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<210> 99

<211> 855

<212> DNA

<213> Streptococcus agalactiae

<400> 99

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aatgacttta atttaaaaac attaaccaat ccacaatcca taaaaaataa ctattactta 780

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<210> 100

<211> 2073

<212> DNA

<213> Streptococcus agalactiae

<400> 100

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<210> 101

<211> 1740

<212> DNA

<213> Streptococcus agalactiae

<400> 101

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<210> 102

<211> 1632

<212> DNA

<213> Streptococcus agalactiae

<400> 102
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<210> 103

<211> 1248

<212> DNA

<213> Streptococcus agalactiae

<400> 103
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ggcatgaaag attcggttac aaatgagatt acaaagtctc agaagaacct tcagatttat 180

tataaaacaa aagaagacca aaaaaatgag gataactttg gagctcaagg ggctttcatg 240

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gcttaccttg aaaaaaaggc aaagacggtt aatataacag gagttaaccg cacttacctt 420

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<210> 104

<211> 1215

<212> DNA

<213> Streptococcus agalactiae

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<210> 105

<211> 360

<212> DNA

<213> Streptococcus agalactiae

<400> 105

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<210> 106

<211> 1026

<212> DNA

<213> Streptococcus agalactiae

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gtcgcgttga taggaaccgt ttctttcatt ggattgatta ttccacattt tattaagctt 840

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atgatctggg tagacttatc atctcgtatt ataaatcccc cttcagagac accaattagt 960

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<210> 107

<211> 567

<212> DNA

<213> Streptococcus agalactiae

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tctaaaaaag tttatgcatt tgatattcaa gaagaagcaa tagcaaaaac gaaagcaaag 180

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<210> 108

<211> 1008

<212> DNA

<213> Streptococcus agalactiae

<400> 108

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<210> 109

<211> 3933

<212> DNA

<213> Streptococcus agalactiae

<400> 109

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<210> 110

<211> 1992

<212> DNA

<213> Streptococcus agalactiae

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ttatctaaaa aagaaaggca agctgaaatt aaagctcttc aacagcaaat gcaagaagca 1920
gctgaattat tggactttga gctagctgca caaatccgag atgttatctt agaactaaaa 1980
gcaatcgatt aa 1992

<210> 111
<211> 2184
<212> DNA
<213> Streptococcus agalactiae

<400> 111
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ggaaaggtca gtgcagaaac tgtgaatatt gtttctgata cagcatacgc tccattcgaa 120
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tatgctatcc ttgcaattat gtatcttgta atcattaccc ttctcacccg tctagcaaaa 2160
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<210> 112

<211> 159

<212> DNA

<213> Streptococcus agalactiae

<400> 112
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gtctggaatg ctgaaaaatt agaagaactc tttaacacat taaatcctaa tcgtaaactt 120
cgtttagaac gcgaaaaatt agcaaaagaa aaaggatag 159

<210> 113

<211> 843

<212> DNA

<213> Streptococcus agalactiae

<400> 113
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caactaactg aaggtgaaga agcttataag gcagtgactc atgctttaaa agttggttat 120
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gactatcatt tagccaaagc ttctattgat gaatctctgc agaaattagg tgttgattat 300
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aattgccaaa tactctatga tcctgaaaat caattacaat cactcaaaga gagattcgaa 420
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ttgcttccta aacatttcga agaaaatatc attaaactat gtcatcacaa ctccaacgaa 720
cacactgtta aagaaacatt aaacgatata ataatgcatc tcgacgtcat gcttaaagaa 780
aattttcaac actttatagg ttaa 804

<210> 116

<211> 804

<212> DNA

<213> Streptococcus agalactiae

<400> 116
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gagtcaattg agcgttctct aaaaggagac cgttatgttg accaaaaact agctgaaaac 120
tcttcaaagg aagctactga acaactaaac aaaaaaacta agcaagcctt aaaagctgat 180
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<210> 117

<211> 690

<212> DNA

<213> Streptococcus agalactiae

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aatattgcag catttcaatt atcagaactg tttgcaaatc aagataatgt tagcttttca 1680

caacattttt accaattgat tgaagatttg agacacccag aaaagtttaa aatacctggt 1740

ctatctgttt cagcttcctt gcgcgattat cagcttacag gtgtccgttg gttaagtatg 1800

ttagatcatt atggctttgc agggatttta gctgatgata tggggcttgg aaaaacactt 1860

caaacgattt cattttaag tacaaaacta actagagatt ctcgtgtgct tattttatca 1920

ccatcaagtt taatttataa ttggcaagat gaattccaca aatttgcgcc agacgtagat 1980

gtagcagttg cctatggttc taagattcgt agagatgaaa ttattgctga acgtcatcaa 2040

gtaatcatta caagttattc atcatttagg caggattttg agacttattc tgaaggaaat 2100

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aagaaagagt tttgaagtt gaaccctaaa caagttgctc gttatatcaa accatttgtg 2340

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ccagctgttg aaatgcaggc gattagtcgc gcacataggt tggggcaaaa agagaatgtc 2940

gaggtttatc gcttgattac tagaggcaca atcgaagaaa aaattctaga aatgcaagaa 3000

actaaaaaac atttggttac aacagttctg gatggaaatg aaacccatgc tagcatgagt 3060

gtagatgata ttcgagagat acttggagtt tctaaataa 3099

<210> 122

<211> 534

<212> DNA

<213> Streptococcus agalactiae

<400> 122

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atcaaagagt cgcttatgga gcgtcattca gagataatgg atatttctga tattcaagtt 120

aaagctattg gtgtttcgaa tttcatgaaa catcacttag aggctttatt tgaaactgcc 480

gaaataaaac ctatggttaa tcaaattatc ctagcaccag gttgtgctca agaggatttg 540

gttcgcttct gtaaaggaaa tgatatctta ttagaagctt acagtccatt tggaacaggt 600

gctatttttg aaaatgaatc tataaaagct attgctgaaa aatatggtaa atcagttgca 660

caagtagctc ttcgctggtc acttgataat ggctttttac cattacctaa gtcagcgact 720

cccaaaaata ttgaagcaaa ccttgatatt tttgattttc aattaaacga agatgatatt 780

actaccttaa tacaactaga ttcaggtatt aaacccaaag atccagataa tgtctcattt 840

taa 843

<210> 114

<211> 468

<212> DNA

<213> Streptococcus agalactiae

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atcgttgaaa caatagaagc aggaattgtt ttgacaggaa cagaaatcaa aagtgtccgc 120

gcagcgcgta ttacattgaa agatggatat gcacaaataa aaaatggtga agcgtggttg 180

attaatgttc atattacacc atacgatcaa ggtaatatat ggaatcaaga tcctgatcgt 240

acacgaaagt tattactaaa aaaacgtgag attgaaaaaa tatcaaatga actgaaaggg 300

actggtatga ctctggtacc tctaaaagtt tacttaaaag atggttttgc taaagttcta 360

ttgggtttgg caaaaggaaa acatgattat gataagcgag agtctatcaa acgtcgtgag 420

caaaaccgtg atattgcccg tcagttaaaa aactataatt cacgatga 468

<210> 115

<211> 804

<212> DNA

<213> Streptococcus agalactiae

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gtttattgtg cagcaactcc tgatatcact agtcgtaaac gtatccttaa caagcactgt 180

cattacattg aacttaacaa tcattactgg gagcttgaag ataatggtac tttaaacgac 240

ggaactgata ttgatattct ctatcgtaac atagataact ttttatcaga cttagaagat 300

gtcgttgaac accacaattc tcgaattgga tacactactt gtttttggca taacctcatc 360

<400> 117
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gaggataaat ctcaagagac agtattatca aatgtatatt acagtggacg ttatggtgaa 120

catgagcttg ttttagtaca gtctggtgtt gggaaagtca tgtcagcgat gagtgttgct 180

attttagtag aaagctttaa agttgatgct attattaata caggatcagc tggtgcagta 240

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gatttaaccg cctttggtta tgactatgga caaatgtcaa tgcagccact ttattttcat 360

tcggataaga cttttgtttc cacttttgaa gcagttttat ctaaagaaga aatgactagt 420

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gctgctcaag ctacaggaaa gccctttgtg gtggtacgtg ctatgagtga tactgcagct 600

catgatgcca atatcacatt tgatgaattt atcattgaag ctggtaaacg ctctgcccaa 660

gtattaatgg catttttgaa agcattataa 690

<210> 118

<211> 1167

<212> DNA

<213> Streptococcus agalactiae

<400> 118
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gtagggtata actgggaatt atcaggaaac gtttcttcgt atggaaattc aatgaagaat 180

ggagctgact tagcagtaaa agaaattaat gctgctggag gggttggcgg caagaagtta 240

aaagtcctat cacaggataa taaatcagaa aatgcagagg cagcaacggt tgccacaaac 300

ttggttacca aaggagctaa tgtcattatc ggaccagcaa catcgggtgc agctgcatct 360

tcaactccaa aagtaaatgc agcagcagtt ccaatgattg cacctgctgc gacacaagac 420

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<210> 119

<211> 1353

<212> DNA

<213> Streptococcus agalactiae

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<210> 120

<211> 1803

<212> DNA

<213> Streptococcus agalactiae

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taa 1803

<210> 121
<211> 3099
<212> DNA
<213> Streptococcus agalactiae

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<210> 123

<211> 579

<212> DNA

<213> Streptococcus agalactiae

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ttattattta aagcattact agaagttgga ggtgtctaa 579

<210> 124

<211> 2829

<212> DNA

<213> Streptococcus agalactiae

<400> 124
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ccagaagaag ttgctgaaaa tcctaaatcc tatacaggat attatttaaa agagaagtta 2820

gcaagatag 2829

<210> 125

<211> 1125

<212> DNA

<213> Streptococcus agalactiae

<400> 125

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atcatgttgc aacaaacaca agttaataca gtaatccctt attataaacg ttttctagag 180

tggtttcctc aaataaaaga tttggcagac gctcctgaag aacaattact aaaggcatgg 240

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<210> 126

<211> 849

<212> DNA

<213> Streptococcus agalactiae

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tatctttaa 849

<210> 127

<211> 981

<212> DNA

<213> Streptococcus agalactiae

<400> 127
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atgaccattc aaagcaagtt tggcaaagac atcgcagttt atactgggga tttacttttc 360

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<210> 128

<211> 1749

<212> DNA

<213> Streptococcus agalactiae

<400> 128

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tatgattttt ccgtcaagaa tttaagtttc cagtataagc cacaagagaa atgggttttg    1080
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<210> 129

<211> 447

<212> DNA

<213> Streptococcus agalactiae

<400> 129
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ggtgtttcag cttcaacttt cacagcaccg caagcaacac atccaaaagc agaacgtcag 180
ttaacagatt cagaaatcta tgaacgtgcc caaaaacaag tgttaccaaa atatatccaa 240
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gtgacaccgc aagtatcaag ccccaaagca gaacgtcagt taacagattc agaaatctat 360
gaacgtgccc aaaaacaagt attgccaaaa tatattcaag gttctctctc aggtatcctt 420
aaccaacatt caactttgaa tgcttaa 447

<210> 130

<211> 510

<212> DNA

<213> Streptococcus agalactiae

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ggggtagtta gctacattta tccgaattaa 510

<210> 131
<211> 942
<212> DNA
<213> Streptococcus agalactiae

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<210> 132
<211> 852
<212> DNA
<213> Streptococcus agalactiae

<400> 132
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tgtcaaaatc ccttgataaa agaaagtaac agcctcaaat gctctgataa tcattgtttt 120
gatttatcca aatttggata tgttaatctt cttggaggaa agaagataga tgaacattat 180
gataaaaaat catttgaaaa tcggcagctt gtcttagaaa acgggtatta taatcatatt 240
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attttagaca ttttttctcc tgcaaattat aaagaattta ggcgggtact gagtgatgat 540
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aattttgaaa ttatttctga gcagaaagtt gttcaaagtt ataactgttc tcaacaagaa 720
cgtcaagctt ttattgatat gacaccgttg ttattcagcg tagataaaac gactattgat 780
tgggcgagta tatcagaaat tacagtaggt gccttaatag taattggaaa aaagcgcagt 840
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<210> 133

<211> 450

<212> DNA

<213> Streptococcus agalactiae

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aaagaatatg aaacgggtta tcttgttctg ggagaccatc aatattttca aggttattgc 120
ctttttctct ctaaaaaaca cgtaacagag ttacatgaat tgcctagaga ttggcgaaat 180
cagtatcttt ccgaaatggc agatgcttct gaaatagttg ctaaggcttt tagagcagat 240
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agaaaaacag gtgatttaag gaactatggg cataatggaa aaggtccagt ttggtggtat 360
ccttttgaga agatgtatgc agatagtgtc agagcaactg gtgcagaaat agaaaaatta 420
aaagagaaat tgttagatgt cttaggatag 450

<210> 134

<211> 1188

<212> DNA

<213> Streptococcus agalactiae

<400> 134
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gttctctttc tctttgcagt gagtaatcgc tacaatcaat attgggatga atatgatgca 120
tataggattg ttaaattagt tgccaaaaat gattatttag gaataccagg cgatgaaccg 180
attgctttgg tgactataga taaccaaaag atggttaaga ttcaaagcaa taatactgat 240
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cgaaaatgga agtcttttat atattccata aaagaatata aagataaaac ctacaccata 360
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<210> 135

<211> 1680

<212> DNA

<213> Streptococcus agalactiae

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cgtgtaggaa tcttgctaac cgaaaaacaa aaagcagcct gtcgtctttt attagatgaa 240
gtaactgatt atagttacgt catgaaaagt agtgagaggt tgcagctgtc tttagtatct 300
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<210> 136

<211> 648

<212> DNA

<213> Streptococcus agalactiae

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atcgttgatg gtgttactac caatccgact attatttcac gtgaggggcg tgactttaaa 120
gaagttatta acgaaatttg ccaaatcgtt gatggcccag ttagtgcaga agtgacaggt 180
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gggattgaaa ctttcttaaa agattgggat agtttcaaga agaagtag 648

<210> 137
<211> 2448
<212> DNA
<213> Streptococcus agalactiae

<400> 137
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<211> 1533

<212> DNA

<213> Streptococcus agalactiae

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<210> 139

<211> 1896

<212> DNA

<213> Streptococcus agalactiae

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tggcgtccag ttgaaaaacg tgttattatt tggtaa 1896

<210> 140

<211> 1008

<212> DNA

<213> Streptococcus agalactiae

<400> 140
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agagctctac aaggctttgg gcaagatact aaactcctct cagccttacc caataatccc 180
ataggtaata gttttcttca atttttaaaa gcacagggta ttgatactca ttctattcag 240
tgggttggag aacgtgttgg gttatatttt ttagaagatt cctttgcttg cagaaaaggt 300
gaggtggtct acgaccgcga tcatagtagt ttacatgact ttaggataaa tcaaattgat 360
ttcgatcaat tatttgaagg agtttctctc tttcatttta gtggtattac actatcattg 420
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acaatctcct tagatctcaa ttttcgcagt aaactaattt ctcctaaaaa tgccaaaatc 540
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gactcacagg acactacctt cttcaatcgc gatgaagcta caatagagga cgtcaaagaa 660
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gctgtcgcta gtgcatcttt aaaatgtgct ttggaagggg acaatatgtt tgagaccgtt 960
accgcagtta acaaagtact aaatcaatcg aaagacatta ttcgttag 1008

<210> 141
<211> 585
<212> DNA
<213> Streptococcus agalactiae

<400> 141
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agtgcatcgg atcaaacgac gacttttatt caaacgattt ctccaacagc tattgaaatt 180
tctaagacct atgatttgta tgcgtcagtc ttattagcac aagctatttt ggaatcatcc 240
agtggacaat cagatttgtc taaggctcct aattataacc tctttggcat caaaggagaa 300
tataaaggta aatctgtcca aatgcctact ttagaagatg atgggaaagg caatatgact 360
caaatccaag ctccttttcg cgcctatcca aattattctg cttcactata tgattatgct 420
gagttagtat ctagtcaaaa gtatgcatct gtttggaaat caaatacctc ttcttataag 480
gatgctactg cagctctaac aggtctttat gcgacagata ctgcttatgc tagtaaatta 540
aaccaaatta ttgaaaccta cagtctagat gcttatgata aatag 585

<210> 142
<211> 1338
<212> DNA
<213> Streptococcus agalactiae

<400> 142
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gcagttatct taacaatggg gtggttctta gggactatcg gagctagcat tcctggtttt 240
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atgggaggaa caggagatgt tgccatttta agtacagcag accgaatgaa cttgatgcca 1260
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<210> 143

<211> 1239

<212> DNA

<213> Streptococcus agalactiae

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ccaaagaaag atttatcaga gtcggaatta aaagcagctc aagaatttct ttcaggaaaa 180
tctgaagcaa atcaagacaa accaaaaaca ggtaaaacag ctcaagaaat ctatgaggca 240
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gactataaga atggtacatt tgtaattcct cataaagatc attaccatta tgtggaatta 360
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gactatttag ctacggctaa atattacatg atgcacccag aaaaacgtcc taaagttgaa 480

ggatggggta aagatgctga aatttataag gaaaaggact ctaataaagc agataaacca 540
agtcctgcac caactgataa taaatcaaca tcaaattcta gtgacaaaaa cttaagtgct 600
gcagaagtat tcaaacaagc aaaaccagaa aaaattgtac cgcttgataa aattgctgct 660
cacatggcat atgcagttgg atttgaagat gatcaattga ttgttcctca tcatgatcat 720
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gatagacaat cttttgaaaa gcaactcatc caattatcaa ataaatatag tgtaagtttt 1140
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gtgcttgttg atattaaaac actaacagaa gtgaaataa 1239

<210> 144

<211> 1446

<212> DNA

<213> Streptococcus agalactiae

<400> 144
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gccatcatta gtgaagaatt gattatgaaa gaccctagct atgtctttaa taaagctgat 360
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<210> 145

<211> 471

<212> DNA

<213> Streptococcus agalactiae

<400> 145
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gcacaaaaca gctctgctat tgaaaccgtg gacgaccagg gggagacgag tagcgaggac 180
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ggcagagcag aactgaaaga gacagagttt tacccttatc cgagatatta g 471

<210> 146

<211> 4713

<212> DNA

<213> Streptococcus agalactiae

<400> 146
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aagccatctg atattgcagt tgaacagcaa gtaaaagaca gtccaacgag catagcaaat 180
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<210> 147

<211> 1932

<212> DNA

<213> Streptococcus agalactiae

<400> 147
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<210> 148

<211> 1623

<212> DNA

<213> Streptococcus agalactiae

<400> 148

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<210> 149

<211> 1542

<212> DNA

<213> Streptococcus agalactiae

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<211> 2577

<212> DNA

<213> Streptococcus agalactiae

<400> 150

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<211> 873

<212> DNA

<213> Streptococcus agalactiae

<400> 151

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<210> 152

<211> 1752

<212> DNA

<213> Streptococcus agalactiae

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<211> 456

<212> DNA

<213> Streptococcus agalactiae

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<210> 154

<211> 678

<212> DNA

<213> Streptococcus agalactiae

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<210> 155

<211> 1482

<212> DNA

<213> Streptococcus agalactiae

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<211> 2580

<212> DNA

<213> Streptococcus agalactiae

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<210> 157

<211> 45

<212> DNA

<213> Streptococcus agalactiae

<400> 157

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tggtttatga agcactcggt tgggaagcgc cacaatttgg tcaca                     45
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<210> 158

<211> 90

<212> DNA

<213> Streptococcus agalactiae

<400> 158
atgaaagatc acctaaggtg cttcctccat taccgatcca aaaacgttgg gaaaaatgga 60

acgagattga agggaggaaa gcctaatgac 90

<210> 159

<211> 99

<212> DNA

<213> Streptococcus agalactiae

<400> 159
gacaaacagc ttttccaatg cgtgcagggc ttccaaataa ggaacctcaa tggcaagaag 60

catgggatca agctgatatt tataaaaaac gtcaagcat 99

<210> 160

<211> 78

<212> DNA

<213> Streptococcus agalactiae

<400> 160
aacgaggaag ccatagatgg ggtgtccaag cttgggaaaa aaatcaccat tctaggaaat 60

aattcatacc tttcttcc 78

<210> 161

<211> 93

<212> DNA

<213> Streptococcus agalactiae

<400> 161
atcaaacaat ggctattggt gatgaagaaa atgaccgtgc tatgcttgaa gttgttggaa 60

atcctgttgt tatgcaaaac ggcaatcctg aac 93

<210> 162

<211> 57

<212> DNA

<213> Streptococcus agalactiae

<400> 162
aggcgcattt caaacaatct aggagtttta aaggaagcga ccgttataca cgccgta 57

<210> 163

<211> 108

<212> DNA

<213> Streptococcus agalactiae

<400> 163
gagctctgcc taaagctgag caacgtcaag ccaatctata tgccttggca cttcgagcaa 60

atcagtttga aaaaacaggt ttcaagggtt tatcacgctt tattcgaa 108

<210> 164

<211> 96

<212> DNA

<213> Streptococcus agalactiae

<400> 164
agaagctgct tcagtaggtg ctatccaaga tttaacagat tcagatatca ttttctcaaa 60

ccaccgtgga cacggacaaa ctattgcaaa aggtat 96

<210> 165

<211> 57

<212> DNA

<213> Streptococcus agalactiae

<400> 165
agatggtttg gttttagata tgacgatggc agaaaattta gctttacaaa cttatta 57

<210> 166

<211> 66

<212> DNA

<213> Streptococcus agalactiae

<400> 166
cccttaaaaa gtttgtcgat gacatcaaga atgaagctat tgaggttatc acaaagaaaa 60

gctatg 66

<210> 167

<211> 90

<212> DNA

<213> Streptococcus agalactiae

<400> 167
aggcacttgc gaaagagaca aaagcaaaat catttaatga atttatgctt tctatgtgcc 60

gtgaaaaaat tgaaaaagga caatttaatt 90

<210> 168

<211> 90

<212> DNA

<213> Streptococcus agalactiae

<400> 168
aagttattta ttcagcctat tcaggaaaat atgaagcagc caatcgagat tatatcaaat 60

tactatgcaa agcttgggtt aatgaaaatc 90

<210> 169

<211> 57

<212> DNA

<213> Streptococcus agalactiae

<400> 169
tatcaaacgt attcgaaaaa ggcaagaaaa tttggttccg tttggcttaa acctaag 57

<210> 170

<211> 84

<212> DNA

<213> Streptococcus agalactiae

<400> 170
acgctgttat tccagatact tctcctgctt tctcatttga aaaagaacat ctttctggag 60

tggaatatgc acgctactta caat 84

<210> 171

<211> 210

<212> DNA

<213> Streptococcus agalactiae

<400> 171
aagaagtttt acgaaataat attagcaacc aagtaccaca catcagtgtt caaatggagt 60

ttaaaactca agaacaagtt gacgaatacc aaaaaaatct cggaagcatc atccgggaaa 120

ttggagatac acttggaaca gcaactgaat tcaatgccaa aagtaacatt agcacttata 180

ctcttggtgg acaaatccaa cgcattattg 210

<210> 172

<211> 333

<212> DNA

<213> Streptococcus agalactiae

<400> 172
ttaaagcaaa tgttccgtcg cgtattgcat ttgctgtttc aagtggtact gatagccgta 60

cgatccttga tgaaaatggt gctgaaaagc tcttgggacg gggtgacatg ctctttaagc 120

ctattgatga gaatcatcca gtacgactac aaggttcctt tatttcagat gatgatgttg 180

aaaggatcgt tggttttatc aaagaccaag ccgaggctga ctatgatgat gcctttgatc 240

ctggagaagt atctgaaaca gataacggct ctggtggtgg cggcggagta cctgaaagtg 300

atcctctttt tgaagaagcc aagggactcg ttt 333

<210> 173

<211> 39

<212> DNA

<213> Streptococcus agalactiae

<400> 173
ggccggaaaa ttaattttag tcgtccatca cgatttgag 39

<210> 174

<211> 81

<212> DNA

<213> Streptococcus agalactiae

<400> 174
agagttaagt ataaaaaatg ggaaccttta tcaatatccc gttcctgcta tgaaaaatct 60

tcgtcaacat caagcagaat t 81

<210> 175

<211> 93

<212> DNA

<213> Streptococcus agalactiae

<400> 175
acttggtcaa gatgttgtat tcccaggtgt tactcgtggt gcaaaattag aagaagcaat 60

caatgctttg gaagatggac aagttctttt ggt 93

<210> 176

<211> 99

<212> DNA

<213> Streptococcus agalactiae

<400> 176
aaggagaatt tcgttcaaag gttgaggagt ctattgaaag caatcagcaa aaatataatc 60

atttatagtc tagtttctct accattagct agacacttg 99

<210> 177

<211> 177

<212> DNA

<213> Streptococcus agalactiae

<400> 177
agtataatca atattaaact agaaatatat gacatatgtc ctaaaactat ctcaaatagg 60

gagtcaatac atggatatag aaaactactg ccaagactac tgtttggaga ctatctttcc 120

aaaacattat ttcaaggatt tacaagtaat caccctaact gccggccaat ccgtctg 177

<210> 178

<211> 48

<212> DNA

<213> Streptococcus agalactiae

<400> 178
ctttctttca gaagaagtcg gcgaattggc tcaagccatt cgcaaata 48

<210> 179

<211> 42

<212> DNA

<213> Streptococcus agalactiae

<400> 179
ttcattttca aggataggtt taaaatgaga cacttcacgg ac 42

<210> 180

<211> 222

<212> DNA

<213> Streptococcus agalactiae

<400> 180
gggttgattt gtgcttgtaa agcctttatc tctgccatac tggctaactt attttgttcc 60

tctgttatcc ccattgccag ttgtcctgaa aatatttgcg ctaaaccaag gactaggttt 120

tcctccacct cagacattgt cttatctcct gcaaagtaca tttttaaggc acccacagtt 180

ttatcattta tttttagagg aactacaata gcagaattta ac 222

<210> 181

<211> 99

<212> DNA

<213> Streptococcus agalactiae

<400> 181
tcctcctctt tggacaccca ttacaaacat agggagcttt tcttagtagc ggacagtcta 60

ggcagtcttt ggttgattct cttagttgct tatttcgtt 99

<210> 182

<211> 75

<212> DNA

<213> Streptococcus agalactiae

<400> 182
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gctctagtcc ataag 75

<210> 183

<211> 72

<212> DNA

<213> Streptococcus agalactiae

<400> 183
gcacacctac acgaagggta tcataagtat ccactaaaaa gacgcaatct ttatgagttt 60

ctgcgtaagc tt 72

<210> 184

<211> 69

<212> DNA

<213> Streptococcus agalactiae

<400> 184
ccattgaaag agctccgcga acattatata attcctcgga aaattcgtct tcaaaacttt 60

ccccataga 69

<210> 185

<211> 63

<212> DNA

<213> Streptococcus agalactiae

<400> 185
aagtatacta ttgcaggctc tcgtgtcacc cagcgtcgac catcattttc tgttactaaa 60

gta 63

<210> 186

<211> 57

<212> DNA

<213> Streptococcus agalactiae

<400> 186
gcagcttttt catcaccagc agctaaaaac agagcattca ttacaacacg atcttca 57

<210> 187

<211> 141

<212> DNA

<213> Streptococcus agalactiae

<400> 187
tccatggtta aacaaatatc gttctctgac catttgatat cacgttttga aggcttatgc 60

ttgaggcgat tttctgtgcg attccgtttg agacgctcac ttagctctgt ttctaattct 120

acaaataata cctcttggtt g 141

<210> 188

<211> 129

<212> DNA

<213> Streptococcus agalactiae

<400> 188
taccacgttc tttctcgata tcatttgaat ccattgcacg ttcttcaagc tctttacgct 60

catcaagagt atgtgattgt tttaataatt catcaacgag agttgtttta ccgtggtcaa 120

cgtgggcaa 129

<210> 189

<211> 54

<212> DNA

<213> Streptococcus agalactiae

<400> 189
gcacagcctt cttcaactag gatatcccct aaaattgatc gttttacacc taag 54

<210> 190

<211> 114

<212> DNA

<213> Streptococcus agalactiae

<400> 190
tggaatagaa ctatcaatta ttttttgaat aacctgcaat tggtgactaa tatcaagttg 60

cccacgagaa aaattttcca gtcccaaaac aagtttctga gcttcatcaa aaac 114

<210> 191

<211> 36

<212> DNA

<213> Streptococcus agalactiae

<400> 191
gtccaagaag gccataaaat tttccctctt caaaga 36

<210> 192

<211> 87

<212> DNA

<213> Streptococcus agalactiae

<400> 192
caacaaagca ataacaccgc caattatagt cgcccctata aaccttggca taaaaagaaa 60

aatggattga gctgcagatg ctttagc 87

<210> 193

<211> 249

<212> DNA

<213> Streptococcus agalactiae

<400> 193
ttctttgatg ataccaaagt taacattcat tggttggaaa tgtttgctgt ctgtatgtgt 60

aatataatgt ggcagtgcac caatagcagt agtttgtggg aaaactactt cactctcccc 120

attaaagcga cgggcagcat tgattcccgc tacaagacca cttgctgccg attctacata 180

accttcaaca ccggtcattt gtccagcaaa gaaaagattt gggttcttac gtgtagcaaa 240

ggtttggtc 249

<210> 194

<211> 243

<212> DNA

<213> Streptococcus agalactiae

<400> 194
gtgtattcgt tacgcatagc gacattggaa ctagaacgaa acttgataga caagcgacgt 60

gggaaaccaa ccgattctag gtcaatagag tttttagagg ttagtttagc aatattatct 120

tgcaagaata agttaatacc tgacatcatg ctagagaaga catttccctt agtttcttct 180

gaagcgaagt cagaagacct aaagtttaaa tcagccatat ctctaaattt ggaaaattgt 240

tct 243

<210> 195

<211> 168

<212> DNA

<213> Streptococcus agalactiae

<400> 195
ggccatagca atggcattaa agagggaaat ggaggtatct tcccagtatt ttgcattgcc 60

attaccgcta ccaggtttcg ttttacgata aatggcttct gcaaccgcat taacccttgt 120

ctgtgtcatt tcatagtaac ccttcttagc tgctgcaatc gcaagagc 168

<210> 196

<211> 489

<212> DNA

<213> Streptococcus agalactiae

<400> 196
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atggtattag gaacaccaga aaaagaacct gtcatttgtt ctgcaaacgg aataatttca 120

attgtaatag ccacacctgc tgatatagaa atacaaatga gtaaagcaga cataatcaaa 180

gctaaacctg ttgaaaaatt attctgtgaa aattctctca ccgaattaac aaaggcagcc 240

cctggcacca taaccattag tgcccctaat ataataatgc tacgatgctc acctaatcct 300

gaaaaatata ataaattagc acttaaagcc actacagaac tacctagaat ggtcaaaaga 360

aatcctgtat gtatacgact ttccatcaaa ttcagaaaat atcctaaaat taagcctgtt 420

acagcagcgg aaaatgaatc taataaggaa ctacctaagg ctaaagaaaa actacccgct 480

ccacaaaaa 489

<210> 197

<211> 267

<212> DNA

<213> Streptococcus agalactiae

<400> 197
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acagcatatg ctatgtcgtc atcagttaca aaaccttctg atgtagaaga attagttacc 120

ataggtgata gaacaaaacg attttctagg ctcaatccat tgggaagtat taatggacga 180

aataaattac cttggacatt attcatctct gctcaccgtc cccttattag ccatagactt 240

agcctgaaat ctatcaaact ctgcaac 267

<210> 198

<211> 54

<212> DNA

<213> Streptococcus agalactiae

<400> 198
gccaaccata atgacaaaaa taatacgata agcgttaata aatttagtgc caaa 54

<210> 199

<211> 153

<212> DNA

<213> Streptococcus agalactiae

<400> 199
tccttctgcg tattttgttg ccattccaaa aaaggcagct acccacatcc aaaacaaagc 60

tcctggtcct ccagatttaa tagccgtagc cacaccaacg atattacctg tccctaccgt 120

tgcagcaaga gcagttgcaa gggcagcata act 153

<210> 200

<211> 90

<212> DNA

<213> Streptococcus agalactiae

<400> 200
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ggtaaatctc ctgattttcc tttgcctggg 90

<210> 201

<211> 180

<212> DNA

<213> Streptococcus agalactiae

<400> 201
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tcagctaatt cttccttaat aatttcttgt gataaggcca cacattcatt acaaatgaaa 120

acaccattac ctgcaataat ttttttact tcatcttggc ttttgccaca aaatgaacaa 180

<210> 202

<211> 105

<212> DNA

<213> Streptococcus agalactiae

<400> 202
ggtgtttata aaaagcagag cctaagcctg attttccatc agattcacct gattgtttat 60
cattttgatt ttttgcatga taggtttgtg ccttattatc gagaa 105

<210> 203
<211> 261
<212> DNA
<213> Streptococcus agalactiae

<400> 203
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ctacataagt tatcatcgcc taaaaacgga caaggcatcg ctttaaatac tttatctcca 120
tcttcatcta cttctaaaaa taaatcttca aaagccgata acttcatccg gaaatgttta 180
gaaatcctag aaatatcagc ttctgtaaat agaggaccca aagttttaca acaattagca 240
catgctgtac aatcaatttc t 261

<210> 204
<211> 390
<212> DNA
<213> Streptococcus agalactiae

<400> 204
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gacttttctt caggacttaa aggatcgttt ggtctgagac tctcttcagt caaatatttt 120
tttccatcta aggtatattg gaggagacca aagaacatac caatagcagc aagtgagaaa 180
ccaagatgga aatttacttc ttgtccgagg taccccacta caatgggtga aataaaagca 240
ccaaggttaa taccaaaaac aaagatacta aaaccagcat cacgacgaga atcattttct 300
ccatataaat taccaaccat ctctgataca tttggtttta atagtccagt accaaggata 360
attagagcaa tcgaaatgaa tagagctgtt 390

<210> 205
<211> 78
<212> DNA
<213> Streptococcus agalactiae

<400> 205
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tctcgattag actgttta 78

<210> 206

<211> 123

<212> DNA

<213> Streptococcus agalactiae

<400> 206
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gttcttgaga aacaaccagg tctttcatcg ctgctaataa tgctgtacca atccccctgac 120

ctt 123

<210> 207

<211> 465

<212> DNA

<213> Streptococcus agalactiae

<400> 207
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tgtgcaaacc ctgcaatacg cttgtcatac tcacgaatac cttcctctgc attaatcacc 120

ataagaacaa catctgagcg gtcgatggcg cgcatagaac gcataacaga atatttctct 180

gtgttttcat ataccttacc agatttacgc ataccagcag tatcaatcat agtatactct 240

tgcccctggc tatcaacgaa attagtatca atagcatcgc gcgtagtacc agcaactggg 300

ctagcaataa cacggtcttc cccaaggatg gcattaatta aactagattt cccaacattt 360

ggacgtccaa tcaaactaaa acgaataata tctggatttt cattttcctc ttctaccgga 420

agattttcca caatagcatc caatatatca ccagtaccaa tacca 465

<210> 208

<211> 72

<212> DNA

<213> Streptococcus agalactiae

<400> 208
tgcccatcct cagatatagc tggaattaat tttaccaaaa atagcggaaa aatagataaa 60

caaaccgtta ca 72

<210> 209

<211> 96

<212> DNA

<213> Streptococcus agalactiae

<400> 209
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acgaaaagca gaattggtaa tacctgccat cggtgc 96

<210> 210

<211> 150

<212> DNA

<213> Streptococcus agalactiae

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atcgctccaa ttcctgtccc acagcctgta ataacaaaat ctgcagcacc gctattaagt 120

aaaatagcag tcagtaaacc attttgtaca 150

<210> 211

<211> 141

<212> DNA

<213> Streptococcus agalactiae

<400> 211
gcaatgccta aacgttgctt cataccaccg gagtatgatg aaatcttctt tttacctaca 60

tcgcctaaac caacaagctc tagtaatcta ggaatttctt gtttagcttt ctttttatca 120

acacctttta aggtagcgat a 141

<210> 212

<211> 147

<212> DNA

<213> Streptococcus agalactiae

<400> 212
cttttactga ttttaaaaaa tccagatact acacataaca ccaccataaa aagacaacct 60

aacaaacccc ctaaagtttt acgaaaaaga actgaaaaaa agagtattaa gcttatgaaa 120

agaataccga taaaccatgt tgcaccg 147

<210> 213

<211> 132

<212> DNA

<213> Streptococcus agalactiae

<400> 213
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tcccttaact ggttgataaa aattgcgatt gtctttgtct tgttaatgga tgctgacaat 120

ttacgcattg ct 132

<210> 214

<211> 141

<212> DNA

<213> Streptococcus agalactiae

<400> 214
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aaatttagcc gttattttac tcaattttcc tttaatataa tcgtacattc tattttccta 120

tctcaatatt tttcattttg g 141

<210> 215

<211> 237

<212> DNA

<213> Streptococcus agalactiae

<400> 215
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gtcaatgaac cttcaagttt ttcagcatca aatgatacga aagctggacg tcctaaagta 120

gcttcaacag cttcaaggat tgcaggtact ttcattgatt tttcacgaac tgaaataact 180

tgtcctggag taacgcggta tgatgggata tcaacacgtt taccatcaac aaggata 237

<210> 216

<211> 111

<212> DNA

<213> Streptococcus agalactiae

<400> 216
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tctcgaaatt cttgtacctt aggatactta gcatttgcag taactaacat t 111

<210> 217

<211> 861

<212> DNA

<213> Streptococcus agalactiae

<400> 217

agaactcgaa atgcaattag atatcctaaa gcaagcagcg gtgattatgg cacaaaaagg 60

gaaataatca ctgctaataa ggataaatac agcatttcaa agatgtgtcg ctggctgaat 120

atgccacgct caagttatta ctatcaagcc gtggagtcag tatctaaaac ggagtttgaa 180

gaaactatta aaagaatttt tctcgatagc gagtctagat acggatccag aaaaatcaaa 240

atatgcttga ataacgaagg tatcacactt tcacgtcgtc ggattcgacg cattatgaag 300

cgactcaatt tggtttctgt ttatcagaaa gccaccttca aaccacattc tagaggcaag 360

aatgaagccc ctattcccaa ccacttagac aggcaattta agcaagaaag accactacaa 420

gccttagtca ctgacttaac ctatgttcgt gtaggcaatc gttgggctta tgtttgcctc 480

atcattgacc tatacaaccg tgaaatcatc ggcctgtctc ttggttggca caagaccgct 540

gaactcgtta agcaagccat acaaagcatc ccttacgccc tgaccaaagt caagatgttc 600

cattcagatc gtggcaaaga gtttgataat cagttaattg atgaaatatt ggaagccttt 660

ggaatcacac gttcgcttag tcaggctggt tgtccttatg acaatgccgt agctgaaagt 720

acgtatcgtg ctttcaaaat tgaatttgtt tatcaagaaa cctttcaatc gctggaagaa 780

ctagctctta agactgaaaa ggcaacactt ttctgtacaa catttataaa gtgttgcctt 840

ttcaggtttt taccaatgct a 861

<210> 218

<211> 428

<212> PRT

<213> Streptococcus agalactiae

<400> 218

Met Lys Lys Val Leu Thr Phe Leu Leu Cys Ser Leu Tyr Phe Val Ser
1               5                   10                  15

Ile Pro Ala Ile Ser Thr Glu Glu Pro Leu Thr Leu Ser Gln Asn Arg
            20                  25                  30

Arg Tyr Ala Leu Thr Gln Thr Val Val Asp Lys Glu Met Tyr Phe Asp
        35                  40                  45

Ala Ile Pro Glu Arg Pro Thr Thr Lys Ile Glu Ile Ser Ser Phe Gln
50 55 60

Asp Glu Ala Leu Thr Ile Thr Gly Glu Thr Leu Val Pro Asn Thr Leu
65 70 75 80

Leu Ser Ile Val Ser Leu Thr Ile Asn Ser Asn Gly Ile Pro Val Phe
85 90 95

Thr Leu Ser Asn Gly Gln Phe Ile Lys Ala Ser Arg Glu Ala Ile Phe
100 105 110

Asn Asp Leu Val Ser Lys Gln Gln Ser Val Ser Leu Asp Tyr Trp Leu
115 120 125

Lys Pro Ser Phe Val Thr Tyr Glu Ala Pro Tyr Thr Asn Gly Val Ser
130 135 140

Glu Val Lys Asn Asn Leu Lys Pro Tyr Ser Arg Val His Leu Val Glu
145 150 155 160

Gln Ala Glu Thr Glu His Gly Ile Tyr Tyr Lys Thr Asp Ser Gly Phe
165 170 175

Trp Ile Ser Val Glu Asp Leu Ser Val Ala Asp Asn Arg Met Ala Lys
180 185 190

Val Gln Glu Val Leu Leu Glu Lys Tyr Asn Lys Asp Lys Tyr Gly Ile
195 200 205

Tyr Ile Lys Gln Leu Asn Thr Gln Thr Val Ala Gly Ile Asn Ile Asp
210 215 220

Arg Ser Met Tyr Ser Ala Ser Ile Ala Lys Leu Ala Thr Leu Tyr Ala
225 230 235 240

Ser Gln Glu Gln Val Lys Leu Gly Lys Leu Ser Leu Asp Ser Lys Phe
245 250 255

Glu Tyr Lys Asp Asn Val Asn Gln Phe Pro Asn Ser Tyr Asp Pro Ser
260 265 270

Gly Ser Gly Lys Leu Glu Lys Lys Ala Asp His Lys Leu Tyr Thr Val
275 280 285

Lys Glu Leu Leu Glu Ala Thr Ala Lys Glu Ser Asp Asn Val Ala Thr
290 295 300

Asn Met Leu Gly Tyr Tyr Val Asn Asn Gln Tyr Asp Ser Met Phe Gln
305 310 315 320

Thr Gln Val Asp Thr Ile Ser Gly Met His Trp Asp Met Lys Lys Arg
325 330 335

Gln Ile Ser Pro Gln Ala Ala Gly Lys Met Met Glu Ala Ile Tyr Tyr
340 345 350

Gln Asn Gly Asp Ile Val Asn Tyr Leu Ser Lys Thr Asp Phe Asp Asn
355 360 365

Thr Arg Ile Pro Lys Asn Ile Pro Val Lys Val Ala His Lys Ile Gly
370 375 380

Asp Ala Tyr Asp Tyr Lys His Asp Ala Ala Ile Val Tyr Ala Glu Gln
385 390 395 400

Pro Phe Ile Met Ile Ile Phe Thr Asp Lys Ser Ser Tyr Asp Asp Ile
405 410 415

Thr Lys Ile Ala Asp Asp Val Tyr Gln Val Leu Lys
420 425

<210> 219

<211> 447

<212> PRT

<213> Streptococcus agalactiae

<400> 219

Met Lys Lys Arg Ile Leu Ser Ala Val Leu Val Ser Gly Val Thr Leu
1 5 10 15

Gly Thr Ala Ala Val Thr Val Asn Ala Asp Asp Phe Asp Ser Lys Ile
20 25 30

Ala Ala Thr Asp Ser Val Ile Asn Thr Leu Ser Gly Gln Gln Ala Ala
35 40 45

Ala Gln Asn Gln Val Thr Ala Ile Lys Gly Gln Val Gly Ala Leu Glu
50 55 60

Ser Gln Gln Ser Glu Leu Glu Ala Gln Asn Ala Gln Leu Glu Ala Val
65 70 75 80

Ser Gln Gln Leu Gly Gln Glu Ile Gln Thr Leu Ser Asn Lys Ile Val
85 90 95

Ala Arg Asn Glu Ser Leu Lys Lys Gln Val Arg Ser Ala Gln Lys Gly
100 105 110

Asn Leu Thr Asn Tyr Ile Asn Thr Ile Leu Asn Ser Lys Ser Val Ser
115 120 125

Asp Ala Val Asn Arg Val Val Ala Ile Arg Glu Val Val Ser Ala Asn
130 135 140

Glu Lys Met Leu Ala Gln Gln Glu Ala Asp Lys Ala Ala Leu Glu Ala
145 150 155 160

Lys Gln Ile Glu Asn Gln Asn Ala Ile Asn Thr Val Ala Ala Asn Lys
165 170 175

Gln Ala Ile Glu Asn Asn Lys Ala Ala Leu Ala Thr Gln Arg Ala Gln
180 185 190

Leu Glu Ala Ala Gln Leu Glu Leu Ser Ala Gln Leu Thr Thr Val Gln
195 200 205

Asn Glu Lys Ala Ser Leu Ile Gln Ala Lys Ala Gln Ala Glu Glu Ala
210 215 220

Ala Arg Lys Ala Ala Glu Ala Gln Ala Ala Ala Glu Ala Lys Ala Gln
225 230 235 240

Ala Glu Ala Lys Ala Gln Ala Glu Ser Val Ala Lys Ala Gln Ala Ala
245 250 255

Ala Gln Val Glu Ser Ala Thr Ala Pro Thr Glu Thr Val Gln Thr Gln
260 265 270

Pro Arg Thr Glu Ile Lys Pro Ser Asn Leu Thr Ala Thr Ser Ser Ala
275 280 285

Thr Thr Val Ala Thr Thr Thr Ala Thr Ala Thr Asn Glu Pro Lys Val
290 295 300

Thr Gln Pro Ser Val Val Thr Lys Ala Val Glu Ala Pro Lys Ala Val
305 310 315 320

Val Ser Ser Thr Pro Arg Ala Val Ser Lys Pro Val Val Arg Ser Tyr
325 330 335

Asp Ser Ser Asn Thr Tyr Pro Met Gly Gln Cys Thr Trp Gly Ala Lys
340 345 350

Ser Met Ala Ser Trp Val Gly Asn Tyr Trp Gly Asn Ala Asn Gln Trp
355 360 365

Gly Ala Ser Ala Arg Ala Ala Gly Tyr Ser Val Gly Thr Thr Pro Arg
370 375 380

Val Gly Ala Val Ala Val Trp Pro Tyr Asp Gly Gly Gly Tyr Gly His
385 390 395 400

Val Ala Val Val Thr Ser Val Ala Asn Asn Ser Ser Ile Gln Val Met
405 410 415

Glu Ser Asn Tyr Ala Gly Asn Met Ser Ile Gly Asn Tyr Arg Gly Ser
420 425 430

Phe Asn Pro Ser Ala Ser Gly Ser Val Tyr Tyr Ile Tyr Pro Asn
435 440 445

<210> 220

<211> 1241

<212> PRT

<213> Streptococcus agalactiae

<400> 220

Met Asn Lys Arg Ile Phe Val Glu Lys Lys Ala Asp Phe Asp Ile Lys
1 5 10 15

Ser Ala Ser Leu Val Lys Glu Leu Thr His Asn Leu Gln Leu Thr Ser
20 25 30

Leu Lys Asp Leu Arg Ile Val Gln Val Tyr Asp Val Phe Asn Leu Ala
35 40 45

Glu Asp Leu Leu Ala Arg Ala Glu Lys His Ile Phe Ser Glu Gln Val
50 55 60

Thr Asp Cys Leu Leu Thr Glu Thr Glu Ile Thr Ala Glu Leu Asp Lys
65 70 75 80

Val Ala Phe Phe Ala Ile Glu Ala Leu Pro Gly Gln Phe Asp Gln Arg
85 90 95

Ala Ala Ser Ser Gln Glu Ser Leu Leu Leu Leu Gly Ser Asp Ser Gln
100 105 110

Val Lys Val Asn Thr Ala Gln Leu Tyr Leu Val Asn Lys Asp Ile Ala
115 120 125

Glu Ala Glu Leu Glu Ala Val Lys Asn Tyr Leu Leu Asn Pro Val Asp
130 135 140

Ser Arg Phe Lys Asp Ile Thr Leu Pro Leu Glu Glu Gln Ala Phe Ser
145 150 155 160

Val Ser Asp Lys Thr Ile Pro Ser Leu Asp Phe Phe Glu Thr Tyr Lys
165 170 175

Ala Asp Asp Phe Ala Ala Tyr Lys Ala Glu Gln Gly Leu Ala Met Glu
180 185 190

Val Asp Asp Leu Leu Phe Ile Gln Asp Tyr Phe Lys Ser Ile Gly Arg
195 200 205

Val Pro Thr Glu Thr Glu Leu Lys Val Leu Asp Thr Tyr Trp Ser Asp
210 215 220

His Cys Arg His Thr Thr Phe Glu Thr Glu Leu Lys Asn Ile Asp Phe
225 230 235 240

Ser Ala Ser Lys Phe Gln Lys Gln Leu Gln Ala Thr Tyr Asp Lys Tyr
245 250 255

Ile Ala Met Arg Asp Glu Leu Gly Arg Ser Glu Lys Pro Gln Thr Leu
260 265 270

Met Asp Met Ala Thr Ile Phe Gly Arg Tyr Glu Arg Ala Asn Gly Arg
275 280 285

Leu Asp Asp Met Glu Val Ser Asp Glu Ile Asn Ala Cys Ser Val Glu
290 295 300

Ile Glu Val Asp Val Asp Gly Val Lys Glu Pro Trp Leu Leu Met Phe
305 310 315 320

Lys Asn Glu Thr His Asn His Pro Thr Glu Ile Glu Pro Phe Gly Gly
325 330 335

Ala Ala Thr Cys Ile Gly Gly Ala Ile Arg Asp Pro Leu Ser Gly Arg
340 345 350

Ser Tyr Val Tyr Gln Ala Met Arg Ile Ser Gly Ala Gly Asp Ile Thr
355 360 365

Thr Pro Ile Ala Glu Thr Arg Ala Gly Lys Leu Pro Gln Gln Val Ile
370 375 380

Ser Lys Thr Ala Ala His Gly Tyr Ser Ser Tyr Gly Asn Gln Ile Gly
385 390 395 400

Leu Ala Thr Thr Tyr Val Arg Glu Tyr Phe His Pro Gly Phe Val Ala
405 410 415

Lys Arg Met Glu Leu Gly Ala Val Val Gly Ala Ala Pro Lys Glu Asn
420 425 430

Val Val Arg Glu Lys Pro Glu Ala Gly Asp Val Val Ile Leu Leu Gly
435 440 445

Gly Lys Thr Gly Arg Asp Gly Val Gly Gly Ala Thr Gly Ser Ser Lys
450 455 460

Val Gln Thr Val Glu Ser Val Glu Thr Ala Gly Ala Glu Val Gln Lys
465 470 475 480

Gly Asn Ala Ile Glu Glu Arg Lys Ile Gln Arg Leu Phe Arg Asn Gly
485 490 495

Asn Val Thr Arg Leu Ile Lys Lys Ser Asn Asp Phe Gly Ala Gly Gly
500 505 510

Val Cys Val Ala Ile Gly Glu Leu Ala Asp Gly Leu Glu Ile Asp Leu
515 520 525

Asp Lys Val Pro Leu Lys Tyr Gln Gly Leu Asn Gly Thr Glu Ile Ala
530 535 540

Ile Ser Glu Ser Gln Glu Arg Met Ser Val Val Val Arg Pro Ser Asp
545 550 555 560

Val Asp Thr Phe Ile Ala Ala Cys Asn Lys Glu Asn Ile Asp Ala Val
565 570 575

Val Val Ala Thr Ile Thr Ala Lys Pro Asn Leu Val Met Thr Trp Asp
580 585 590

Gly Glu Thr Ile Val Asp Leu Glu Arg Arg Phe Leu Asp Thr Asn Gly
595 600 605

Val Arg Val Val Val Asp Ala Lys Val Val Asp Lys Asp Leu Thr Val
610 615 620

Pro Glu Val Arg Thr Thr Ser Ala Glu Thr Leu Glu Ala Asp Thr Leu
625 630 635 640

Lys Val Leu Ser Asp Leu Asn His Ala Ser Gln Lys Gly Leu Gln Thr
645 650 655

Ile Phe Asp Ser Ser Val Gly Arg Ser Thr Val Asn His Pro Ile Gly
660 665 670

Gly Arg Tyr Gln Ile Thr Pro Thr Glu Ser Ser Val Gln Lys Leu Pro
675 680 685

Val Gln His Gly Val Thr Thr Thr Ala Ser Val Met Ala Gln Gly Tyr
690 695 700

Asn Pro Tyr Ile Ala Glu Trp Ser Pro Tyr His Gly Ala Ala Tyr Ala
705 710 715 720

Val Ile Glu Ala Thr Ala Arg Leu Val Ala Thr Gly Ala Asp Trp Ser
725 730 735

Arg Ala Arg Phe Ser Tyr Gln Glu Tyr Phe Glu Arg Met Asp Lys Gln
740 745 750

Ala Glu Arg Phe Gly Gln Pro Val Ser Ala Leu Leu Gly Ser Ile Glu
755 760 765

Ala Gln Ile Gln Leu Gly Leu Pro Ser Ile Gly Gly Lys Asp Ser Met
770 775 780

Ser Gly Thr Phe Glu Glu Leu Thr Val Pro Pro Thr Leu Val Ala Phe
785 790 795 800

Gly Val Thr Thr Ala Asp Ser Arg Lys Val Leu Ser Pro Glu Phe Lys
805 810 815

Ala Ala Gly Glu Asn Ile Tyr Tyr Ile Pro Gly Gln Ala Ile Ser Glu
820 825 830

Asp Ile Asp Phe Asp Leu Ile Lys Ala Asn Phe Ser Gln Phe Glu Thr
835 840 845

Ile Gln Ala Gln His Lys Ile Thr Ala Ala Ser Ala Val Lys Tyr Gly
850 855 860

Gly Val Leu Glu Ser Leu Ala Leu Met Thr Phe Gly Asn Arg Ile Gly
865 870 875 880

Ala Ser Val Glu Ile Ala Glu Leu Asp Ser Ser Leu Thr Ala Gln Leu
885 890 895

Gly Gly Phe Val Phe Thr Ser Ala Glu Glu Ile Ala Asp Ser Val Lys
900 905 910

Ile Gly Gln Thr Gln Ala Ala Phe Thr Leu Thr Val Asn Gly Asn Asp
915 920 925

Leu Ala Gly Ala Ser Leu Leu Ser Val Phe Glu Gly Lys Leu Glu Glu
930 935 940

Val Tyr Pro Thr Glu Phe Glu Gln Ala Asp Ala Leu Glu Glu Val Pro
945 950 955 960

Ala Val Val Ser Asp Thr Val Ile Lys Ala Lys Glu Thr Ile Glu Lys
965 970 975

Pro Val Val Tyr Ile Pro Val Phe Pro Gly Thr Asn Ser Glu Tyr Asp
980 985 990

Ser Ala Lys Ala Phe Glu Gln Val Gly Ala Ser Val Asn Leu Val Ala
995 1000 1005

Phe Val Thr Leu Asn Glu Ala Ala Ile Ala Asp Ser Val Asp Thr
1010 1015 1020

Met Val Ala Asn Ile Ala Lys Ala Asn Ile Ile Phe Phe Ala Gly
1025 1030 1035

Gly Phe Ser Ala Ala Asp Glu Pro Asp Gly Ser Ala Lys Phe Ile
1040 1045 1050

Val Asn Ile Leu Leu Asn Lys Lys Val Arg Ala Ala Ile Asp Ser
1055 1060 1065

Phe Ile Glu Lys Gly Gly Leu Ile Ile Gly Ile Cys Asn Gly Phe
1070 1075 1080

Gln Ala Leu Val Lys Ser Gly Leu Leu Pro Tyr Gly Asn Phe Glu
1085 1090 1095

Glu Ala Gly Glu Thr Ser Pro Thr Leu Phe Tyr Asn Asp Ala Asn
1100 1105 1110

Gln His Val Ala Lys Met Val Glu Thr Arg Ile Ala Asn Thr Asn
1115 1120 1125

Ser Pro Trp Leu Val Gly Val Glu Val Gly Asp Ile His Ala Ile
1130 1135 1140

Pro Val Ser His Gly Glu Gly Lys Phe Val Val Ser Ala Ser Glu
1145 1150 1155

Phe Ala Glu Leu Arg Asp Asn Gly Gln Ile Trp Ser Gln Tyr Val
1160 1165 1170

Asp Phe Asp Gly Gln Pro Ser Met Asp Ser Lys Tyr Asn Pro Asn
1175 1180 1185

Gly Ser Val Asn Ala Ile Glu Gly Ile Thr Ser Lys Asn Gly Gln
1190 1195 1200

Ile Ile Gly Lys Met Gly His Ser Glu Arg Trp Glu Asp Gly Leu
1205 1210 1215

Phe Gln Asn Ile Pro Gly Asn Lys Asp Gln Ala Leu Phe Ala Ser
1220 1225 1230

Ala Val Lys Tyr Phe Thr Gly Lys
1235 1240

<210> 221

<211> 434

<212> PRT

<213> Streptococcus agalactiae

<400> 221

Met Lys Met Asn Lys Lys Val Leu Leu Thr Ser Thr Met Ala Ala Ser
1 5 10 15

Leu Leu Ser Val Ala Ser Val Gln Ala Gln Glu Thr Asp Thr Thr Trp
20 25 30

Thr Ala Arg Thr Val Ser Glu Val Lys Ala Asp Leu Val Lys Gln Asp
35 40 45

Asn Lys Ser Ser Tyr Thr Val Lys Tyr Gly Asp Thr Leu Ser Val Ile
50 55 60

Ser Glu Ala Met Ser Ile Asp Met Asn Val Leu Ala Lys Ile Asn Asn
65 70 75 80

Ile Ala Asp Ile Asn Leu Ile Tyr Pro Glu Thr Thr Leu Thr Val Thr
85 90 95

Tyr Asp Gln Lys Ser His Thr Ala Thr Ser Met Lys Ile Glu Thr Pro
100 105 110

Ala Thr Asn Ala Ala Gly Gln Thr Thr Ala Thr Val Asp Leu Lys Thr
115 120 125

Asn Gln Val Ser Val Ala Asp Gln Lys Val Ser Leu Asn Thr Ile Ser
130 135 140

Glu Gly Met Thr Pro Glu Ala Ala Thr Thr Ile Val Ser Pro Met Lys
145 150 155 160

Thr Tyr Ser Ser Ala Pro Ala Leu Lys Ser Lys Glu Val Leu Ala Gln
165 170 175

Glu Gln Ala Val Ser Gln Ala Ala Ala Asn Glu Gln Val Ser Pro Ala
180 185 190

Pro Val Lys Ser Ile Thr Ser Glu Val Pro Ala Ala Lys Glu Glu Val
195 200 205

Lys Pro Thr Gln Thr Ser Val Ser Gln Ser Thr Thr Val Ser Pro Ala
    210                 215                     220

Ser Val Ala Ala Glu Thr Pro Ala Pro Val Ala Lys Val Ala Pro Val
225                 230                 235                 240

Arg Thr Val Ala Ala Pro Arg Val Ala Ser Val Lys Val Val Thr Pro
                245                 250                 255

Lys Val Glu Thr Gly Ala Ser Pro Glu His Val Ser Ala Pro Ala Val
            260                 265                 270

Pro Val Thr Thr Thr Ser Pro Ala Thr Asp Ser Lys Leu Gln Ala Thr
        275                 280                 285

Glu Val Lys Ser Val Pro Val Ala Gln Lys Ala Pro Thr Ala Thr Pro
    290                 295                 300

Val Ala Gln Pro Ala Ser Thr Thr Asn Ala Val Ala Ala His Pro Glu
305                 310                 315                 320

Asn Ala Gly Leu Gln Pro His Val Ala Ala Tyr Lys Glu Lys Val Ala
                325                 330                 335

Ser Thr Tyr Gly Val Asn Glu Phe Ser Thr Tyr Arg Ala Gly Asp Pro
            340                 345                 350

Gly Asp His Gly Lys Gly Leu Ala Val Asp Phe Ile Val Gly Thr Asn
        355                 360                 365

Gln Ala Leu Gly Asn Lys Val Ala Gln Tyr Ser Thr Gln Asn Met Ala
    370                 375                 380

Ala Asn Asn Ile Ser Tyr Val Ile Trp Gln Gln Lys Phe Tyr Ser Asn
385                 390                 395                 400

Thr Asn Ser Ile Tyr Gly Pro Ala Asn Thr Trp Asn Ala Met Pro Asp
                405                 410                 415

Arg Gly Gly Val Thr Ala Asn His Tyr Asp His Val His Val Ser Phe
            420                 425                 430

Asn Lys

<210> 222

<211> 300

<212> PRT

<213> Streptococcus agalactiae

<400> 222

Met Leu Lys His Phe Gly Ser Lys Val Arg Asn Leu Arg Val Thr Arg
1               5                   10                  15

Asn Ile Thr Arg Glu Asp Phe Cys Gly Asp Glu Thr Glu Leu Ser Val
            20                  25                  30

Arg Gln Leu Ala Arg Ile Glu Ser Gly Gln Ser Ile Pro Asn Leu Thr
        35                  40                  45

Lys Ala His Tyr Ile Ala Lys Gln Leu Asn Val Lys Leu Asp Ile Leu
    50                  55                  60

Thr Gly Gly Glu Ser Leu Glu Leu Pro Lys Arg Tyr Lys Glu Leu Lys
65                  70                  75                  80

Tyr Lys Leu Leu Arg Thr Pro Thr Tyr Gly Asp Ala Asn Arg Leu Ala
                85                  90                  95

Val Arg Glu Ala Tyr Phe Asp Glu Ile Tyr Glu Val Phe Tyr Glu Glu
            100                 105                 110

Leu Pro Glu Asp Glu Arg Leu Ile Ile Asp Cys Met Gln Ser Lys Leu
        115                 120                 125

Asp Val His Phe Ser Val Asn Asp Asn Phe Gly Ile Thr Ile Leu His
    130                 135                 140

Asp Tyr Phe Asp Gln Ile Lys Lys Lys Lys Glu Tyr Thr Thr Asn Asp
145                 150                 155                 160

Phe Val Met Ile Asp Leu Tyr Leu Leu Cys Phe Ser Ile Asn Tyr Gly
                165                 170                 175

Met Lys Ser Leu Tyr Ser Leu Glu Asn Tyr His Phe Ile Met Ser Lys
            180                 185                 190

Leu Leu Glu Gln Asp Asn Leu Leu Pro Glu Asp Asn Phe Gln Leu Asn
        195                 200                 205

Asn Val Leu Leu Asn His Val Glu Leu Ala Phe Gln Phe Lys Gln Lys
    210                 215                 220

Lys Tyr Val Gln Gln Ile Ile His Arg Ser Asn Ala Ile Met Thr Glu
225                 230                 235                 240

Ile His Asp Phe Gln Lys Arg Pro Ile Leu Ser Leu Ile Glu Trp Lys
                245                 250                 255

Tyr Leu Leu Ile Ile Glu Lys Asp Arg Thr Lys Ala Glu Thr Cys Phe
260 265 270

Lys Gln Ser Ile Leu Phe Ala Glu Leu Ile Gly Asp Leu Tyr Leu Lys
275 280 285

Gly Lys Leu Ile Glu Glu Trp Asn Lys Asp Leu Thr
290 295 300

<210> 223

<211> 880

<212> PRT

<213> Streptococcus agalactiae

<400> 223

Met Thr Glu Lys Thr Lys Ala Val Glu Thr Thr Asp Val Ala Leu Ala
1 5 10 15

Ile Asp Thr Leu Val Gln Asn Gly Leu Lys Ala Leu Asp Glu Met Arg
20 25 30

Gln Leu Asn Gln Glu Gln Val Asp Tyr Ile Val Ala Lys Ala Ser Val
35 40 45

Ala Ala Leu Asp Ala His Gly Glu Leu Ala Leu His Ala Val Glu Glu
50 55 60

Thr Gly Arg Gly Val Phe Glu Asp Lys Ala Thr Lys Asn Leu Phe Ala
65 70 75 80

Cys Glu His Val Val Asn Asn Met Arg His Thr Lys Thr Val Gly Val
85 90 95

Ile Glu Glu Asp Asp Val Thr Gly Leu Thr Leu Ile Ala Glu Pro Val
100 105 110

Gly Val Val Cys Gly Ile Thr Pro Thr Thr Asn Pro Thr Ser Thr Ala
115 120 125

Ile Phe Lys Ser Leu Ile Ser Leu Lys Thr Arg Asn Pro Ile Ile Phe
130 135 140

Ala Phe His Pro Ser Ala Gln Glu Ser Ser Ala His Ala Ala Arg Ile
145 150 155 160

Val Arg Asp Ala Ala Ile Ala Ala Gly Ala Pro Glu Asn Cys Val Gln
165 170 175

Trp Ile Glu Gln Pro Ser Ile Asp Ala Thr Asn Ala Leu Met Asn His
180 185 190

Asp Gly Ile Ala Thr Ile Leu Ala Thr Gly Gly Asn Ala Met Val Lys
195 200 205

Ala Ala Tyr Ser Cys Gly Lys Pro Ala Leu Gly Val Gly Ala Gly Asn
210 215 220

Val Pro Ala Tyr Val Glu Lys Ser Ala Asn Ile Arg Gln Ala Ala His
225 230 235 240

Asp Ile Val Met Ser Lys Ser Phe Asp Asn Gly Met Val Cys Ala Ser
245 250 255

Glu Gln Ala Val Ile Ile Asp Lys Glu Ile Tyr Lys Glu Phe Val Glu
260 265 270

Glu Phe Lys Ser Tyr His Thr Tyr Phe Val Asn Lys Lys Glu Lys Ala
275 280 285

Leu Leu Glu Glu Phe Cys Phe Gly Ala Lys Ala Asn Ser Lys Asn Cys
290 295 300

Ala Gly Ala Lys Leu Asn Pro Asn Ile Val Gly Lys Ser Ala Val Trp
305 310 315 320

Ile Ala Glu Gln Ala Gly Phe Thr Val Pro Glu Gly Thr Asn Ile Leu
325 330 335

Ala Ala Glu Cys Thr Glu Val Ser Glu Lys Glu Pro Leu Thr Arg Glu
340 345 350

Lys Leu Ser Pro Val Ile Ala Val Leu Lys Ala Glu Ser Thr Glu Asp
355 360 365

Gly Val Glu Lys Ala Arg Gln Met Val Glu Phe Asn Gly Leu Gly His
370 375 380

Ser Ala Ala Ile His Thr Lys Asp Ala Asp Leu Ala Arg Glu Phe Gly
385 390 395 400

Thr Arg Ile Arg Ala Ile Arg Val Ile Trp Asn Ser Pro Ser Thr Phe
405 410 415

Gly Gly Ile Gly Asp Val Tyr Asn Ala Phe Leu Pro Ser Leu Thr Leu
420 425 430

Gly Cys Gly Ser Tyr Gly Arg Asn Ser Val Gly Asp Asn Val Ser Ala
435 440 445

Ile Asn Leu Leu Asn Ile Lys Lys Val Gly Arg Arg Arg Asn Asn Met
450 455 460

Gln Trp Phe Lys Val Pro Ser Lys Thr Tyr Phe Glu Arg Asp Ser Ile
465 470 475 480

Gln Tyr Leu Gln Lys Cys Arg Asp Val Glu Arg Val Met Ile Val Thr
485 490 495

Asp His Ala Met Val Glu Leu Gly Phe Leu Asp Arg Ile Ile Glu Gln
500 505 510

Leu Asp Leu Arg Arg Asn Lys Val Val Tyr Gln Ile Phe Ala Glu Val
515 520 525

Glu Pro Asp Pro Asp Ile Thr Thr Val Met Lys Gly Thr Asp Leu Met
530 535 540

Arg Thr Phe Lys Pro Asp Thr Ile Ile Ala Leu Gly Gly Gly Ser Pro
545 550 555 560

Met Asp Ala Ala Lys Val Met Trp Leu Phe Tyr Glu Gln Pro Glu Val
565 570 575

Asp Phe His Asp Leu Val Gln Lys Phe Met Asp Ile Arg Lys Arg Ala
580 585 590

Phe Lys Phe Pro Glu Leu Gly Lys Lys Thr Lys Phe Val Ala Ile Pro
595 600 605

Thr Thr Ser Gly Thr Gly Ser Glu Val Thr Pro Phe Ala Val Ile Ser
610 615 620

Asp Lys Ala Asn Asn Arg Lys Tyr Pro Ile Ala Asp Tyr Ser Leu Thr
625 630 635 640

Pro Thr Val Ala Ile Val Asp Pro Ala Leu Val Met Thr Val Pro Gly
645 650 655

Phe Ile Ala Ala Asp Thr Gly Met Asp Val Leu Thr His Ala Thr Glu
660 665 670

Ala Tyr Val Ser Gln Met Ala Asn Asp Tyr Thr Asp Gly Leu Ala Leu
675 680 685

Gln Ala Ile Lys Ile Val Phe Asp Tyr Leu Glu Arg Ser Val Lys Asp
690 695 700

Ala Asp Phe Glu Ala Arg Glu Lys Met His Asn Ala Ser Thr Met Ala
705 710 715 720

Gly Met Ala Phe Ala Asn Ala Phe Leu Gly Ile Ser His Ser Met Ala
725 730 735

His Lys Ile Gly Ala Gln Phe His Thr Val His Gly Arg Thr Asn Ala
740 745 750

Ile Leu Leu Pro Tyr Val Ile Arg Tyr Asn Gly Thr Arg Pro Ala Lys
755 760 765

Thr Ala Thr Trp Pro Lys Tyr Asn Tyr Tyr Arg Ala Asp Glu Lys Tyr
770 775 780

Gln Asp Ile Ala Lys Leu Leu Gly Leu Pro Ala Ala Thr Pro Glu Glu
785 790 795 800

Ala Val Glu Ser Tyr Ala Lys Ala Val Tyr Asp Leu Gly Thr Arg Leu
805 810 815

Gly Ile Lys Met Asn Phe Arg Asp Gln Gly Ile Asp Glu Lys Glu Trp
820 825 830

Lys Glu Lys Ser Arg Glu Leu Ala Phe Leu Ala Tyr Glu Asp Gln Cys
835 840 845

Ser Pro Ala Asn Pro Arg Leu Pro Met Val Asp His Met Gln Glu Ile
850 855 860

Ile Glu Asp Ala Tyr Tyr Gly Tyr Glu Glu Arg Pro Gly Arg Arg Lys
865 870 875 880

<210> 224

<211> 277

<212> PRT

<213> Streptococcus agalactiae

<400> 224

Val Gly Ile Lys Val Tyr Lys Pro Thr Thr Asn Gly Arg Arg Asn Met
1 5 10 15

Thr Ser Leu Asp Phe Ala Glu Ile Thr Thr Asn Thr Pro Glu Lys Ser
20 25 30

Leu Leu Val Ser Leu Lys Asn Lys Ala Gly Arg Asn Asn Asn Gly Arg
35 40 45

Ile Thr Val Arg His Gln Gly Gly Gly His Lys Arg His Tyr Arg Leu
50 55 60

Ile Asp Phe Lys Arg Asn Lys Asp Gly Val Glu Ala Val Val Lys Thr
65 70 75 80

Ile Glu Tyr Asp Pro Asn Arg Thr Ala Asn Ile Ala Leu Val His Tyr
85 90 95

Thr Asp Gly Val Lys Ala Tyr Ile Leu Ala Pro Lys Gly Leu Glu Val
100 105 110

Gly Gln Arg Ile Ile Ser Gly Pro Glu Ala Asp Ile Lys Val Gly Asn
115 120 125

Ala Leu Pro Leu Ala Asn Ile Pro Val Gly Thr Val Ile His Asn Ile
130 135 140

Glu Leu Gln Pro Gly Lys Gly Ala Glu Leu Ile Arg Ala Ala Gly Ala
145 150 155 160

Ser Ala Gln Val Leu Gly Gln Glu Gly Lys Tyr Val Leu Val Arg Leu
165 170 175

Gln Ser Gly Glu Val Arg Met Ile Leu Gly Thr Cys Arg Ala Thr Ile
180 185 190

Gly Thr Val Gly Asn Glu Gln Gln Ser Leu Val Asn Ile Gly Lys Ala
195 200 205

Gly Arg Asn Arg Trp Lys Gly Val Arg Pro Thr Val Arg Gly Ser Val
210 215 220

Met Asn Pro Asn Asp His Pro His Gly Gly Gly Glu Gly Lys Ala Pro
225 230 235 240

Val Gly Arg Lys Ala Pro Ser Thr Pro Trp Gly Lys Pro Ala Leu Gly
245 250 255

Leu Lys Thr Arg Asn Lys Lys Ala Lys Ser Asp Lys Leu Ile Val Arg
260 265 270

Arg Arg Asn Gln Lys
275

<210> 225

<211> 312

<212> PRT

<213> Streptococcus agalactiae

<400> 225

Met Ile Glu Phe Glu Lys Pro Ile Ile Thr Lys Ile Asp Glu Asn Lys
1               5                   10                  15

Asp Tyr Gly Arg Phe Val Ile Glu Pro Leu Glu Arg Gly Tyr Gly Thr
            20                  25                  30

Thr Leu Gly Asn Ser Leu Arg Arg Val Leu Leu Ser Ser Leu Pro Gly
        35                  40                  45

Ala Ala Val Thr Ser Ile Lys Ile Asp Gly Val Leu His Glu Phe Asp
    50                  55                  60

Thr Ile Pro Gly Val Arg Glu Asp Val Met Gln Ile Ile Leu Asn Val
65                  70                  75                  80

Lys Gly Leu Ala Val Lys Ser Tyr Val Glu Asp Glu Lys Ile Ile Glu
                85                  90                  95

Leu Asp Val Glu Gly Pro Ala Glu Ile Thr Ala Gly Asp Ile Leu Thr
            100                 105                 110

Asp Ser Asp Ile Glu Ile Val Asn Pro Asp His Tyr Leu Phe Thr Ile
        115                 120                 125

Ala Glu Gly His Ser Leu Lys Ala Thr Met Thr Val Ala Lys Asn Arg
    130                 135                 140

Gly Tyr Val Pro Ala Glu Gly Asn Lys Lys Asp Asp Ala Pro Val Gly
145                 150                 155                 160

Thr Leu Ala Val Asp Ser Ile Tyr Thr Pro Val Lys Lys Val Asn Tyr
                165                 170                 175

Gln Val Glu Pro Ala Arg Val Gly Ser Asn Asp Gly Phe Asp Lys Leu
            180                 185                 190

Thr Ile Glu Ile Met Thr Asn Gly Thr Ile Ile Pro Glu Asp Ala Leu
        195                 200                 205

Gly Leu Ser Ala Arg Val Leu Ile Glu His Leu Asn Leu Phe Thr Asp
    210                 215                 220

Leu Thr Glu Val Ala Lys Ala Thr Glu Val Met Lys Glu Thr Glu Lys
225                 230                 235                 240

Val Asn Asp Glu Lys Val Leu Asp Arg Thr Ile Glu Glu Leu Asp Leu
                245                 250                 255

Ser Val Arg Ser Tyr Asn Cys Leu Lys Arg Ala Gly Ile Asn Thr Val
            260                 265                 270

Phe Asp Leu Thr Glu Lys Thr Glu Pro Glu Met Met Lys Val Arg Asn
275 280 285

Leu Gly Arg Lys Ser Leu Glu Glu Val Lys Ile Lys Leu Ala Asp Leu
290 295 300

Gly Leu Gly Leu Lys Asn Asp Lys
305 310

<210> 226

<211> 308

<212> PRT

<213> Streptococcus agalactiae

<400> 226

Met Lys Lys Ile Arg Leu Ser Lys Phe Ile Lys Met Ile Val Val Ile
1 5 10 15

Leu Phe Leu Ile Ser Val Ala Ala Ser Phe Tyr Phe Phe His Val Ala
20 25 30

Gln Val Arg Asp Asp Lys Ser Phe Ile Ser Asn Gly Gln Arg Lys Pro
35 40 45

Gly Asn Ser Leu Tyr Ala Tyr Asp Lys Ser Phe Asp Lys Leu Leu Lys
50 55 60

Gln Lys Ile Glu Met Thr Asn Gln Asn Ile Lys Gln Val Ala Trp Tyr
65 70 75 80

Val Pro Ala Ala Lys Lys Thr His Lys Thr Ala Val Val Val His Gly
85 90 95

Phe Ala Asn Ser Lys Glu Asn Met Lys Ala Tyr Gly Trp Leu Phe His
100 105 110

Lys Leu Gly Tyr Asn Val Leu Met Pro Asp Asn Ile Ala His Gly Glu
115 120 125

Ser His Gly Gln Leu Ile Gly Tyr Gly Trp Asn Asp Arg Glu Asn Ile
130 135 140

Ile Lys Trp Thr Glu Met Ile Val Asp Lys Asn Pro Ser Ser Gln Ile
145 150 155 160

Thr Leu Phe Gly Val Ser Met Gly Gly Ala Thr Val Met Met Ala Ser
165 170 175

Gly Glu Lys Leu Pro Ser Gln Val Val Asn Ile Ile Glu Asp Cys Gly
180 185 190

Tyr Ser Ser Val Trp Asp Glu Leu Lys Phe Gln Ala Lys Glu Met Tyr
195 200 205

Gly Leu Pro Ala Phe Pro Leu Leu Tyr Glu Val Ser Thr Ile Ser Lys
210 215 220

Ile Arg Ala Gly Phe Ser Tyr Gly Gln Ala Ser Ser Val Glu Gln Leu
225 230 235 240

Lys Lys Asn Asn Leu Pro Ala Leu Phe Ile His Gly Asp Lys Asp Asn
245 250 255

Phe Val Pro Thr Ser Met Val Tyr Asp Asn Tyr Lys Ala Thr Ala Gly
260 265 270

Lys Lys Glu Leu Tyr Ile Val Lys Gly Ala Lys His Ala Lys Ser Phe
275 280 285

Glu Thr Glu Pro Glu Lys Tyr Glu Lys Arg Ile Ser Ser Phe Leu Lys
290 295 300

Lys Tyr Glu Lys
305

<210> 227

<211> 148

<212> PRT

<213> Streptococcus agalactiae

<400> 227

Met Ser Lys Val Arg Gly Phe Glu Leu Val Ser Gln Phe Ser Asn Lys
1 5 10 15

Glu Leu Leu Pro Lys Arg Glu Thr Ala His Ala Ala Gly Tyr Asp Leu
20 25 30

Lys Val Ala Lys Lys Thr Val Ile Glu Pro Gly Glu Ile Thr Leu Val
35 40 45

Pro Thr Gly Ile Lys Ala His Met Gln Pro Gly Glu Val Leu Tyr Leu
50 55 60

Tyr Asp Arg Ser Ser Asn Pro Arg Lys Lys Gly Ile Val Leu Ile Asn
65 70 75 80

Ser Val Gly Val Ile Asp Gly Asp Tyr Tyr Asn Asn Gln Val Asn Glu
85 90 95

Gly His Ile Phe Ala Gln Met Gln Asn Ile Thr Asp Gln Ala Val Ile
100 105 110

Leu Glu Glu Gly Glu Arg Ile Val Gln Ala Val Phe Ala Pro Phe Leu
115 120 125

Leu Ala Asp Asp Asp Gln Ala Thr Gly Met Arg Thr Gly Gly Phe Gly
130 135 140

Ser Thr Gly Lys
145

<210> 228

<211> 322

<212> PRT

<213> Streptococcus agalactiae

<400> 228

Met Lys Phe Gly Lys Lys Leu Gly Phe Leu Ala Leu Leu Met Ser Ile
1 5 10 15

Val Leu Ile Leu Gly Ala Cys Gly Lys Thr Gly Leu Gly Asn Ser Thr
20 25 30

Gly Asn Ser Thr Lys Asn Val Thr Lys Lys Ser Ala Lys Asn Leu Lys
35 40 45

Leu Gly Val Ser Ile Ser Thr Thr Asn Asn Pro Tyr Phe Val Ala Met
50 55 60

Lys Asp Gly Ile Asp Lys Tyr Ala Ser Asn Lys Lys Ile Ser Ile Lys
65 70 75 80

Val Ala Asp Ala Gln Asp Asp Ala Ala Arg Gln Ala Asp Asp Val Gln
85 90 95

Asn Phe Ile Ser Gln Asn Val Asp Ala Ile Leu Ile Asn Pro Val Asp
100 105 110

Ser Lys Ala Ile Val Thr Ala Ile Lys Ser Ala Asn Asn Ala Asn Ile
115 120 125

Pro Val Ile Leu Met Asp Arg Gly Ser Glu Gly Gly Lys Val Leu Thr
130 135 140

Thr Val Ala Ser Asp Asn Val Ala Ala Gly Lys Met Ala Ala Asp Tyr
145 150 155 160

Ala Val Lys Lys Leu Gly Lys Lys Ala Lys Ala Phe Glu Leu Ser Gly
165 170 175

Val Pro Gly Ala Ser Ala Thr Val Asp Arg Gly Lys Gly Phe His Ser
180 185 190

Val Ala Lys Ser Lys Leu Asp Ile Leu Ser Ser Gln Ser Ala Asn Phe
195 200 205

Asp Arg Ala Lys Ala Leu Asn Thr Thr Gln Asn Met Ile Gln Gly His
210 215 220

Lys Asp Val Gln Ile Ile Phe Ala Gln Asn Asp Glu Met Ala Leu Gly
225 230 235 240

Ala Ala Gln Ala Val Lys Ser Ala Gly Leu Gln Asn Val Leu Ile Val
245 250 255

Gly Ile Asp Gly Gln Pro Asp Ala His Asp Ala Ile Lys Lys Gly Asp
260 265 270

Ile Ser Ala Thr Ile Ala Gln Gln Pro Ala Lys Met Gly Glu Ile Ala
275 280 285

Ile Gln Ala Ala Ile Asp His Tyr Lys Gly Lys Lys Val Glu Lys Glu
290 295 300

Thr Ile Ser Pro Ile Tyr Leu Val Thr Lys Asp Asn Val Glu Lys Tyr
305 310 315 320

Asn Trp

<210> 229

<211> 396

<212> PRT

<213> Streptococcus agalactiae

<400> 229

Met Gly Lys Glu Lys Leu Ile Leu Ala Tyr Ser Gly Gly Leu Asp Thr
1 5 10 15

Ser Val Ala Ile Ala Trp Leu Lys Lys Asp Tyr Asp Val Ile Ala Val
20 25 30

Cys Met Asp Val Gly Glu Gly Lys Asp Leu Asp Phe Ile His Asp Lys
35 40 45

Ala Leu Thr Ile Gly Ala Ile Glu Ser Tyr Ile Leu Asp Val Lys Asp
50 55 60

Glu Phe Ala Glu His Phe Val Leu Pro Ala Leu Gln Ala His Ala Met
65 70 75 80

Tyr Glu Gln Lys Tyr Pro Leu Val Ser Ala Leu Ser Arg Pro Ile Ile
85 90 95

Ala Gln Lys Leu Val Glu Met Ala His Gln Thr Gly Ala Thr Thr Ile
100 105 110

Ala His Gly Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe Glu Val
115 120 125

Ala Ile Ala Ala Leu Asp Pro Glu Leu Lys Val Ile Ala Pro Val Arg
130 135 140

Glu Trp Lys Trp His Arg Glu Glu Glu Ile Thr Phe Ala Lys Ala Asn
145 150 155 160

Gly Val Pro Ile Pro Ala Asp Leu Asp Asn Pro Tyr Ser Ile Asp Gln
165 170 175

Asn Leu Trp Gly Arg Ala Asn Glu Cys Gly Val Leu Glu Asn Pro Trp
180 185 190

Asn Gln Ala Pro Glu Glu Ala Phe Gly Ile Thr Lys Ser Pro Glu Glu
195 200 205

Ala Pro Asp Cys Ala Glu Tyr Ile Asp Ile Thr Phe Gln Asn Gly Lys
210 215 220

Pro Ile Ala Ile Asn Asn Gln Glu Met Thr Leu Ala Asp Leu Ile Leu
225 230 235 240

Ser Leu Asn Glu Ile Ala Gly Lys His Gly Ile Gly Arg Ile Asp His
245 250 255

Val Glu Asn Arg Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu Cys
260 265 270

Pro Ala Ala Met Val Leu Leu Ala Ala His Lys Glu Ile Glu Asp Leu
275 280 285

Thr Leu Val Arg Glu Val Ser His Phe Lys Pro Ile Leu Glu Asn Glu
290 295 300

Leu Ser Asn Leu Ile Tyr Asn Ala Leu Trp Phe Ser Pro Ala Thr Lys
305 310 315 320

Ala Ile Ile Ala Tyr Val Lys Glu Thr Gln Lys Val Val Asn Gly Thr
325 330 335

Thr Lys Val Lys Leu Tyr Lys Gly Ser Ala Lys Val Val Ala Arg His
340 345 350

Ser Ser Asn Ser Leu Tyr Asp Glu Asn Leu Ala Thr Tyr Thr Ala Ala
355 360 365

Asp Asn Phe Asp Gln Asp Ala Ala Val Gly Phe Ile Lys Leu Trp Gly
370 375 380

Leu Pro Thr Gln Val Asn Ala Gln Val Asn Lys Gly
385 390 395

<210> 230

<211> 62

<212> PRT

<213> Streptococcus agalactiae

<400> 230

Met Ala Lys Val Cys Tyr Phe Thr Gly Arg Lys Thr Val Ser Gly Asn
1 5 10 15

Asn Arg Ser His Ala Met Asn Gln Thr Lys Arg Thr Val Lys Pro Asn
20 25 30

Leu Gln Lys Val Thr Val Leu Ile Asp Gly Lys Pro Lys Lys Val Trp
35 40 45

Val Ser Ala Arg Ala Leu Lys Ser Gly Lys Val Glu Arg Val
50 55 60

<210> 231

<211> 551

<212> PRT

<213> Streptococcus agalactiae

<400> 231

Met Ala Lys Gln Lys Asn Asn Trp Arg Arg Val Gly Val Gly Val Leu
1 5 10 15

Thr Leu Ala Ser Val Ala Thr Leu Ala Ala Cys Gly Ser Lys Ser Ala
20 25 30

Ser Gln Asp Ser Asn Gly Ala Ile Asn Trp Ala Ile Pro Thr Glu Ile
35 40 45

Asn Thr Leu Asp Leu Ser Lys Val Thr Asp Thr Tyr Ser Asn Leu Ala
50 55 60

Ile Gly Asn Ser Ser Ser Asn Phe Leu Arg Leu Asp Lys Asp Gly Lys
65 70 75 80

Thr Arg Pro Asp Leu Ala Thr Lys Val Asp Val Ser Lys Asp Gly Leu
85 90 95

Thr Tyr Thr Ala Thr Leu Arg Lys Gly Leu Lys Trp Ser Asp Gly Ser
100 105 110

Lys Leu Thr Ala Lys Asp Phe Val Tyr Ser Trp Gln Arg Leu Val Asp
115 120 125

Pro Lys Thr Ala Ser Gln Tyr Ala Tyr Leu Ala Val Glu Gly His Val
130 135 140

Leu Asn Ala Asp Lys Ile Asn Glu Gly Gln Glu Lys Asp Leu Asn Lys
145 150 155 160

Leu Gly Val Lys Ala Glu Gly Asp Asp Lys Val Val Ile Thr Leu Ser
165 170 175

Ser Pro Ser Pro Gln Phe Ile Tyr Tyr Leu Ala Phe Thr Asn Phe Met
180 185 190

Pro Gln Lys Gln Glu Val Val Glu Lys Tyr Gly Lys Asp Tyr Ala Thr
195 200 205

Thr Ser Lys Asn Thr Val Tyr Ser Gly Pro Tyr Thr Val Glu Gly Trp
210 215 220

Asn Gly Ser Asn Gly Thr Phe Thr Leu Lys Lys Asn Lys Asn Tyr Trp
225 230 235 240

Asp Ala Lys Asn Val Lys Thr Lys Glu Val Arg Ile Gln Thr Val Lys
245 250 255

Lys Pro Asp Thr Ala Val Gln Met Tyr Lys Arg Gly Glu Leu Asp Ala
260 265 270

Ala Asn Ile Ser Asn Thr Ser Ala Ile Tyr Gln Ala Asn Lys Asn Asn
275 280 285

Lys Asp Val Thr Asp Val Leu Glu Ala Thr Thr Ala Tyr Met Gln Tyr
290 295 300

Asn Thr Thr Gly Ser Val Lys Gly Leu Asp Asn Val Lys Ile Arg Arg
305 310 315 320

Ala Leu Asn Leu Ala Thr Asn Arg Lys Gly Val Val Gln Ala Ala Val
325 330 335

Asp Thr Gly Ser Lys Pro Ala Ile Ala Phe Ala Pro Thr Gly Leu Ala
340 345 350

Lys Thr Pro Asp Gly Thr Asp Leu Ala Lys Tyr Val Ala Pro Gly Tyr
355 360 365

Glu Tyr Asn Lys Thr Glu Ala Ala Lys Leu Phe Lys Glu Gly Leu Ala
370 375 380

Glu Ser Gly Leu Thr Lys Leu Lys Leu Thr Ile Thr Ala Asp Ala Asp
385 390 395 400

Val Pro Ala Ala Lys Asn Ser Val Asp Tyr Ile Lys Ser Thr Trp Glu
405 410 415

Ala Ala Leu Pro Gly Leu Thr Val Glu Glu Lys Phe Val Thr Phe Lys
420 425 430

Gln Arg Leu Glu Asp Ser Arg Lys Gln Asn Phe Asp Ile Val Val Ser
435 440 445

Val Trp Gly Gly Asp Tyr Pro Glu Gly Ser Thr Phe Tyr Gly Leu Phe
450 455 460

Lys Ser Asp Ser Gln Asn Asn Asp Gly Lys Phe Ala Asn Lys Asp Tyr
465 470 475 480

Asp Ala Ala Tyr Asn Lys Ala Ile Ser Glu Asp Ala Leu Lys Pro Glu
485 490 495

Glu Ser Ala Lys Asp Tyr Lys Glu Ala Glu Lys Ile Leu Phe Glu Gln
500 505 510

Gly Ala Tyr Asn Pro Leu Tyr Phe Arg Ser Gly Lys Gly Leu Gln Asn
515 520 525

Pro Lys Leu Lys Gly Val Ile Arg Asn Thr Thr Gly Leu Ser Ile Asp
530 535 540

Phe Thr His Ala Tyr Lys Lys
545 550

<210> 232

<211> 242

<212> PRT

<213> Streptococcus agalactiae

<400> 232

Met Glu Leu Leu Lys Thr Pro Ile Phe Gly Ile Cys Phe Ser Leu Ile
1               5                   10                  15

Leu Tyr Thr Ile Gly Gln His Leu Phe Lys Lys Ser Lys Gly Phe Phe
            20                  25                  30

Leu Leu Gln Pro Leu Phe Phe Ala Met Val Ser Gly Ile Val Ile Leu
        35                  40                  45

Trp Leu Met Ser Lys Gly Leu Gly Thr Asp Val Lys Thr Phe Tyr Thr
    50                  55                  60

Gln Ala Tyr Lys Pro Gly Gly Asp Leu Ile Phe Trp Phe Leu Asn Pro
65                  70                  75                  80

Ala Thr Ile Ala Phe Ala Val Pro Leu Tyr Lys Lys Asn Asp Val Val
                85                  90                  95

Lys Lys Tyr Trp Val Glu Ile Leu Ser Ser Leu Val Ile Gly Met Ile
            100                 105                 110

Val Ser Leu Met Leu Ile Val Ala Ile Ser Lys Met Val Gly Leu Ser
        115                 120                 125

Gln Val Gly Ile Ala Ser Met Leu Pro Gln Ala Ala Thr Thr Ala Ile
    130                 135                 140

Ala Leu Pro Ile Thr Ala Ala Ile Gly Gly Asn Thr Ala Val Thr Ala
145                 150                 155                 160

Met Ala Cys Ile Leu Asn Ala Val Ile Ile Tyr Ala Leu Gly Lys Lys
                165                 170                 175

Leu Val Ser Phe Phe His Leu Asn Asp Ser Lys Ile Gly Ala Gly Leu
            180                 185                 190

Gly Leu Gly Thr Ser Gly His Thr Val Gly Ala Ala Phe Ala Leu Glu
        195                 200                 205

Leu Gly Glu Leu Gln Gly Ala Met Ala Ala Ile Ala Val Val Val Ile
    210                 215                 220

Gly Leu Val Val Asp Leu Val Ile Pro Ile Phe Ser His Leu Ile Gly
225 230 235 240

Leu Leu

<210> 233

<211> 542

<212> PRT

<213> Streptococcus agalactiae

<400> 233

Val Thr Lys Tyr Leu Lys Tyr Ile Ser Phe Val Ala Leu Phe Leu Ala
1 5 10 15

Ser Ile Phe Leu Val Ala Cys Gln Asn Gln Asn Ser Gln Thr Lys Glu
20 25 30

Arg Thr Arg Lys Gln Arg Pro Lys Asp Glu Leu Val Val Ser Met Gly
35 40 45

Ala Lys Leu Pro His Glu Phe Asp Pro Lys Asp Arg Tyr Gly Ile His
50 55 60

Asn Glu Gly Asn Ile Thr His Ser Thr Leu Leu Lys Arg Ser Pro Glu
65 70 75 80

Leu Asp Ile Lys Gly Glu Leu Ala Lys Lys Tyr Lys Ile Ser Lys Asp
85 90 95

Gly Leu Thr Trp Ser Phe Asp Leu Asn Asp Asp Phe Lys Phe Ser Asn
100 105 110

Gly Glu Pro Val Thr Ala Asp Asp Val Lys Phe Thr Tyr Asp Met Leu
115 120 125

Lys Ala Asp Gly Lys Ala Trp Asp Leu Thr Phe Ile Lys Asn Val Glu
130 135 140

Val Val Gly Lys Asn Gln Val Asn Ile His Leu Thr Glu Ala His Ser
145 150 155 160

Thr Phe Thr Ala Gln Leu Thr Glu Ile Pro Ile Val Pro Lys Lys His
165 170 175

Tyr Asn Asp Lys Tyr Lys Ser Asn Pro Ile Gly Ser Gly Pro Tyr Met
180 185 190

Val Lys Glu Tyr Lys Ala Gly Glu Gln Ala Ile Phe Val Arg Asn Pro
195 200 205

Tyr Trp His Gly Lys Lys Pro Tyr Phe Lys Lys Trp Thr Trp Val Leu
210 215 220

Leu Asp Glu Asn Thr Ala Leu Ala Ala Leu Glu Ser Gly Asp Val Asp
225 230 235 240

Met Ile Tyr Ala Thr Pro Glu Leu Ala Ser Lys Lys Val Lys Gly Thr
245 250 255

Arg Leu Leu Asp Ile Ala Ser Asn Asp Val Arg Gly Leu Ser Leu Pro
260 265 270

Tyr Val Lys Lys Gly Val Val Lys Asn Ser Pro Asp Gly Tyr Pro Val
275 280 285

Gly Asn Asp Val Thr Ser Asp Pro Ala Ile Arg Lys Ala Leu Thr Ile
290 295 300

Gly Leu Asn Arg Gln Lys Val Leu Asp Thr Val Leu Asn Gly Tyr Gly
305 310 315 320

Lys Pro Ala Tyr Ser Ile Ile Asp Arg Thr Pro Phe Trp Asn Pro Lys
325 330 335

Thr Ala Ile Lys Asp Asn Lys Val Ala Lys Ala Lys Gln Leu Leu Thr
340 345 350

Lys Ala Gly Trp Lys Glu Gln Ala Asp Gly Ser Arg Lys Lys Gly Asn
355 360 365

Leu Lys Ala Glu Phe Asp Leu Tyr Tyr Pro Thr Asn Asp Gln Leu Arg
370 375 380

Ala Asn Leu Ala Val Glu Val Ala Glu Gln Ala Lys Ala Leu Gly Ile
385 390 395 400

Thr Ile Lys Leu Lys Ala Ser Asn Trp Asp Glu Met Ala Thr Lys Ser
405 410 415

His Asp Ser Ala Leu Leu Tyr Ala Gly Gly Arg His His Ala Gln Gln
420 425 430

Phe Tyr Glu Ser His Tyr Pro Ser Leu Ala Gly Lys Gly Trp Thr Asn
435 440 445

Ile Thr Phe Tyr Asn Asn Pro Thr Val Thr Lys Tyr Leu Asp Lys Ala
450 455 460

Met Thr Ser Pro Asp Leu Asp Lys Ala Asn Lys Tyr Trp Lys Leu Ala
465 470 475 480

Gln Trp Asp Gly Lys Thr Gly Ala Ser Thr Leu Gly Asp Leu Pro Asn
485 490 495

Val Trp Leu Val Ser Leu Asn His Thr Tyr Ile Gly Asp Lys Arg Ile
500 505 510

Asn Val Gly Lys Gln Gly Val His Ser His Gly His Asp Trp Ser Leu
515 520 525

Leu Thr Asn Ile Ala Glu Trp Thr Trp Asp Glu Ser Ala Lys
530 535 540

<210> 234

<211> 381

<212> PRT

<213> Streptococcus agalactiae

<400> 234

Met Gly Gln Glu Pro Ile Ile Glu Tyr Gln Asn Ile Asn Lys Val Tyr
1 5 10 15

Gly Glu Asn Val Ala Val Glu Asp Ile Asn Leu Lys Ile Tyr Pro Gly
20 25 30

Asp Phe Val Cys Phe Ile Gly Thr Ser Gly Ser Gly Lys Thr Thr Leu
35 40 45

Met Arg Met Val Asn His Met Leu Lys Pro Thr Asn Gly Thr Leu Leu
50 55 60

Phe Lys Gly Lys Asp Ile Ser Thr Ile Asn Pro Ile Glu Leu Arg Arg
65 70 75 80

Arg Ile Gly Tyr Val Ile Gln Asn Ile Gly Leu Met Pro His Met Thr
85 90 95

Ile Tyr Glu Asn Ile Val Leu Val Pro Lys Leu Leu Lys Trp Ser Glu
100 105 110

Glu Ala Lys Arg Ala Lys Ala Arg Glu Leu Ile Lys Leu Val Glu Leu
115 120 125

Pro Glu Glu Tyr Leu Asp Arg Tyr Pro Ser Glu Leu Ser Gly Gly Gln
130 135 140

Gln Gln Arg Ile Gly Val Ile Arg Ala Leu Ala Ala Asp Gln Asp Ile
145                 150                 155                 160

Ile Leu Met Asp Glu Pro Phe Gly Ala Leu Asp Pro Ile Thr Arg Glu
                165                 170                 175

Gly Ile Gln Asp Leu Val Lys Ser Leu Gln Glu Glu Met Gly Lys Thr
            180                 185                 190

Ile Ile Leu Val Thr His Asp Met Asp Glu Ala Leu Lys Leu Ala Thr
        195                 200                 205

Lys Ile Ile Val Met Asp Asn Gly Lys Met Val Gln Glu Gly Thr Pro
    210                 215                 220

Asn Asp Leu Leu His His Pro Ala Thr Ser Phe Val Glu Gln Met Ile
225                 230                 235                 240

Gly Glu Glu Arg Leu Leu His Ala Gln Ala Asp Ile Thr Pro Val Lys
                245                 250                 255

Gln Ile Met Leu Asn Asn Pro Val Ser Ile Thr Ala Glu Lys Thr Leu
            260                 265                 270

Thr Glu Ala Ile Thr Leu Met Arg Gln Lys Arg Val Asp Ser Leu Leu
        275                 280                 285

Val Thr Asp Asn Gly Lys Leu Ile Gly Phe Ile Asp Leu Glu Ser Leu
    290                 295                 300

Ser Ser Lys Tyr Lys Lys Asp Arg Leu Val Ser Asp Ile Leu Lys His
305                 310                 315                 320

Thr Asp Phe Tyr Val Met Glu Asp Asp Leu Leu Arg Asn Thr Ala Glu
                325                 330                 335

Arg Ile Leu Lys Arg Gly Leu Lys Tyr Ala Pro Val Val Asp His Glu
            340                 345                 350

Asn Asn Leu Lys Gly Ile Val Thr Arg Ala Ser Leu Val Asp Met Leu
        355                 360                 365

Tyr Asp Ile Ile Trp Gly Asp Thr Glu Thr Glu Asp Gln
    370                 375                 380

<210> 235

<211> 235

<212> PRT

<213> Streptococcus agalactiae

<400> 235

Met Lys Ile Asp Lys Lys Glu Phe Leu Ala Leu Ile Ala Ser Ile Ile
1               5                   10                  15

Leu Leu Ile Phe Ala Ser Val Thr Phe Phe Leu Phe Lys Asp His Gly
            20                  25                  30

Thr Thr Gln Met Asp Thr Val Glu Ser Ser Val Asn His Val Ser Asp
        35                  40                  45

Ser Gln Leu Thr Glu Ala Gln Asp Met Leu Asp Lys Phe Glu Lys Lys
    50                  55                  60

Pro Ser Glu Lys Leu Leu Lys Asp Val Glu Leu Ala Leu Asn Lys Leu
65                  70                  75                  80

Ser Asn Ser Ser Lys Lys Glu Ala Leu Gln Lys Arg Phe Lys Lys Ala
                85                  90                  95

Lys Asp Lys Tyr Leu Lys Asp Glu Ala Asp Lys Lys Ala Thr Lys Asp
            100                 105                 110

Ala Thr Asp Leu Val Glu Ile Leu Glu Gln Ala Pro Ser Glu Glu Asn
        115                 120                 125

Val Leu Lys Ala Glu Ala Ala Val Asn Lys Leu Thr Val Lys Glu Ser
    130                 135                 140

Lys Glu Ala Leu Gln Lys Arg Ile Asp Thr Val Lys Thr Gln Tyr Gly
145                 150                 155                 160

Leu Ile Gly Asn Gln Thr Pro Ser Ser Ser Val Ala Glu Thr Thr Glu
                165                 170                 175

Gln Gly Thr Ala Asn Pro Ala Ser Gln Asp Thr Ser Ser Tyr Val Asn
            180                 185                 190

Gln Asn Val Ala Pro Thr Tyr Glu Gln Pro Gln Thr Asn Asn Thr Pro
        195                 200                 205

Val Thr Pro Gly Val Asn Asn Thr Val Pro Thr Pro Gly Thr Gly Thr
    210                 215                 220

Ala Pro Ala Thr Asn Gly Thr Gly Val Ala Gln
225                 230                 235

<210> 236

<211> 679

<212> PRT

<213> Streptococcus agalactiae

<400> 236

Met Thr Lys Asp Leu Leu Leu Glu Leu Gly Leu Glu Glu Leu Pro Ala
1               5                   10                  15

Tyr Val Val Thr Pro Ser Glu Lys Gln Leu Gly Gln Lys Met Val Lys
            20                  25                  30

Phe Leu Glu Asp His Arg Leu Ser Phe Glu Thr Val Gln Thr Phe Ser
        35                  40                  45

Thr Pro Arg Arg Leu Ala Val Arg Val Lys Gly Leu Ala Asp Gln Gln
    50                  55                  60

Thr Asp Leu Thr Glu Asp Phe Lys Gly Pro Ser Lys Lys Ile Ala Leu
65                  70                  75                  80

Asp Ala Glu Gly Asn Phe Ser Lys Ala Ala Gln Gly Phe Val Arg Gly
                85                  90                  95

Lys Gly Leu Ser Val Asp Asp Ile Glu Phe Arg Glu Val Lys Gly Glu
            100                 105                 110

Glu Tyr Val Tyr Val Thr Lys His Glu Thr Gly Lys Ser Ala Ile Asp
        115                 120                 125

Val Leu Ala Ser Val Thr Glu Val Leu Thr Glu Leu Thr Phe Pro Val
    130                 135                 140

Asn Met His Trp Ala Asn Asn Ser Phe Glu Tyr Ile Arg Pro Val His
145                 150                 155                 160

Thr Leu Val Val Leu Leu Asp Asp Gln Ala Leu Glu Leu Asp Phe Leu
                165                 170                 175

Asp Ile His Ser Gly Arg Ile Ser Arg Gly His Arg Phe Leu Gly Ser
            180                 185                 190

Asp Thr Glu Ile Leu Ser Ala Ser Ser Tyr Glu Asp Asp Leu Arg Gln
        195                 200                 205

Gln Phe Val Ile Ala Asp Ala Lys Glu Arg Gln Gln Met Ile Val Asp
    210                 215                 220

Gln Ile His Ala Ile Glu Glu Lys Glu Asn Ile Ser Val Glu Ile Asp
225                 230                 235                 240

Glu Asp Leu Leu Asn Glu Val Leu Asn Leu Val Glu Tyr Pro Thr Ala
245 250 255

Phe Leu Gly Ser Phe Asp Glu Lys Tyr Leu Asp Val Pro Glu Glu Val
260 265 270

Leu Val Thr Ser Met Lys Asn His Gln Arg Tyr Phe Val Val Arg Asp
275 280 285

Arg Asp Gly Lys Leu Leu Pro Asn Phe Ile Ser Val Arg Asn Gly Asn
290 295 300

Ala Glu His Ile Glu Asn Val Ile Lys Gly Asn Glu Lys Val Leu Val
305 310 315 320

Ala Arg Leu Glu Asp Gly Glu Phe Phe Trp Gln Glu Asp Gln Lys Leu
325 330 335

Asn Ile Ala Asp Leu Val Glu Lys Leu Lys Gln Val Thr Phe His Glu
340 345 350

Lys Ile Gly Ser Leu Tyr Glu His Met Asp Arg Val Lys Val Ile Ser
355 360 365

Gln Tyr Leu Ala Glu Lys Ala Asp Leu Ser Asp Glu Glu Lys Leu Ala
370 375 380

Val Leu Arg Ala Ala Ser Ile Tyr Lys Phe Asp Leu Leu Thr Gly Met
385 390 395 400

Val Asp Glu Phe Asp Glu Leu Gln Gly Ile Met Gly Glu Lys Tyr Ala
405 410 415

Leu Leu Ala Gly Glu Gln Pro Ala Val Ala Ala Ala Ile Arg Glu His
420 425 430

Tyr Met Pro Thr Ser Ala Asp Gly Glu Leu Pro Glu Thr Arg Val Gly
435 440 445

Ala Ile Leu Ala Leu Ala Asp Lys Phe Asp Thr Leu Leu Ser Phe Phe
450 455 460

Ser Val Gly Leu Ile Pro Ser Gly Ser Asn Asp Pro Tyr Ala Leu Arg
465 470 475 480

Arg Ala Thr Gln Gly Ile Val Arg Ile Leu Glu Ala Phe Gly Trp Asp
485 490 495

Ile Pro Leu Asp Glu Leu Val Thr Asn Leu Tyr Gly Leu Ser Phe Ala
500 505 510

Ser Leu Asp Tyr Ala Asn Gln Lys Glu Val Met Ala Phe Ile Ser Ala
515 520 525

Arg Ile Glu Lys Met Ile Gly Ser Lys Val Pro Lys Asp Ile Arg Glu
530 535 540

Ala Val Leu Glu Ser Asp Thr Tyr Ile Val Ser Leu Ile Leu Glu Ala
545 550 555 560

Ser Gln Ala Leu Val Gln Lys Ser Lys Asp Ala Gln Tyr Lys Val Ser
565 570 575

Ile Glu Ser Leu Ser Arg Ala Phe Asn Leu Ala Glu Lys Val Thr His
580 585 590

Ser Val Ser Val Asp Tyr Ser Leu Phe Glu Asn Asn Gln Glu Lys Ala
595 600 605

Leu Tyr Gln Ala Ile Leu Ser Leu Glu Leu Thr Glu Asp Met His Asp
610 615 620

Asn Leu Asp Lys Leu Phe Ala Leu Ser Pro Ile Ile Asn Asp Phe Phe
625 630 635 640

Asp Asn Thr Met Val Met Thr Asp Asp Glu Lys Met Lys Gln Asn Arg
645 650 655

Leu Ala Leu Leu Asn Ser Leu Val Ala Lys Ala Arg Thr Val Ala Ala
660 665 670

Phe Asn Leu Leu Asn Thr Lys
675

<210> 237

<211> 661

<212> PRT

<213> Streptococcus agalactiae

<400> 237

Met Thr Phe Asp Thr Ile Asp Gln Leu Ala Val Asn Thr Val Arg Thr
1 5 10 15

Leu Ser Ile Asp Ala Ile Gln Ala Ala Asn Ser Gly His Pro Gly Leu
20 25 30

Pro Met Gly Ala Ala Pro Met Ala Tyr Val Leu Trp Asn Lys Phe Leu
35 40 45

Asn Val Asn Pro Lys Thr Ser Arg Asn Trp Thr Asn Arg Asp Arg Phe
50 55 60

Val Leu Ser Ala Gly His Gly Ser Ala Leu Leu Tyr Ser Leu Leu His
65 70 75 80

Leu Ala Gly Tyr Asp Leu Ser Ile Asp Asp Leu Lys Gln Phe Arg Gln
85 90 95

Trp Gly Ser Lys Thr Pro Gly His Pro Glu Val Asn His Thr Asp Gly
100 105 110

Val Glu Ala Thr Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val
115 120 125

Gly Met Ala Met Ala Glu Ala His Leu Ala Ala Lys Phe Asn Lys Pro
130 135 140

Gly Phe Asp Leu Val Asp His Tyr Thr Tyr Thr Leu His Gly Asp Gly
145 150 155 160

Cys Leu Met Glu Gly Val Ser Gln Glu Ala Ala Ser Leu Ala Gly His
165 170 175

Leu Lys Leu Gly Lys Leu Val Leu Leu Tyr Asp Ser Asn Asp Ile Ser
180 185 190

Leu Asp Gly Pro Thr Ser Gln Ser Phe Thr Glu Asp Val Lys Gly Arg
195 200 205

Phe Glu Ser Tyr Gly Trp Gln His Ile Leu Val Lys Asp Gly Asn Asp
210 215 220

Leu Glu Ala Ile Ala Ala Ala Ile Glu Ala Ala Lys Ala Glu Thr Asp
225 230 235 240

Lys Pro Thr Ile Ile Glu Val Lys Thr Ile Ile Gly Phe Gly Ala Glu
245 250 255

Lys Gln Gly Thr Ser Ser Val His Gly Ala Pro Leu Gly Ala Glu Gly
260 265 270

Ile Thr Phe Ala Lys Lys Ala Tyr Gly Trp Glu Tyr Pro Asp Phe Thr
275 280 285

Val Pro Ala Glu Val Val Ala Arg Phe Ala Ser Asp Leu Gln Ala Arg
290 295 300

Gly Ala Lys Ala Glu Glu Ala Trp Asn Asp Leu Phe Ala Lys Tyr Glu
305 310 315 320

Val Glu Tyr Pro Glu Leu Ala Ala Glu Tyr Lys Glu Ala Phe Ala Gly
325 330 335

Gln Ala Glu Thr Val Glu Leu Lys Ala His Asp Leu Gly Ser Ser Val
340 345 350

Ala Ser Arg Val Ser Ser Gln Gln Ala Ile Gln Gln Leu Ser Thr Gln
355 360 365

Leu Pro Asn Leu Trp Gly Gly Ser Ala Asp Leu Ser Ala Ser Asn Asn
370 375 380

Thr Met Val Ala Ala Glu Thr Asp Phe Gln Ala Ser Asn Tyr Ala Gly
385 390 395 400

Arg Asn Ile Trp Phe Gly Val Arg Glu Phe Ala Met Ala Ala Ala Met
405 410 415

Asn Gly Ile Ala Leu His Gly Gly Thr Arg Val Tyr Gly Gly Thr Phe
420 425 430

Phe Val Phe Ser Asn Tyr Leu Leu Pro Ala Val Arg Met Ala Ala Leu
435 440 445

Gln Asn Leu Pro Thr Val Tyr Val Met Thr His Asp Ser Ile Ala Val
450 455 460

Gly Glu Asp Gly Pro Thr His Glu Pro Ile Glu Gln Leu Ala Ser Val
465 470 475 480

Arg Ser Met Pro Asn Leu Asn Val Ile Arg Pro Ala Asp Gly Asn Glu
485 490 495

Thr Asn Ala Ala Trp Gln Arg Ala Val Ser Glu Thr Asp Arg Pro Thr
500 505 510

Met Leu Val Leu Thr Arg Gln Asn Leu Pro Val Leu Glu Gly Thr Ser
515 520 525

Glu Leu Ala Gln Glu Gly Val Asn Lys Gly Ala Tyr Ile Leu Ser Glu
530 535 540

Ala Lys Gly Glu Leu Asp Gly Ile Ile Ile Ala Thr Gly Ser Glu Val
545 550 555 560

Lys Leu Ala Leu Asp Thr Gln Asp Lys Leu Glu Ser Glu Gly Ile His
565 570 575

Val Arg Val Val Ser Met Pro Ala Gln Asn Ile Phe Asp Glu Gln Glu
580 585 590

Ala Ser Tyr Gln Glu Gln Val Leu Pro Ser Ala Val Thr Lys Arg Leu
595 600 605

Ala Ile Glu Ala Gly Ser Ser Phe Gly Trp Gly Lys Tyr Val Gly Leu
610 615 620

Asn Gly Leu Thr Leu Thr Ile Asp Thr Trp Gly Ala Ser Ala Pro Gly
625 630 635 640

Asn Arg Ile Phe Glu Glu Tyr Gly Phe Thr Val Glu Asn Ala Val Ser
645 650 655

Leu Tyr Lys Glu Leu
660

<210> 238

<211> 273

<212> PRT

<213> Streptococcus agalactiae

<400> 238

Met Thr Leu Gln Asp Gln Ile Ile Lys Glu Leu Gly Val Lys Pro Val
1 5 10 15

Ile Asn Pro Ser Gln Glu Ile Arg Arg Ser Val Glu Phe Leu Lys Asp
20 25 30

Tyr Leu Leu Lys His Ser Phe Leu Lys Thr Tyr Val Leu Gly Ile Ser
35 40 45

Gly Gly Gln Asp Ser Thr Leu Ala Gly Arg Leu Ala Gln Leu Ala Val
50 55 60

Glu Glu Leu Arg Ala Asp Thr Gly Glu Asn Tyr Gln Phe Ile Ala Ile
65 70 75 80

Arg Leu Pro Tyr Gly Ile Gln Ala Asp Glu Glu Asp Ala Gln Lys Ala
85 90 95

Leu Asp Phe Ile Lys Pro Asp Ile Ala Leu Thr Ile Asn Ile Lys Glu
100 105 110

Ala Val Asp Gly Gln Val Arg Ala Leu Asn Ala Ala Gly Val Glu Ile
115 120 125

Thr Asp Phe Asn Lys Gly Asn Ile Lys Ala Arg Gln Arg Met Ile Ser
130 135 140

Gln Tyr Ala Val Ala Gly Gln Tyr Ala Gly Ala Val Ile Gly Thr Asp
145 150 155 160

His Ala Ala Glu Asn Ile Thr Gly Phe Phe Thr Lys Phe Gly Asp Gly
165 170 175

Gly Ala Asp Leu Leu Pro Leu Phe Arg Leu Asn Lys Ser Gln Gly Lys
180 185 190

Gln Leu Leu Ala Glu Leu Gly Ala Asp Lys Ala Leu Tyr Glu Lys Ile
195 200 205

Pro Thr Ala Asp Leu Glu Glu Asn Lys Pro Gly Ile Ala Asp Glu Ile
210 215 220

Ala Leu Gly Val Thr Tyr Gln Glu Ile Asp Ala Tyr Leu Glu Gly Lys
225 230 235 240

Val Val Ser Asp Lys Ser Arg Gly Ile Ile Glu Asn Trp Trp Tyr Lys
245 250 255

Gly Gln His Lys Arg His Leu Pro Ile Thr Ile Phe Asp Asp Phe Trp
260 265 270

Lys

<210> 239

<211> 745

<212> PRT

<213> Streptococcus agalactiae

<400> 239

Ile Lys Lys Glu Ser Val Ile Lys Leu Leu Lys Tyr Ala Phe Gly Ile
1 5 10 15

Ile Met Gly Phe Ile Ile Leu Ala Ile Val Ile Gly Gly Leu Leu Phe
20 25 30

Ala Tyr Tyr Val Ser Arg Ser Pro Lys Leu Thr Asp Gln Ala Leu Lys
35 40 45

Ser Val Asn Ser Ser Leu Val Tyr Asp Gly Asn Asn Lys Leu Ile Ala
50 55 60

Asp Leu Gly Ser Glu Lys Arg Glu Ser Val Ser Ala Asp Ser Ile Pro
65 70 75 80

Leu Asn Leu Val Asn Ala Ile Thr Ser Ile Glu Asp Lys Arg Phe Phe
85 90 95

Lys His Arg Gly Val Asp Ile Tyr Arg Ile Leu Gly Ala Ala Trp His
100 105 110

Asn Leu Val Ser Ser Asn Thr Gln Gly Gly Ser Thr Leu Asp Gln Gln
115 120 125

Leu Ile Lys Leu Ala Tyr Phe Ser Thr Asn Lys Ser Asp Gln Thr Leu
130 135 140

Lys Arg Lys Ser Gln Glu Val Trp Leu Ala Leu Gln Met Glu Arg Lys
145 150 155 160

Tyr Thr Lys Glu Glu Ile Leu Thr Phe Tyr Ile Asn Lys Val Tyr Met
165 170 175

Gly Asn Gly Asn Tyr Gly Met Arg Thr Thr Ala Lys Ser Tyr Phe Gly
180 185 190

Lys Asp Leu Lys Glu Leu Ser Ile Ala Gln Leu Ala Leu Leu Ala Gly
195 200 205

Ile Pro Gln Ala Pro Thr Gln Tyr Asp Pro Tyr Lys Asn Pro Glu Ser
210 215 220

Ala Gln Thr Arg Arg Asn Thr Val Leu Gln Gln Met Tyr Gln Asp Lys
225 230 235 240

Asn Ile Ser Lys Lys Glu Tyr Asp Gln Ala Val Ala Thr Pro Val Thr
245 250 255

Asp Gly Leu Lys Glu Leu Lys Gln Lys Ser Thr Tyr Pro Lys Tyr Met
260 265 270

Asp Asn Tyr Leu Lys Gln Val Ile Ser Glu Val Lys Gln Lys Thr Gly
275 280 285

Lys Asp Ile Phe Thr Ala Gly Leu Lys Val Tyr Thr Asn Ile Asn Thr
290 295 300

Asp Ala Gln Lys Gln Leu Tyr Asp Ile Tyr Asn Ser Asp Thr Tyr Ile
305 310 315 320

Ala Tyr Pro Asn Asn Glu Leu Gln Ile Ala Ser Thr Ile Met Asp Ala
325 330 335

Thr Asn Gly Lys Val Ile Ala Gln Leu Gly Gly Arg His Gln Asn Glu
340 345 350

Asn Ile Ser Phe Gly Thr Asn Gln Ser Val Leu Thr Asp Arg Asp Trp
355 360 365

Gly Ser Thr Met Lys Pro Ile Ser Ala Tyr Ala Pro Ala Ile Asp Ser
370 375 380

Gly Val Tyr Asn Ser Thr Gly Gln Ser Leu Asn Asp Ser Val Tyr Tyr
385 390 395 400

Trp Pro Gly Thr Ser Thr Gln Leu Tyr Asp Trp Asp Arg Gln Tyr Met
405 410 415

Gly Trp Met Ser Met Gln Thr Ala Ile Gln Gln Ser Arg Asn Val Pro
420 425 430

Ala Val Arg Ala Leu Glu Ala Ala Gly Leu Asp Glu Ala Lys Ser Phe
435 440 445

Leu Glu Lys Leu Gly Ile Tyr Tyr Pro Glu Met Asn Tyr Ser Asn Ala
450 455 460

Ile Ser Ser Asn Asn Ser Ser Ser Asp Ala Lys Tyr Gly Ala Ser Ser
465 470 475 480

Glu Lys Met Ala Ala Ala Tyr Ser Ala Phe Ala Asn Gly Gly Thr Tyr
485 490 495

Tyr Lys Pro Gln Tyr Val Asn Lys Ile Glu Phe Ser Asp Gly Thr Asn
500 505 510

Asp Thr Tyr Ala Ala Ser Gly Ser Arg Ala Met Lys Glu Thr Thr Ala
515 520 525

Tyr Met Met Thr Asp Met Leu Lys Thr Val Leu Thr Phe Gly Thr Gly
530 535 540

Thr Lys Ala Ala Ile Pro Gly Val Ala Gln Ala Gly Lys Thr Gly Thr
545 550 555 560

Ser Asn Tyr Thr Glu Asp Glu Leu Ala Lys Ile Glu Ala Thr Thr Gly
565 570 575

Ile Tyr Asn Ser Ala Val Gly Thr Met Ala Pro Asp Glu Asn Phe Val
580 585 590

Gly Tyr Thr Ser Lys Tyr Thr Met Ala Ile Trp Thr Gly Tyr Lys Asn
595 600 605

Arg Leu Thr Pro Leu Tyr Gly Ser Gln Leu Asp Ile Ala Thr Glu Val
610 615 620

Tyr Arg Ala Met Met Ser Tyr Leu Thr Gly Gly Tyr Ser Ala Asp Trp
625 630 635 640

Thr Met Pro Glu Gly Leu Tyr Arg Ser Gly Ser Tyr Leu Tyr Ile Asn
645 650 655

Gly Thr Thr Thr Thr Gly Thr Tyr Ser Ser Ser Val Tyr Lys Asn Ile
660 665 670

Tyr Gln Asn Ser Gly Gln Ser Ser Gln Ser Ser Ser Ser Thr Ser Ser
675 680 685

Glu Lys Gln Lys Glu Asp Lys Asn Thr Ala Asn Asp Ala Asn Ser Ser
690 695 700

Ser Pro Gln Val Glu Thr Pro Asn Asn Gly Asn Ala Thr Thr Pro Asn
705 710 715 720

Asn Ser Asn Gln Thr Val Pro Gly Thr Gly His Gly Asn Gly Asn Gly
725 730 735

Asn Asn Asn Thr Val Pro Asn Gly Asn
740 745

<210> 240

<211> 425

<212> PRT

<213> Streptococcus agalactiae

<400> 240

Met Leu Asp Leu Lys Arg Ile Arg Thr Asp Phe Asp Val Val Ala Lys
1 5 10 15

Lys Leu Ala Thr Arg Gly Val Asp Gln Glu Thr Leu Thr Thr Leu Lys
20 25 30

Glu Leu Asp Ile Lys Arg Arg Glu Leu Leu Ile Lys Ala Glu Glu Ala
35 40 45

Lys Ala Gln Arg Asn Val Ala Ser Ala Ala Ile Ala Gln Ala Lys Arg
50 55 60

Asn Lys Glu Asn Ala Asp Glu Gln Ile Ala Ala Met Gln Thr Leu Ser
65 70 75 80

Ala Asp Ile Lys Ala Ile Asp Ala Glu Leu Ala Asp Val Asp Ala Asn
85 90 95

Leu Gln Ser Met Val Thr Val Leu Pro Asn Thr Pro Ala Asp Asp Val
100 105 110

Pro Leu Gly Ala Asp Glu Asp Glu Asn Val Glu Val Arg Arg Trp Gly
115 120 125

Thr Pro Arg Glu Phe Asp Phe Glu Thr Lys Ala His Trp Asp Leu Gly
130 135 140

Glu Ser Leu Gly Ile Leu Asp Trp Glu Arg Gly Ala Lys Val Thr Gly
145 150 155 160

Ser Arg Phe Leu Phe Tyr Lys Gly Leu Gly Ala Arg Leu Glu Arg Ala
165 170 175

Ile Tyr Ser Phe Met Leu Asp Glu His Ala Lys Glu Gly Tyr Thr Glu
180 185 190

Val Ile Pro Pro Tyr Met Val Asn His Asp Ser Met Phe Gly Thr Gly
195 200 205

Gln Tyr Pro Lys Phe Lys Glu Asp Thr Phe Glu Leu Ala Asp Ser Pro
210 215 220

Phe Val Leu Ile Pro Thr Ala Glu Val Pro Leu Thr Asn Tyr Tyr Arg
225 230 235 240

Asp Glu Ile Ile Asp Gly Lys Glu Leu Pro Ile Tyr Phe Thr Ala Met
245 250 255

Ser Pro Ser Phe Arg Ser Glu Ala Gly Ser Ala Gly Arg Asp Thr Arg
260 265 270

Gly Leu Ile Arg Leu His Gln Phe His Lys Val Glu Met Val Lys Phe
275 280 285

Ala Lys Pro Glu Glu Ser Tyr Gln Glu Leu Glu Lys Met Thr Ala Asn
290 295 300

Ala Glu Asn Ile Leu Gln Lys Leu Asn Leu Pro Tyr Arg Val Ile Thr
305 310 315 320

Leu Cys Thr Gly Asp Met Gly Phe Ser Ala Ala Lys Thr Tyr Asp Leu
325 330 335

Glu Val Trp Ile Pro Ala Gln Asn Thr Tyr Arg Glu Ile Ser Ser Cys
340 345 350

Ser Asn Thr Glu Asp Phe Gln Ala Arg Arg Ala Gln Ile Arg Tyr Arg
355 360 365

Asp Glu Val Asp Gly Lys Val Arg Leu Leu His Thr Leu Asn Gly Ser
370 375 380

Gly Leu Ala Val Gly Arg Thr Val Ala Ala Ile Leu Glu Asn Tyr Gln
385 390 395 400

Asn Glu Asp Gly Ser Val Thr Ile Pro Glu Val Leu Arg Pro Tyr Met
405 410 415

Gly Asn Ile Asp Ile Ile Lys Pro Asn
420 425

<210> 241

<211> 266

<212> PRT

<213> Streptococcus agalactiae

<400> 241

Val Thr Ile Ser Asn Gln Glu Leu Thr Leu Thr Pro Leu Arg Gly Lys
1 5 10 15

Ser Gly Lys Ala Tyr Ile Gly Thr Tyr Pro Asn Gly Glu Arg Val Phe
20 25 30

Val Lys Tyr Asn Thr Thr Pro Ile Leu Pro Ala Leu Ala Lys Glu Gln
35 40 45

Ile Ala Pro Gln Leu Leu Trp Ala Arg Arg Thr Ser Asn Gly Asp Met
50 55 60

Met Ser Ala Gln Glu Trp Leu Asp Gly Arg Thr Leu Thr Lys Glu Asp
65 70 75 80

Met Gly Ser Lys Gln Ile Ile His Ile Leu Leu Arg Leu His Lys Ser
85 90 95

Arg Pro Leu Val Asn Gln Leu Leu Gln Leu Gly Tyr Lys Ile Glu Asn
100 105 110

Pro Tyr Asp Leu Leu Met Asp Trp Glu Lys Gln Thr Pro Ile Gln Ile
115 120 125

Arg Glu Asn Thr Tyr Leu Gln Ser Ile Val Thr Glu Leu Lys Arg Ser
130 135 140

Leu Pro Glu Phe Arg Thr Glu Val Ala Thr Ile Val His Gly Asp Ile
145 150 155 160

Lys His Ser Asn Trp Val Ile Thr Thr Ser Gly Leu Ile Tyr Leu Val
165 170 175

Asp Trp Asp Ser Val Arg Leu Thr Asp Arg Met Tyr Asp Val Ala Tyr
180 185 190

Ile Leu Ser His Tyr Ile Pro Gln Lys His Trp Lys Asp Trp Leu Ser
195 200 205

Tyr Tyr Gly Tyr Lys Asp Asn Glu Lys Val Trp Ser Lys Ile Ile Trp
210 215 220

Tyr Gly Gln Phe Ser Tyr Leu Ser Gln Ile Ile Lys Cys Phe Asp Lys
225 230 235 240

Arg Asp Met Glu His Val Asn Gln Glu Ile Tyr Glu Leu Arg Lys Phe
245 250 255

Arg Glu Leu Ile Lys Lys His Asn Ala Ser
260 265

<210> 242

<211> 521

<212> PRT

<213> Streptococcus agalactiae

<400> 242

Met Lys Ile Ser Gln Tyr Asn Lys Trp Ser Ile Arg Arg Leu Lys Val
1 5 10 15

Gly Ala Ala Ser Val Met Ile Ala Ser Gly Ser Ile Val Ala Leu Gly
20 25 30

Gln Ser His Ile Val Ser Ala Asp Glu Met Ser Gln Pro Lys Thr Thr
35 40 45

Ile Thr Ala Pro Thr Ala Asn Thr Ser Thr Asn Val Glu Ser Ser Thr
50 55 60

Asp Lys Ala Leu Ser Lys Val Thr Thr Met Glu Thr Ser Ser Glu Met
65 70 75 80

Pro Lys Met Gln Asn Met Ala Lys Val Glu Lys Thr Ser Asp Lys Pro
85 90 95

Met Met Val Ala Thr Ser Val Arg Lys Met Met Ala Thr Pro Thr Pro
100 105 110

Val Ala Met Thr Lys Thr Thr Ser Val Asp Glu Val Lys Lys Ser Thr
115 120 125

Asp Thr Ala Phe Lys Gln Thr Val Asp Val Pro Ala His Tyr Val Asn
130 135 140

Ala Ala Lys Gly Asn Gly Pro Phe Leu Ala Gly Val Asn Gln Thr Ile
145 150 155 160

Pro Tyr Glu Ala Phe Gly Gly Asp Gly Met Leu Thr Arg Leu Ile Leu
165 170 175

Lys Ser Ser Glu Gly Ala Lys Trp Ser Asp Asn Gly Val Asp Lys Asn
180 185 190

Ser Pro Leu Leu Pro Leu Lys Gly Leu Thr Lys Gly Lys Tyr Phe Tyr
195 200 205

Gln Val Ser Leu Asn Gly Asn Thr Thr Gly Lys Glu Gly Gln Ala Leu
210 215 220

Leu Asp Gln Ile Lys Ala Asn Asp Lys His Ser Tyr Gln Ala Thr Ile
225 230 235 240

Arg Val Tyr Gly Ala Lys Asp Gly Lys Val Asp Leu Lys Asn Met Ile
245 250 255

Ser Gln Lys Met Val Thr Ile Asn Ile Pro His Ile Thr Thr Asp Met
260 265 270

Glu Val Lys Asn Ser Leu Lys Met Ala Phe Lys Glu Lys Val Asp Val
275 280 285

Pro Ala Lys Tyr Val Ser Ala Ala Lys Ala Lys Gly Pro Phe Leu Ala
290 295 300

Gly Val Asn Glu Thr Ile Pro Tyr Glu Ala Phe Gly Gly Asp Gly Met
305 310 315 320

Leu Thr Arg Leu Ile Leu Lys Ala Ser Glu Gly Ala Lys Trp Ser Asp
325 330 335

Asn Gly Val Asp Lys Asn Ser Pro Leu Leu Pro Leu Lys Asp Leu Thr
340 345 350

Lys Gly Lys Tyr Phe Tyr Gln Val Ser Leu Asn Gly Asn Thr Ala Gly
355 360 365

Lys Lys Gly Gln Ala Leu Leu Asp Gln Ile Lys Ala Asn Gly Ser His
370 375 380

Thr Tyr Gln Ala Thr Ile Thr Ile Tyr Gly Thr Lys Asp Gly Lys Val
385 390 395 400

Asp Met Asn Thr Ile Leu Gly Gln Lys Thr Val Met Ile His Ile Asn
405 410 415

Val Ala Lys Lys Asp Met Asn Ser Thr Ser Met Met Met Lys Lys Asp
420 425 430

Lys Met Thr Met Pro Met Lys Lys Glu Met Thr Ser Ser Lys Ile Asn
435 440 445

Thr Gly Met Met Met Ser Asn Asn Lys Met Ser Ala Asn Met Gln Met
450 455 460

Ser Ser Gln Ala Lys Ser Asn Asp Lys Ala Gly Lys Lys Met Ser Met
465 470 475 480

Met Ser Lys Asn Leu Pro Asn Thr Gly Glu Thr Lys Gln Gln Asn Val
485 490 495

Gly Val Leu Gly Met Leu Ser Leu Ala Phe Ala Thr Gly Leu Thr Ala
500 505 510

Leu Gly Leu Lys Lys Ser Lys Gln Arg
515 520

<210> 243

<211> 449

<212> PRT

<213> Streptococcus agalactiae

<400> 243

Met Thr His Ile Thr Phe Asp Tyr Ser Lys Val Leu Gly Gln Phe Val
1 5 10 15

Gly Glu His Glu Leu Asp Tyr Leu Gln Pro Gln Val Ser Ala Ala Asp
20 25 30

Ala Phe Leu Arg Gln Gly Thr Gly Pro Gly Ser Asp Phe Leu Gly Trp
35 40 45

Met Asp Leu Pro Glu Asn Tyr Asp Lys Glu Glu Phe Ser Arg Ile Gln
50 55 60

Lys Ala Ala Glu Lys Ile Lys Ser Asp Ser Glu Val Leu Val Val Ile
65 70 75 80

Gly Ile Gly Gly Ser Tyr Leu Gly Ala Lys Ala Ala Ile Asp Phe Leu
85 90 95

Asn Asn His Phe Ala Asn Leu Gln Thr Ala Glu Glu Arg Lys Ala Pro
100 105 110

Gln Ile Leu Tyr Ala Gly Asn Ser Ile Ser Ser Thr Tyr Leu Ala Asp
115 120 125

Leu Val Glu Tyr Val Gln Asp Lys Glu Phe Ser Val Asn Val Ile Ser
130 135 140

Lys Ser Gly Thr Thr Thr Glu Pro Ala Ile Ala Phe Arg Val Phe Lys
145 150 155 160

Glu Leu Leu Val Lys Lys Tyr Gly Gln Glu Glu Ala Asn Lys Arg Ile
165 170 175

Tyr Ala Thr Thr Asp Lys Val Lys Gly Ala Val Lys Val Glu Ala Asp
180 185 190

Ala Asn Asn Trp Glu Thr Phe Val Val Pro Asp Asn Val Gly Gly Arg
195 200 205

Phe Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Ala Ser Gly
210 215 220

Ala Asp Ile Thr Ala Leu Met Glu Gly Ala Asn Ala Ala Arg Lys Asp
225 230 235 240

Leu Ser Ser Asp Lys Ile Ser Glu Asn Ile Ala Tyr Gln Tyr Ala Ala
245 250 255

Val Arg Asn Val Leu Tyr Arg Lys Gly Tyr Ile Thr Glu Ile Leu Ala
260 265 270

Asn Tyr Glu Pro Ser Leu Gln Tyr Phe Gly Glu Trp Trp Lys Gln Leu
275 280 285

Ala Gly Glu Ser Glu Gly Lys Asp Gln Lys Gly Ile Tyr Pro Thr Ser
290 295 300

Ala Asn Phe Ser Thr Asp Leu His Ser Leu Gly Gln Phe Ile Gln Glu
305 310 315 320

Gly Tyr Arg Asn Leu Phe Glu Thr Val Val Arg Val Glu Lys Pro Arg
325 330 335

Lys Asn Val Thr Ile Pro Glu Leu Thr Glu Asp Leu Asp Gly Leu Gly
340 345 350

Tyr Leu Gln Gly Lys Asp Val Asp Phe Val Asn Lys Lys Ala Thr Asp
355 360 365

Gly Val Leu Leu Ala His Thr Asp Gly Gly Val Pro Asn Met Phe Val
370 375 380

Thr Leu Pro Thr Gln Asp Ala Tyr Thr Leu Gly Tyr Thr Ile Tyr Phe
385 390 395 400

Phe Glu Leu Ala Ile Gly Leu Ser Gly Tyr Leu Asn Ser Val Asn Pro
405 410 415

Phe Asp Gln Pro Gly Val Glu Ala Tyr Lys Arg Asn Met Phe Ala Leu
420 425 430

Leu Gly Lys Pro Gly Phe Glu Glu Leu Ser Ala Glu Leu Asn Ala Arg
435 440 445

Leu

<210> 244

<211> 105

<212> PRT

<213> Streptococcus agalactiae

<400> 244

Met Lys Glu Lys Gln Thr Ala Gly Arg Arg Gln Leu Glu Glu Phe Ala
1 5 10 15

Pro Glu Phe Ala Arg Tyr Asn Asp Asp Ile Leu Phe Gly Glu Val Trp
20 25 30

Ala Lys Glu Asp His Leu Thr Asp Lys Thr Arg Ser Ile Ile Thr Ile
35 40 45

Ser Ala Leu Ile Ser Gly Gly Asn Leu Glu Gln Leu Glu His His Leu
50 55 60

Gln Phe Ala Lys Gln Asn Gly Val Thr Lys Glu Glu Ile Ala Asp Ile
65 70 75 80

Ile Thr His Leu Ala Phe Tyr Val Gly Trp Pro Lys Ala Trp Ser Ala
85 90 95

Phe Asn Lys Ala Lys Glu Ile Trp Ile
100 105

<210> 245

<211> 156

<212> PRT

<213> Streptococcus agalactiae

<400> 245

Ala Trp Arg Ala Leu Glu Asp Ala Gln Lys Ser Gly Lys Val Lys Ser
1 5 10 15

Ile Gly Val Ser Asn Phe Leu Glu Lys Asp Leu Glu Asn Ile Leu Lys
20 25 30

Asn Gly His Val Lys Pro Ala Val Asn Gln Ile Leu Ala His Ile Gly
35 40 45

Asn Thr Pro Phe Asp Leu Ile Asp Tyr Cys Gln Ser Lys Gly Ile Gln
50 55 60

Val Glu Ala Tyr Ser Pro Ile Ala His Gly Gln Ala Leu Lys Ser Asp
65 70 75 80

Gly Ile Gln Lys Met Ala Glu Lys Tyr Gly Val Ser Val Ala Gln Leu
85 90 95

Cys Ile Gln Tyr Leu Leu Gln Leu Asn Leu Ile Val Leu Pro Lys Ala
100 105 110

Ser Ser Lys Glu His Leu Gln Ser Asn Leu Asp Phe Asp Phe Val Ile
115 120 125

Ser Asp Glu Asp Met Ser Ile Leu Lys Ser Leu Met Phe Asp Asp Tyr
130 135 140

Gly Glu Phe Ser Asn Phe Pro Val Phe Ser Glu Lys
145 150 155

<210> 246

<211> 1126

<212> PRT

<213> Streptococcus agalactiae

<400> 246

Met Phe Arg Arg Ser Lys Asn Asn Ser Tyr Asp Thr Ser Gln Thr Lys
1 5 10 15

Gln Arg Phe Ser Ile Lys Lys Phe Lys Phe Gly Ala Ala Ser Val Leu
20 25 30

Ile Gly Leu Ser Phe Leu Gly Gly Val Thr Gln Gly Asn Leu Asn Ile
35 40 45

Phe Glu Glu Ser Ile Val Ala Ala Ser Thr Ile Pro Gly Ser Ala Ala
50 55 60

Thr Leu Asn Thr Ser Ile Thr Lys Asn Ile Gln Asn Gly Asn Ala Tyr
65 70 75 80

Ile Asp Leu Tyr Asp Val Lys Asn Gly Leu Ile Asp Pro Gln Asn Leu
85 90 95

Ile Val Leu Asn Pro Ser Ser Tyr Ser Ala Asn Tyr Tyr Ile Lys Gln
100 105 110

Gly Ala Lys Tyr Tyr Ser Asn Pro Ser Glu Ile Thr Thr Thr Gly Ser
115 120 125

Ala Thr Ile Thr Phe Asn Ile Leu Asp Glu Thr Gly Asn Pro His Lys
130 135 140

Lys Ala Asp Gly Gln Ile Asp Ile Val Ser Val Asn Leu Thr Ile Tyr
145 150 155 160

Asp Ser Thr Ala Leu Arg Asn Arg Ile Asp Glu Val Ile Asn Asn Ala
165 170 175

Asn Asp Pro Lys Trp Ser Asp Gly Ser Arg Asp Glu Val Leu Thr Gly
180 185 190

Leu Glu Lys Ile Lys Lys Asp Ile Asp Asn Asn Pro Lys Thr Gln Ile
195 200 205

Asp Ile Asp Asn Lys Ile Asn Glu Val Asn Glu Ile Glu Lys Leu Leu
210 215 220

Val Val Ser Leu Pro Asp Lys Ile Lys Tyr Ser Pro Glu Ala Lys His
225 230 235 240

Arg Thr Val Glu Gln His Ala Glu Leu Asp Ala Lys Asp Ser Ile Ala
245 250 255

Asn Thr Asp Glu Leu Pro Ser Asn Ser Thr Tyr Asn Trp Lys Asn Gly
260 265 270

His Lys Pro Asp Thr Ser Thr Ser Gly Glu Lys Asp Gly Ile Val Glu
275 280 285

Val His Tyr Pro Asp Gly Thr Val Asp Asp Val Asn Val Lys Val Thr
    290                 295                 300

Val Thr Ser Lys Lys Thr Asp Asn Thr Ala Pro Thr Leu Thr Val Thr
305                 310                 315                 320

Pro Glu Gln Gln Thr Val Lys Val Asp Glu Asp Ile Thr Phe Thr Val
                325                 330                 335

Thr Ala Glu Asp Glu Asn Glu Val Glu Leu Gly Leu Asp Asp Leu Lys
            340                 345                 350

Ala Lys Tyr Glu Asn Asp Ile Ile Gly Ala Arg Val Lys Ile Lys Tyr
        355                 360                 365

Leu Thr Lys Glu Pro Asn Lys Lys Val Met Glu Val Thr Ile Met Lys
    370                 375                 380

Ala Thr Leu Ala Asp Lys Gly Ala Ile Thr Phe Thr Ala Lys Asp Lys
385                 390                 395                 400

Ala Gly Asn Gln Ala Glu Pro Lys Thr Val Thr Ile Asn Val Leu Pro
                405                 410                 415

Pro Asp Lys Ile Lys Tyr Ser Pro Glu Ala Lys His Arg Thr Val Glu
            420                 425                 430

Gln His Ala Glu Leu Asp Ala Lys Asp Ser Ile Ala Asn Thr Asp Glu
        435                 440                 445

Leu Pro Ser Asn Ser Thr Tyr Asn Trp Lys Asn Gly His Lys Pro Asp
    450                 455                 460

Thr Ser Thr Ser Gly Glu Lys Asp Gly Ile Val Glu Val His Tyr Pro
465                 470                 475                 480

Asp Gly Thr Val Asp Asp Val Asn Val Lys Val Thr Val Thr Ser Lys
                485                 490                 495

Lys Thr Asp Asn Thr Ala Pro Thr Leu Thr Val Thr Pro Glu Gln Gln
            500                 505                 510

Thr Val Lys Val Asp Glu Asp Ile Thr Phe Thr Val Thr Ala Glu Asp
        515                 520                 525

Glu Asn Glu Val Glu Leu Gly Leu Asp Asp Leu Lys Ala Lys Tyr Glu
    530                 535                 540

Asn Asp Ile Ile Gly Ala Arg Val Lys Ile Lys Tyr Leu Thr Lys Glu
545                 550                 555                 560

Pro Asn Lys Lys Val Met Glu Val Thr Ile Met Lys Ala Thr Leu Ala
565 570 575

Asp Lys Gly Ala Ile Thr Phe Thr Ala Lys Asp Lys Ala Gly Asn Gln
580 585 590

Ala Glu Pro Lys Thr Val Thr Ile Asn Val Leu Pro Pro Asp Lys Ile
595 600 605

Lys Tyr Ser Pro Glu Ala Lys His Arg Thr Val Glu Gln His Ala Glu
610 615 620

Leu Asp Ala Lys Asp Ser Ile Ala Asn Thr Asp Glu Leu Pro Ser Asn
625 630 635 640

Ser Thr Tyr Asn Trp Lys Asn Gly His Lys Pro Asp Thr Ser Thr Pro
645 650 655

Gly Glu Lys Asn Ala Val Val Val Val Thr Tyr Pro Asp Lys Ser Thr
660 665 670

Asp Glu Val Pro Val Lys Val Thr Val Val Asp Pro Arg Thr Asp Ala
675 680 685

Glu Lys Asn Asp Pro Ala Gly Lys Asp Gln Thr Val Lys Val Gly Glu
690 695 700

Gln Pro Asp Pro Thr Lys Ser Leu Glu Ala Val Pro Ala Gly Ser Thr
705 710 715 720

Val Ala Tyr Lys Glu Pro Val Asp Thr Lys Thr Pro Gly Glu Lys Asn
725 730 735

Ala Ile Val Val Val Thr Tyr Pro Asp Lys Ser Thr Asp Glu Val Pro
740 745 750

Val Lys Val Thr Val Val Asp Pro Arg Thr Asp Ala Glu Lys Asn Asp
755 760 765

Pro Ala Gly Lys Asp Gln Thr Val Lys Val Gly Glu Gln Pro Asp Pro
770 775 780

Thr Lys Ser Leu Glu Ala Val Pro Ala Gly Ser Thr Val Ala Tyr Lys
785 790 795 800

Glu Pro Val Asp Thr Lys Thr Pro Gly Glu Lys Asn Ala Ile Val Val
805 810 815

Val Thr Tyr Pro Asp Lys Ser Thr Asp Glu Val Pro Val Lys Val Thr
820 825 830

Val Val Asp Pro Arg Thr Asp Ala Glu Lys Asn Asp Pro Ala Gly Lys
835 840 845

Asp Gln Thr Val Lys Val Gly Glu Gln Pro Asp Pro Thr Lys Ser Leu
850 855 860

Glu Ala Val Pro Ala Gly Ser Thr Val Ala Tyr Lys Glu Pro Val Asp
865 870 875 880

Thr Lys Thr Pro Gly Glu Lys Asn Ala Val Val Val Val Thr Tyr Pro
885 890 895

Asp Lys Ser Thr Asp Glu Val Pro Val Lys Val Thr Val Val Asp Pro
900 905 910

Arg Thr Asp Ala Glu Lys Asn Asp Pro Ala Gly Lys Asp Gln Thr Val
915 920 925

Lys Val Gly Glu Gln Pro Asp Pro Thr Lys Ser Leu Glu Ala Val Pro
930 935 940

Ala Gly Ser Thr Val Ala Tyr Lys Glu Pro Val Asp Thr Lys Thr Pro
945 950 955 960

Gly Glu Lys Asn Ala Val Val Val Val Thr Tyr Pro Asp Lys Ser Thr
965 970 975

Asp Glu Val Pro Val Lys Val Thr Val Val Asp Pro Arg Thr Asp Ala
980 985 990

Glu Lys Asn Asp Pro Ala Gly Gly Glu Thr Thr Val Pro Gln Gly Thr
995 1000 1005

Pro Ile Ser Asp Glu Glu Ile Thr Gly Leu Val Lys Ile Pro Glu
1010 1015 1020

Gly Ser Asn Gly Val Pro Lys Val Val Gly Asp Arg Pro Asn Thr
1025 1030 1035

Asp Val Pro Gly Asp Tyr Lys Val Thr Val Glu Val Thr Tyr Pro
1040 1045 1050

Asp Gly Thr Lys Asp Thr Val Ala Val Thr Val His Val Thr Pro
1055 1060 1065

Lys Pro Val Pro Asp Lys Asp Lys Tyr Asp Pro Thr Gly Lys Ser
1070 1075 1080

Gln Gln Val Asn Gly Lys Gly Asn Lys Leu Pro Ala Thr Gly Glu
1085 1090 1095

Ser Ala Thr Pro Phe Phe Asn Val Ala Ala Leu Thr Ile Ile Ser
    1100                1105                1110

Ser Val Gly Leu Leu Ser Val Ser Lys Lys Lys Glu Asp
    1115                1120                1125

<210> 247

<211> 189

<212> PRT

<213> Streptococcus agalactiae

<400> 247

Met Gln Ile Leu Glu Asp Tyr Asp Gly Arg Ala Leu Pro Lys Leu Glu
1               5                   10                  15

Thr Asp Arg Leu Ile Leu Arg Gln Arg Thr Val Gly Asp Val Pro Ala
            20                  25                  30

Met Phe Asp Tyr Val Cys Leu Glu Glu Val Ala Tyr Pro Ala Gly Leu
        35                  40                  45

Ser Pro Ile Ala Ser Leu Glu Asp Glu Tyr Asp Tyr Phe Glu Asn Arg
    50                  55                  60

Tyr Tyr Gln Asn Leu Glu Lys Ala Lys Leu Pro Ser Gly Tyr Gly Ile
65                  70                  75                  80

Thr Val Lys Gly Ser Asp Arg Ile Ile Gly Ser Cys Ala Phe Asn His
                85                  90                  95

Arg Arg Glu Asp Asp Val Phe Glu Ile Gly Tyr Leu Leu His Pro Asp
            100                 105                 110

Tyr Trp Gly His Gly Tyr Met Thr Glu Ala Val Ala Ala Leu Ile Glu
        115                 120                 125

Val Gly Phe Thr Leu Leu Asn Leu His Lys Ile Glu Ile Arg Cys Tyr
    130                 135                 140

Asp Tyr Asn Lys Gln Ser Gln Arg Val Ala Glu Lys Leu Gly Phe Thr
145                 150                 155                 160

Leu Glu Ala Thr Ile Arg Asp Arg Lys Asp Asn Gln Gly Asn Arg Cys
                165                 170                 175

Val Asn Leu Ile Tyr Gly Leu Leu Arg Ser Glu Trp Glu
            180                 185

<210> 248

<211> 884

<212> PRT

<213> Streptococcus agalactiae

<400> 248

Met Ser Lys Glu Leu Ser Pro Lys Tyr Asn Pro Ala Glu Val Glu Glu
1 5 10 15

Gly Arg Tyr Gln Thr Trp Leu Asp Gln Asp Val Phe Lys Pro Ser Gly
20 25 30

Asp Thr Glu Ala Lys Pro Tyr Ser Ile Val Ile Pro Pro Pro Asn Val
35 40 45

Thr Gly Lys Leu His Leu Gly His Ala Trp Asp Thr Thr Leu Gln Asp
50 55 60

Ile Ile Ile Arg Gln Lys Arg Met Gln Gly Phe Asp Thr Leu Trp Leu
65 70 75 80

Pro Gly Met Asp His Ala Gly Ile Ala Thr Gln Ala Lys Val Glu Glu
85 90 95

Arg Leu Arg Glu Gln Gly Ile Ser Arg Tyr Asp Leu Gly Arg Glu Lys
100 105 110

Phe Leu Asp Lys Val Trp Glu Trp Lys Asp Glu Tyr Ala Ala Thr Ile
115 120 125

Lys Ser Gln Trp Gly Lys Met Gly Leu Ser Val Asp Tyr Ser Arg Glu
130 135 140

Arg Phe Thr Leu Asp Glu Gly Leu Ser Lys Ala Val Arg Lys Val Phe
145 150 155 160

Val Asp Leu Tyr Asn Lys Gly Trp Ile Tyr Arg Gly Glu Phe Ile Ile
165 170 175

Asn Trp Asp Pro Ala Ala Arg Thr Ala Leu Ser Asp Ile Glu Val Ile
180 185 190

His Lys Asp Val Glu Gly Ala Phe Tyr His Met Asn Tyr Met Leu Glu
195 200 205

Asp Gly Ser Arg Ala Leu Glu Val Ala Thr Thr Arg Pro Glu Thr Met
210 215 220

Phe Gly Asp Val Ala Val Ala Val Asn Pro Glu Asp Pro Arg Tyr Lys
225 230 235 240

Asp Leu Ile Gly Gln Asn Val Ile Leu Pro Ile Ile Asn Lys Pro Ile
245 250 255

Pro Ile Ile Ala Asp Glu His Ala Asp Pro Glu Phe Gly Thr Gly Val
260 265 270

Val Lys Ile Thr Pro Ala His Asp Pro Asn Asp Phe Ala Val Gly Gln
275 280 285

Arg His Asn Leu Pro Gln Val Asn Val Met Asn Asp Asp Gly Thr Met
290 295 300

Asn Glu Leu Ala Asp Glu Phe Asn Gly Met Asp Arg Phe Glu Ala Arg
305 310 315 320

Lys Ala Val Val Ala Lys Leu Glu Ser Leu Gly Asn Leu Val Lys Ile
325 330 335

Glu Lys Met Thr His Ser Val Gly His Ser Glu Arg Thr Gly Val Val
340 345 350

Val Glu Pro Arg Leu Ser Thr Gln Trp Phe Val Lys Met Asp Gln Leu
355 360 365

Ala Lys Asn Ala Ile Ala Asn Gln Asp Thr Glu Asp Lys Val Glu Phe
370 375 380

Tyr Pro Pro Arg Phe Asn Asp Thr Phe Met Ser Trp Met Glu Asn Val
385 390 395 400

His Asp Trp Val Ile Ser Arg Gln Leu Trp Trp Gly His Gln Ile Pro
405 410 415

Ala Trp Tyr Asn Val Asn Gly Glu Met Tyr Val Gly Glu Asp Ala Pro
420 425 430

Glu Gly Asp Gly Trp Thr Gln Asp Glu Asp Val Leu Asp Thr Trp Phe
435 440 445

Ser Ser Ala Leu Trp Pro Phe Ser Thr Met Gly Trp Pro Asp Thr Glu
450 455 460

Ala Ala Asp Phe Lys Arg Tyr Phe Pro Thr Ser Thr Leu Val Thr Gly
465 470 475 480

Tyr Asp Ile Ile Phe Phe Trp Val Ser Arg Met Ile Phe Gln Ser Leu
485 490 495

Glu Phe Thr Gly Arg Gln Pro Phe Ser Asn Val Leu Ile His Gly Leu
500 505 510

Ile Arg Asp Glu Glu Gly Arg Lys Met Ser Lys Ser Leu Gly Asn Gly
515 520 525

Ile Asp Pro Met Asp Val Ile Glu Lys Tyr Gly Ala Asp Ala Leu Arg
530 535 540

Trp Phe Leu Ser Asn Gly Ser Ala Pro Gly Gln Asp Val Arg Phe Ser
545 550 555 560

Tyr Glu Lys Met Asp Ala Ser Trp Asn Phe Ile Asn Lys Ile Trp Asn
565 570 575

Ile Ser Arg Tyr Ile Leu Met Asn Asn Glu Gly Leu Thr Leu Asp Gln
580 585 590

Ala Arg Glu Asn Val Glu Lys Val Val Asn Ser Gln Val Gly Asn Val
595 600 605

Thr Asp Arg Trp Ile Leu His Asn Leu Asn Glu Thr Val Gly Lys Val
610 615 620

Thr Glu Ser Phe Asp Lys Phe Glu Phe Gly Val Ala Gly His Ile Leu
625 630 635 640

Tyr Asn Phe Ile Trp Glu Glu Phe Ala Asn Trp Tyr Val Glu Leu Thr
645 650 655

Lys Glu Val Leu Tyr Ser Asp Asn Glu Asp Glu Lys Val Val Thr Arg
660 665 670

Ser Val Leu Leu Tyr Thr Leu Asp Gln Ile Leu Arg Leu Leu His Pro
675 680 685

Ile Met Pro Phe Val Thr Glu Glu Ile Phe Gly Gln Tyr Ala Glu Gly
690 695 700

Ser Ile Val Leu Ala Ser Tyr Pro Gln Val Asn Ala Thr Phe Glu Asn
705 710 715 720

Gln Thr Ala His Lys Gly Val Glu Ser Leu Lys Asp Leu Ile Arg Ser
725 730 735

Val Arg Asn Ser Arg Ala Glu Val Asn Val Ala Pro Ser Lys Pro Ile
740 745 750

Thr Ile Leu Val Lys Thr Ser Asp Ser Glu Leu Glu Ser Phe Phe Lys
755 760 765

Asp Asn Ser Asn Tyr Ile Lys Arg Phe Thr Asn Pro Glu Thr Leu Glu
770 775 780

Ile Ser Ser Ala Ile Thr Ala Pro Glu Leu Ala Met Thr Ser Ile Ile
785 790 795 800

Thr Gly Ala Glu Ile Phe Leu Pro Leu Ala Asp Leu Leu Asn Val Glu
805 810 815

Glu Glu Leu Ala Arg Leu Glu Lys Glu Leu Ala Lys Trp Gln Lys Glu
820 825 830

Leu Asn Met Val Gly Lys Lys Leu Ser Asn Glu Arg Phe Val Ala Asn
835 840 845

Ala Lys Pro Glu Val Val Gln Lys Glu Lys Asp Lys Gln Thr Asp Tyr
850 855 860

Gln Thr Lys Tyr Asp Ala Thr Ile Ala Arg Ile Glu Glu Met Lys Lys
865 870 875 880

Leu Asn Asn Asp

<210> 249

<211> 244

<212> PRT

<213> Streptococcus agalactiae

<400> 249

Met Val Glu Pro Ile Ile Ser Ile Gln Gly Leu His Lys Ser Phe Gly
1 5 10 15

Lys Asn Glu Val Leu Lys Gly Ile Asp Leu Asp Ile His Gln Gly Glu
20 25 30

Val Val Val Ile Ile Gly Pro Ser Gly Ser Gly Lys Ser Thr Phe Leu
35 40 45

Arg Thr Met Asn Leu Leu Glu Val Pro Thr Lys Gly Thr Val Thr Phe
50 55 60

Glu Gly Ile Asp Ile Thr Asp Lys Lys Asn Asp Ile Phe Lys Met Arg
65 70 75 80

Glu Lys Met Gly Met Val Phe Gln Gln Phe Asn Leu Phe Pro Asn Met
85 90 95

Thr Val Leu Glu Asn Ile Thr Leu Ser Pro Ile Lys Thr Lys Gly Leu
100 105 110

Ser Lys Leu Asp Ala Gln Thr Lys Ala Tyr Glu Leu Leu Glu Lys Val
115 120 125

Gly Leu Lys Glu Lys Ala Asn Ala Tyr Pro Ala Ser Leu Ser Gly Gly
130 135 140

Gln Gln Gln Arg Ile Ala Ile Ala Arg Gly Leu Ala Met Asn Pro Asp
145 150 155 160

Val Leu Leu Phe Asp Glu Pro Thr Ser Ala Leu Asp Pro Glu Met Val
165 170 175

Gly Glu Val Leu Thr Val Met Gln Asp Leu Ala Lys Ser Gly Met Thr
180 185 190

Met Val Ile Val Thr His Glu Met Gly Phe Ala Arg Glu Val Ala Asp
195 200 205

Arg Val Ile Phe Met Asp Ala Gly Ile Ile Val Glu Gln Gly Thr Pro
210 215 220

Lys Glu Val Phe Glu Gln Thr Lys Glu Ile Arg Thr Arg Asp Phe Leu
225 230 235 240

Ser Lys Val Leu

<210> 250

<211> 564

<212> PRT

<213> Streptococcus agalactiae

<400> 250

Met Asn Tyr Lys Glu Ile Tyr Gln Glu Trp Leu Glu Asn Asp Ser Leu
1 5 10 15

Gly Lys Asp Ile Lys Ser Asp Leu Glu Ala Ile Lys Gly Asp Glu Ser
20 25 30

Glu Ile Gln Asp Arg Phe Tyr Lys Thr Leu Glu Phe Gly Thr Ala Gly
35 40 45

Leu Arg Gly Lys Leu Gly Ala Gly Thr Asn Arg Met Asn Thr Tyr Met
50 55 60

Val Gly Lys Ala Ala Gln Ala Leu Ala Asn Thr Ile Ile Asp His Gly
65 70 75 80

Pro Glu Ala Ile Ala Arg Gly Ile Ala Val Ser Tyr Asp Val Arg Tyr
85 90 95

Gln Ser Lys Glu Phe Ala Glu Leu Thr Cys Ser Ile Met Ala Ala Asn
100 105 110

Gly Ile Lys Ser Tyr Ile Tyr Lys Gly Ile Arg Pro Thr Pro Met Cys
115 120 125

Ser Tyr Ala Ile Arg Ala Leu Gly Cys Val Ser Gly Val Met Val Thr
130 135 140

Ala Ser His Asn Pro Gln Ala Tyr Asn Gly Tyr Lys Ala Tyr Trp Lys
145 150 155 160

Glu Gly Ser Gln Ile Leu Asp Asp Ile Ala Asp Gln Ile Ala Asn His
165 170 175

Met Asp Ala Ile Thr Asp Tyr Gln Gln Ile Arg Gln Ile Pro Phe Glu
180 185 190

Glu Ala Leu Ala Ser Gly Leu Ala Ser Tyr Ile Asp Glu Ser Ile Glu
195 200 205

Glu Ala Tyr Lys Lys Glu Val Leu Gly Leu Thr Ile Asn Asp Thr Asn
210 215 220

Ile Asp Lys Ser Val Arg Val Val Tyr Thr Pro Leu Asn Gly Val Gly
225 230 235 240

Asn Leu Pro Val Arg Glu Val Leu Arg Arg Arg Gly Phe Glu Asn Val
245 250 255

Tyr Val Val Pro Glu Gln Glu Met Pro Asp Pro Asp Phe Thr Thr Val
260 265 270

Gly Tyr Pro Asn Pro Glu Val Pro Lys Ala Phe Ala Tyr Ser Glu Ser
275 280 285

Leu Gly Lys Ser Val Asp Ala Asp Ile Leu Leu Ala Thr Asp Pro Asp
290 295 300

Cys Asp Arg Val Ala Leu Glu Val Lys Asp Ser Lys Gly Glu Tyr Ile
305 310 315 320

Phe Leu Asn Gly Asn Lys Ile Gly Ala Leu Leu Ser Tyr Tyr Ile Phe
325 330 335

Ser Gln Arg Cys Ala Leu Gly Asn Leu Pro His His Pro Val Leu Val
340 345 350

Lys Ser Ile Val Thr Gly Asp Leu Ser Lys Val Ile Ala Asp Lys Tyr
355 360 365

Asn Ile Glu Thr Val Glu Thr Leu Thr Gly Phe Lys Asn Ile Cys Gly
370 375 380

Lys Ala Asn Glu Tyr Asp Ile Ser Lys Asp Lys Thr Tyr Leu Phe Gly
385 390 395 400

Tyr Glu Glu Ser Ile Gly Phe Cys Tyr Gly Thr Phe Val Arg Asp Lys
405 410 415

Asp Ala Val Ser Ala Ser Met Met Val Val Glu Met Thr Ala Tyr Tyr
420 425 430

Lys Glu Arg Gly Gln Thr Leu Leu Asp Val Leu Gln Thr Ile Tyr Asp
435 440 445

Glu Phe Gly Tyr Tyr Asn Glu Arg Gln Phe Ser Leu Glu Leu Glu Gly
450 455 460

Ala Glu Gly Gln Glu Arg Ile Ser Arg Ile Met Glu Asp Phe Arg Gln
465 470 475 480

Asp Pro Ile Leu Gln Val Gly Glu Met Arg Leu Glu Asn Ser Ile Asp
485 490 495

Phe Lys Asp Gly Tyr Lys Asp Phe Pro Lys Gln Asn Cys Leu Lys Tyr
500 505 510

Tyr Phe Asn Glu Gly Ser Trp Tyr Ala Leu Arg Pro Ser Gly Thr Glu
515 520 525

Pro Lys Ile Lys Cys Tyr Leu Tyr Thr Ile Gly Cys Thr Glu Ala Asp
530 535 540

Ser Leu Ser Lys Leu Asn Ala Ile Glu Ser Ala Cys Arg Ala Lys Met
545 550 555 560

Asn Ser Thr Lys

<210> 251

<211> 403

<212> PRT

<213> Streptococcus agalactiae

<400> 251

Met Tyr Arg Glu Ile Thr Ala Val Glu His Asp Arg Phe Val Ser Glu
1               5                   10                  15

Ser Asn Gln Thr Asn Leu Leu Gln Ser Ser Asn Trp Pro Lys Val Lys
            20                  25                  30

Asp Asn Trp Gly Ser Gln Leu Leu Gly Phe Phe Asp Gly Glu Thr Gln
        35                  40                  45

Ile Ala Ser Ala Ser Ile Leu Ile Lys Ser Leu Pro Leu Gly Phe Ser
    50                  55                  60

Met Leu Tyr Ile Pro Arg Gly Pro Ile Met Asp Tyr Ser Asn Leu Asp
65                  70                  75                  80

Ile Val Thr Lys Val Leu Lys Asp Leu Lys Ala Phe Gly Lys Lys Gln
                85                  90                  95

Arg Ala Leu Phe Ile Lys Cys Asp Pro Leu Ile Tyr Leu Lys Met Val
            100                 105                 110

Asn Ala Lys Asp Phe Glu Asn Ser Pro Asp Glu Lys Glu Gly Leu Ile
        115                 120                 125

Ala Ile Asp His Leu Gln Arg Ala Gly Ala Asp Trp Thr Gly Arg Thr
    130                 135                 140

Thr Asp Leu Ala His Thr Ile Gln Pro Arg Phe Gln Ala Asn Leu Tyr
145                 150                 155                 160

Ala Asn Gln Phe Gly Leu Asp Lys Met Ser Lys Lys Thr Arg Gln Ala
                165                 170                 175

Ile Arg Thr Ser Lys Asn Lys Gly Val Asp Ile Gln Phe Gly Ser His
            180                 185                 190

Glu Leu Leu Glu Asp Phe Ala Glu Leu Met Lys Lys Thr Glu Asp Arg
        195                 200                 205

Lys Gly Ile Asn Leu Arg Gly Ile Asp Tyr Tyr Gln Lys Leu Leu Asp
    210                 215                 220

Thr Tyr Pro Asn Asn Ser Tyr Ile Thr Met Ala Ser Leu Asp Val Ala
225                 230                 235                 240

Lys Arg Leu Glu Lys Ile Glu Lys Glu Cys Gln Ile Ala Gln Ser Glu
                245                 250                 255

Arg Ile Lys Ser Leu Glu Leu Asn Arg Glu Lys Lys Val Lys Gln His
260 265 270

Gln Gly Thr Ile Asp Arg Leu Asn Lys Glu Ile Asp Phe Leu Lys Glu
275 280 285

Ala Gln Lys Ala Tyr Asp Arg Asp Ile Ile Pro Leu Ala Ala Thr Leu
290 295 300

Thr Leu Glu Phe Gly Asn Thr Ser Glu Asn Ile Tyr Ala Gly Met Asp
305 310 315 320

Asp Tyr Phe Lys Ser Tyr Ser Ala Pro Ile Tyr Thr Trp Phe Glu Thr
325 330 335

Ala Gln Arg Ala Phe Glu Arg Gly Asn Ile Trp Gln Asn Met Gly Gly
340 345 350

Ile Glu Asn Asp Leu Ser Gly Gly Leu Tyr His Phe Lys Ser Lys Phe
355 360 365

Glu Pro Ile Ile Glu Glu Phe Ile Gly Glu Phe Asn Ile Pro Val Asn
370 375 380

Arg Leu Leu Tyr Lys Ala Ser Asn Tyr Val Tyr Ala Leu Arg Lys Lys
385 390 395 400

Arg Asn Ser

<210> 252

<211> 465

<212> PRT

<213> Streptococcus agalactiae

<400> 252

Met Ala Cys Thr Thr Ile Leu Val Gly Lys Lys Ala Ser Tyr Asp Gly
1 5 10 15

Ser Thr Met Ile Ala Arg Thr Glu Asp Ser Val Asn Gly Asp Phe Thr
20 25 30

Pro Lys Lys Leu Lys Val Met Thr Ser Lys Asp Gln Pro Arg His Tyr
35 40 45

Lys Ser Val Leu Ser Asn Phe Glu Val Asp Leu Pro Asp Asn Pro Leu
50 55 60

Pro Tyr Thr Ser Val Pro Asp Ala Leu Gly Lys Asp Gly Ile Trp Gly
65 70 75 80

Glu Ala Gly Ile Asn Ser Lys Asn Val Ala Met Ser Ala Thr Glu Thr
85 90 95

Ile Thr Thr Asn Ser Arg Val Leu Gly Ala Asp Pro Leu Val Ser Asp
100 105 110

Gly Ile Gly Glu Glu Asp Ile Leu Thr Leu Val Leu Pro Tyr Ile Gln
115 120 125

Ser Ala Arg Glu Gly Val Glu Arg Leu Gly Ala Ile Leu Glu Lys Tyr
130 135 140

Gly Thr Tyr Glu Ser Asn Gly Ile Ala Phe Ser Asp Thr Glu Glu Ile
145 150 155 160

Trp Trp Leu Glu Thr Ile Gly Gly His His Trp Ile Ala Arg Arg Val
165 170 175

Pro Asp Asp Val Tyr Val Thr Asn Pro Asn Gln Leu Gly Ile Asp His
180 185 190

Phe Glu Phe Asn Asn Cys Asp Asp Tyr Met Cys Ser Ser Asp Leu Lys
195 200 205

Glu Phe Ile Glu Gln Tyr His Leu Asp Leu Thr Tyr Ser Asn Glu His
210 215 220

Phe Asn Pro Arg Tyr Ala Phe Gly Ser Gln Arg Asp Lys Asp Arg His
225 230 235 240

Tyr Asn Thr Pro Arg Ser Trp Ala Met Gln Arg Phe Leu Asn Pro Glu
245 250 255

Ile Glu Gln Asp Pro Arg Ser Leu Phe Ile Pro Trp Cys Gln Lys Pro
260 265 270

Tyr Arg Lys Ile Thr Val Glu Asp Ile Lys Tyr Val Leu Ser Asp His
275 280 285

Tyr Gln Asp Ser Val Tyr Asp Pro Tyr Gly Pro Glu Gly Asp Ala Val
290 295 300

Ser Arg Arg Ala Phe Arg Ser Val Gly Ile Asn Arg Thr Ser Gln Thr
305 310 315 320

Ser Ile Leu Gln Leu Arg Pro Asn Lys Ser Leu Glu Thr Thr Gly Val
325 330 335

Gln Trp Leu Ser Tyr Gly Ser Met Pro Phe Ala Thr Met Val Pro Leu
340 345 350

Phe Thr Gln Val Glu Thr Val Pro Asn Tyr Phe Ser Asn Thr Thr Lys
355 360 365

Asp Ala Ser Thr Asp Asn Phe Tyr Trp Thr Asn Arg Leu Ile Ala Ala
370 375 380

Leu Ala Asp Pro His Phe Tyr Gln His Glu Ala Asp Ile Glu Ser Tyr
385 390 395 400

Ile Glu Arg Thr Met Ala Gln Gly His Ala His Ile Asn Gly Val Asp
405 410 415

Arg Glu Val Ala Glu Asn Lys Glu Ile Asp Phe Gln Gln Lys Asn Gln
420 425 430

Glu Met Ser Asp Tyr Ile Gln Lys Glu Ser Gln Glu Leu Leu Asn Arg
435 440 445

Ile Leu Phe Asp Ala Ser Asn Leu Met Thr Asn Arg Phe Ser Met Gly
450 455 460

Asp
465

<210> 253

<211> 506

<212> PRT

<213> Streptococcus agalactiae

<400> 253

Met Arg Lys Lys Phe Leu Leu Leu Met Ser Phe Val Ala Met Phe Ala
1 5 10 15

Ala Trp Gln Leu Val Gln Val Lys Gln Val Trp Ala Asp Ser Lys Leu
20 25 30

Lys Val Val Thr Thr Phe Tyr Pro Val Tyr Glu Phe Thr Lys Asn Val
35 40 45

Val Gly Asp Lys Ala Asp Val Ser Met Leu Ile Lys Ala Gly Thr Glu
50 55 60

Pro His Asp Phe Glu Pro Ser Thr Lys Asn Ile Ala Ala Ile Gln Asp
65 70 75 80

Ser Asn Ala Phe Val Tyr Met Asp Asp Asn Met Glu Thr Trp Ala Pro
85 90 95

Lys Val Ala Lys Ser Val Lys Ser Lys Lys Val Thr Thr Ile Lys Gly
100 105 110

Thr Gly Asp Met Leu Leu Thr Lys Gly Val Glu Glu Glu Gly Glu Glu
115 120 125

His Glu Gly His Gly His Glu Gly His His His Glu Leu Asp Pro His
130 135 140

Val Trp Leu Ser Pro Glu Arg Ala Ile Ser Val Val Glu Asn Ile Arg
145 150 155 160

Asn Lys Phe Val Lys Ala Tyr Pro Lys Asp Ala Ala Ser Phe Asn Lys
165 170 175

Asn Ala Asp Ala Tyr Ile Ala Lys Leu Lys Glu Leu Asp Lys Glu Tyr
180 185 190

Lys Asn Gly Leu Ser Asn Ala Lys Gln Lys Ser Phe Val Thr Gln His
195 200 205

Ala Ala Phe Gly Tyr Met Ala Leu Asp Tyr Gly Leu Asn Gln Val Pro
210 215 220

Ile Ala Gly Leu Thr Pro Asp Ala Glu Pro Ser Ser Lys Arg Leu Gly
225 230 235 240

Glu Leu Ala Lys Tyr Ile Lys Lys Tyr Asn Ile Asn Tyr Ile Tyr Phe
245 250 255

Glu Glu Asn Ala Ser Asn Lys Val Ala Lys Thr Leu Ala Asp Glu Val
260 265 270

Gly Val Lys Thr Ala Val Leu Ser Pro Leu Glu Gly Leu Ser Lys Lys
275 280 285

Glu Met Ala Ala Gly Glu Asp Tyr Phe Ser Val Met Arg Arg Asn Leu
290 295 300

Lys Val Leu Lys Lys Thr Thr Asp Val Ala Gly Lys Glu Val Ala Pro
305 310 315 320

Glu Glu Asp Lys Thr Lys Thr Val Glu Thr Gly Tyr Phe Lys Thr Lys
325 330 335

Asp Val Lys Asp Arg Lys Leu Thr Asp Tyr Ser Gly Asn Trp Gln Ser
340 345 350

Val Tyr Pro Leu Leu Gln Asp Gly Thr Leu Asp Pro Val Trp Asp Tyr
355 360 365

Lys Ala Lys Ser Lys Lys Asp Met Thr Ala Ala Glu Tyr Lys Lys Tyr
370 375 380

Tyr Thr Ala Gly Tyr Lys Thr Asp Val Glu Ser Ile Lys Ile Asp Gly
385 390 395 400

Lys Lys His Gln Met Thr Phe Val Arg Asn Gly Lys Ser Gln Thr Phe
405 410 415

Thr Tyr Lys Tyr Ala Gly Tyr Lys Ile Leu Thr Tyr Lys Lys Gly Asn
420 425 430

Arg Gly Val Arg Tyr Leu Phe Glu Ala Lys Glu Lys Asp Ala Gly Gln
435 440 445

Phe Lys Tyr Ile Gln Phe Ser Asp His Gly Ile Lys Pro Asn Lys Ala
450 455 460

Glu His Phe His Ile Phe Trp Gly Ser Glu Ser Gln Glu Lys Leu Phe
465 470 475 480

Glu Glu Met Glu Asn Trp Pro Thr Tyr Phe Pro Ala Lys Met Ser Gly
485 490 495

Arg Glu Val Ala Gln Asp Leu Met Ser His
500 505

<210> 254

<211> 554

<212> PRT

<213> Streptococcus agalactiae

<400> 254

Met Lys Leu Ser Lys Lys Leu Leu Phe Ser Ala Ala Val Leu Thr Met
1 5 10 15

Val Ala Gly Ser Thr Val Glu Pro Val Ala Gln Phe Ala Thr Gly Met
20 25 30

Ser Ile Val Arg Ala Ala Glu Val Ser Gln Glu Arg Pro Ala Lys Thr
35 40 45

Thr Val Asn Ile Tyr Lys Leu Gln Ala Asp Ser Tyr Lys Ser Glu Ile
50 55 60

Thr Ser Asn Gly Gly Ile Glu Asn Lys Asp Gly Glu Val Ile Ser Asn
65 70 75 80

Tyr Ala Lys Leu Gly Asp Asn Val Lys Gly Leu Gln Gly Val Gln Phe
85 90 95

Lys Arg Tyr Lys Val Lys Thr Asp Ile Ser Val Asp Glu Leu Lys Lys
100 105 110

Leu Thr Thr Val Glu Ala Ala Asp Ala Lys Val Gly Thr Ile Leu Glu
115 120 125

Glu Gly Val Ser Leu Pro Gln Lys Thr Asn Ala Gln Gly Leu Val Val
130 135 140

Asp Ala Leu Asp Ser Lys Ser Asn Val Arg Tyr Leu Tyr Val Glu Asp
145 150 155 160

Leu Lys Asn Ser Pro Ser Asn Ile Thr Lys Ala Tyr Ala Val Pro Phe
165 170 175

Val Leu Glu Leu Pro Val Ala Asn Ser Thr Gly Thr Gly Phe Leu Ser
180 185 190

Glu Ile Asn Ile Tyr Pro Lys Asn Val Val Thr Asp Glu Pro Lys Thr
195 200 205

Asp Lys Asp Val Lys Lys Leu Gly Gln Asp Asp Ala Gly Tyr Thr Ile
210 215 220

Gly Glu Glu Phe Lys Trp Phe Leu Lys Ser Thr Ile Pro Ala Asn Leu
225 230 235 240

Gly Asp Tyr Glu Lys Phe Glu Ile Thr Asp Lys Phe Ala Asp Gly Leu
245 250 255

Thr Tyr Lys Ser Val Gly Lys Ile Lys Ile Gly Ser Lys Thr Leu Asn
260 265 270

Arg Asp Glu His Tyr Thr Ile Asp Glu Pro Thr Val Asp Asn Gln Asn
275 280 285

Thr Leu Lys Ile Thr Phe Lys Pro Glu Lys Phe Lys Glu Ile Ala Glu
290 295 300

Leu Leu Lys Gly Met Thr Leu Val Lys Asn Gln Asp Ala Leu Asp Lys
305 310 315 320

Ala Thr Ala Asn Thr Asp Asp Ala Ala Phe Leu Glu Ile Pro Val Ala
325 330 335

Ser Thr Ile Asn Glu Lys Ala Val Leu Gly Lys Ala Ile Glu Asn Thr
340 345 350

Phe Glu Leu Gln Tyr Asp His Thr Pro Asp Lys Ala Asp Asn Pro Lys
355 360 365

Pro Ser Asn Pro Pro Arg Lys Pro Glu Val His Thr Gly Gly Lys Arg
370 375 380

Phe Val Lys Lys Asp Ser Thr Glu Thr Gln Thr Leu Gly Gly Ala Glu
385 390 395 400

Phe Asp Leu Leu Ala Ser Asp Gly Thr Ala Val Lys Trp Thr Asp Ala
405 410 415

Leu Ile Lys Ala Asn Thr Asn Lys Asn Tyr Ile Ala Gly Glu Ala Val
420 425 430

Thr Gly Gln Pro Ile Lys Leu Lys Ser His Thr Asp Gly Thr Phe Glu
435 440 445

Ile Lys Gly Leu Ala Tyr Ala Val Asp Ala Asn Ala Glu Gly Thr Ala
450 455 460

Val Thr Tyr Lys Leu Lys Glu Thr Lys Ala Pro Glu Gly Tyr Val Ile
465 470 475 480

Pro Asp Lys Glu Ile Glu Phe Thr Val Ser Gln Thr Ser Tyr Asn Thr
485 490 495

Lys Pro Thr Asp Ile Thr Val Asp Ser Ala Asp Ala Thr Pro Asp Thr
500 505 510

Ile Lys Asn Asn Lys Arg Pro Ser Ile Pro Asn Thr Gly Gly Ile Gly
515 520 525

Thr Ala Ile Phe Val Ala Ile Gly Ala Ala Val Met Ala Phe Ala Val
530 535 540

Lys Gly Met Lys Arg Arg Thr Lys Asp Asn
545 550

<210> 255

<211> 890

<212> PRT

<213> Streptococcus agalactiae

<400> 255

Met Lys Lys Arg Gln Lys Ile Trp Arg Gly Leu Ser Val Thr Leu Leu
1               5                   10                  15

Ile Leu Ser Gln Ile Pro Phe Gly Ile Leu Val Gln Gly Glu Thr Gln
            20                  25                  30

Asp Thr Asn Gln Ala Leu Gly Lys Val Ile Val Lys Lys Thr Gly Asp
        35                  40                  45

Asn Ala Thr Pro Leu Gly Lys Ala Thr Phe Val Leu Lys Asn Asp Asn
    50                  55                  60

Asp Lys Ser Glu Thr Ser His Glu Thr Val Glu Gly Ser Gly Glu Ala
65                  70                  75                  80

Thr Phe Glu Asn Ile Lys Pro Gly Asp Tyr Thr Leu Arg Glu Glu Thr
                85                  90                  95

Ala Pro Ile Gly Tyr Lys Lys Thr Asp Lys Thr Trp Lys Val Lys Val
            100                 105                 110

Ala Asp Asn Gly Ala Thr Ile Ile Glu Gly Met Asp Ala Asp Lys Ala
        115                 120                 125

Glu Lys Arg Lys Glu Val Leu Asn Ala Gln Tyr Pro Lys Ser Ala Ile
    130                 135                 140

Tyr Glu Asp Thr Lys Glu Asn Tyr Pro Leu Val Asn Val Glu Gly Ser
145                 150                 155                 160

Lys Val Gly Glu Gln Tyr Lys Ala Leu Asn Pro Ile Asn Gly Lys Asp
                165                 170                 175

Gly Arg Arg Glu Ile Ala Glu Gly Trp Leu Ser Lys Lys Ile Thr Gly
            180                 185                 190

Val Asn Asp Leu Asp Lys Asn Lys Tyr Lys Ile Glu Leu Thr Val Glu
        195                 200                 205

Gly Lys Thr Thr Val Glu Thr Lys Glu Leu Asn Gln Pro Leu Asp Val
    210                 215                 220

Val Val Leu Leu Asp Asn Ser Asn Ser Met Asn Asn Glu Arg Ala Asn
225                 230                 235                 240

Asn Ser Gln Arg Ala Leu Lys Ala Gly Glu Ala Val Glu Lys Leu Ile
                245                 250                 255

Asp Lys Ile Thr Ser Asn Lys Asp Asn Arg Val Ala Leu Val Thr Tyr
            260                 265                 270

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Ala Ser Thr Ile Phe Asp Gly Thr Glu Ala Thr Val Ser Lys Gly Val
        275                 280                 285

Ala Asp Gln Asn Gly Lys Ala Leu Asn Asp Ser Val Ser Trp Asp Tyr
    290                 295                 300

His Lys Thr Thr Phe Thr Ala Thr Thr His Asn Tyr Ser Tyr Leu Asn
305                 310                 315                     320

Leu Thr Asn Asp Ala Asn Glu Val Asn Ile Leu Lys Ser Arg Ile Pro
                325                 330                 335

Lys Glu Ala Glu His Ile Asn Gly Asp Arg Thr Leu Tyr Gln Phe Gly
            340                 345                 350

Ala Thr Phe Thr Gln Lys Ala Leu Met Lys Ala Asn Glu Ile Leu Glu
        355                 360                 365

Thr Gln Ser Ser Asn Ala Arg Lys Lys Leu Ile Phe His Val Thr Asp
    370                 375                 380

Gly Val Pro Thr Met Ser Tyr Ala Ile Asn Phe Asn Pro Tyr Ile Ser
385                 390                 395                     400

Thr Ser Tyr Gln Asn Gln Phe Asn Ser Phe Leu Asn Lys Ile Pro Asp
                405                 410                 415

Arg Ser Gly Ile Leu Gln Glu Asp Phe Ile Ile Asn Gly Asp Asp Tyr
            420                 425                 430

Gln Ile Val Lys Gly Asp Gly Glu Ser Phe Lys Leu Phe Ser Asp Arg
        435                 440                 445

Lys Val Pro Val Thr Gly Gly Thr Thr Gln Ala Ala Tyr Arg Val Pro
    450                 455                 460

Gln Asn Gln Leu Ser Val Met Ser Asn Glu Gly Tyr Ala Ile Asn Ser
465                 470                 475                     480

Gly Tyr Ile Tyr Leu Tyr Trp Arg Asp Tyr Asn Trp Val Tyr Pro Phe
                485                 490                 495

Asp Pro Lys Thr Lys Lys Val Ser Ala Thr Lys Gln Ile Lys Thr His
            500                 505                 510

Gly Glu Pro Thr Thr Leu Tyr Phe Asn Gly Asn Ile Arg Pro Lys Gly
        515                 520                 525

Tyr Asp Ile Phe Thr Val Gly Ile Gly Val Asn Gly Asp Pro Gly Ala
    530                 535                 540
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Thr Pro Leu Glu Ala Glu Lys Phe Met Gln Ser Ile Ser Ser Lys Thr
545 550 555 560

Glu Asn Tyr Thr Asn Val Asp Asp Thr Asn Lys Ile Tyr Asp Glu Leu
565 570 575

Asn Lys Tyr Phe Lys Thr Ile Val Glu Glu Lys His Ser Ile Val Asp
580 585 590

Gly Asn Val Thr Asp Pro Met Gly Glu Met Ile Glu Phe Gln Leu Lys
595 600 605

Asn Gly Gln Ser Phe Thr His Asp Asp Tyr Val Leu Val Gly Asn Asp
610 615 620

Gly Ser Gln Leu Lys Asn Gly Val Ala Leu Gly Gly Pro Asn Ser Asp
625 630 635 640

Gly Gly Ile Leu Lys Asp Val Thr Val Thr Tyr Asp Lys Thr Ser Gln
645 650 655

Thr Ile Lys Ile Asn His Leu Asn Leu Gly Ser Gly Gln Lys Val Val
660 665 670

Leu Thr Tyr Asp Val Arg Leu Lys Asp Asn Tyr Ile Ser Asn Lys Phe
675 680 685

Tyr Asn Thr Asn Asn Arg Thr Thr Leu Ser Pro Lys Ser Glu Lys Glu
690 695 700

Pro Asn Thr Ile Arg Asp Phe Pro Ile Pro Lys Ile Arg Asp Val Arg
705 710 715 720

Glu Phe Pro Val Leu Thr Ile Ser Asn Gln Lys Lys Met Gly Glu Val
725 730 735

Glu Phe Ile Lys Val Asn Lys Asp Lys His Ser Glu Ser Leu Leu Gly
740 745 750

Ala Lys Phe Gln Leu Gln Ile Glu Lys Asp Phe Ser Gly Tyr Lys Gln
755 760 765

Phe Val Pro Glu Gly Ser Asp Val Thr Thr Lys Asn Asp Gly Lys Ile
770 775 780

Tyr Phe Lys Ala Leu Gln Asp Gly Asn Tyr Lys Leu Tyr Glu Ile Ser
785 790 795 800

Ser Pro Asp Gly Tyr Ile Glu Val Lys Thr Lys Pro Val Val Thr Phe
805 810 815

Thr Ile Gln Asn Gly Glu Val Thr Asn Leu Lys Ala Asp Pro Asn Ala
820 825 830

Asn Lys Asn Gln Ile Gly Tyr Leu Glu Gly Asn Gly Lys His Leu Ile
835 840 845

Thr Asn Thr Pro Lys Arg Pro Pro Gly Val Phe Pro Lys Thr Gly Gly
850 855 860

Ile Gly Thr Ile Val Tyr Ile Leu Val Gly Ser Thr Phe Met Ile Leu
865 870 875 880

Thr Ile Cys Ser Phe Arg Arg Lys Gln Leu
885 890

<210> 256

<211> 201

<212> PRT

<213> Streptococcus agalactiae

<400> 256

Gly Ala Lys Lys Ala Gly Trp Thr Glu Tyr Ala Arg Met Leu Glu Val
1 5 10 15

Arg Glu Gln Val Asp His Val Met Ile Pro Lys Ile Asn Gln Asp Leu
20 25 30

Pro Ile Tyr Ala Gly Pro Glu Glu Asp Asn Leu Gln Arg Gly Val Gly
35 40 45

His Leu Glu Gly Ile Ser Leu Pro Ile Gly Gly Ala Ser Thr His Ala
50 55 60

Val Leu Ser Gly Gln Arg Gly Met Pro Ala Ala Arg Leu Phe Ala Asp
65 70 75 80

Leu Asp Lys Met Lys Lys Gly Asp Tyr Phe Tyr Val Thr Asn Leu Lys
85 90 95

Glu Thr Leu Ala Tyr Gln Val Asp Arg Ile Met Val Ile Glu Pro Ser
100 105 110

Gln Leu Asp Ala Val Ser Ile Glu Glu Asp Lys Asp Tyr Val Thr Leu
115 120 125

Leu Thr Cys Thr Pro Tyr Met Gly Ser Leu Ser Thr Val Met Gly Asp
130 135 140

Leu Ser Leu Thr Thr Arg Glu Asn Gln Leu Gly Ser Leu Ser Phe Trp
145 150 155 160

Met Phe Lys Ala Met Arg Ile Leu Leu Leu Lys Phe Leu Lys Leu Arg
165 170 175

Lys Pro Lys Ala Cys Arg Leu Met Ser Leu Ile Ser Leu Leu Val Ala
180 185 190

Ser Asn Leu Ala Leu Glu Arg Asp Ser
195 200

<210> 257

<211> 352

<212> PRT

<213> Streptococcus agalactiae

<400> 257

Met Ser Asp Val Val Glu Lys Gln Thr Ala Lys Ser Phe Ile Met Asn
1 5 10 15

Val Leu Asn Gly Leu Ala Leu Gly Thr Val Ile Val Leu Ile Pro Gly
20 25 30

Ala Ile Leu Gly Glu Leu Met Lys Ala Leu Leu Pro Met Trp Ser Gly
35 40 45

Phe Ala Thr Leu Ile Ala Ala Thr Ala Val Ala Thr Ser Met Met Gly
50 55 60

Leu Val Ile Gly Ile Met Val Gly Leu Asn Phe Lys Phe Asn Pro Ile
65 70 75 80

Gln Ser Ala Ser Leu Gly Leu Ala Val Met Phe Ala Gly Gly Ala Ala
85 90 95

Thr Phe Leu Lys Gly Ala Ile Met Leu Lys Gly Thr Gly Asp Ile Ile
100 105 110

Asn Met Gly Ile Thr Ala Ala Leu Gly Val Leu Leu Ile Gln Phe Leu
115 120 125

Ser Asp Lys Thr Lys Ser Phe Thr Leu Ile Val Ile Pro Thr Val Thr
130 135 140

Leu Leu Leu Val Gly Gly Val Gly His Val Leu Leu Pro Tyr Val Lys
145 150 155 160

Met Ile Thr Thr Met Ile Gly Gln Gly Ile Ala Ser Leu Leu Gly Leu
165 170 175

Gln Pro Val Leu Met Ser Ile Leu Ile Ala Met Ile Phe Cys Phe Leu
180 185 190

Ile Val Ser Pro Ile Thr Thr Val Gly Ile Ala Leu Ala Ile Ser Leu
195 200 205

Ser Gly Ile Gly Ser Gly Ala Ala Asn Leu Gly Ile Cys Ala Ala Ser
210 215 220

Phe Gly Leu Cys Met Ala Gly Trp Ser Val Asn Ser Lys Gly Thr Ala
225 230 235 240

Leu Ala His Val Leu Gly Ser Pro Lys Ile Ser Met Ala Asn Val Leu
245 250 255

Ala Lys Pro Lys Ile Met Leu Pro Met Ile Ser Ser Ala Ala Ile Leu
260 265 270

Gly Ile Leu Gly Ala Leu Phe Asn Ile Gln Gly Thr Pro Ala Ser Ala
275 280 285

Gly Phe Gly Ile Ser Gly Leu Ile Gly Pro Ile Asn Ala Leu Asn Leu
290 295 300

Ala Lys Gly Gly Trp Ser Val Met Asn Met Leu Leu Ile Ile Ile Ile
305 310 315 320

Phe Val Ala Ala Pro Ile Ile Leu Asn Phe Ile Phe Asn Tyr Leu Phe
325 330 335

Ile Lys Val Leu Lys Ile Ile Asp Pro Met Asp Tyr Lys Leu Asp Ile
340 345 350

<210> 258

<211> 223

<212> PRT

<213> Streptococcus agalactiae

<400> 258

Met Ala Arg Pro Leu Val Glu Gln Thr Ala Asp Arg Leu Leu His Leu
1 5 10 15

Ile Leu Glu Arg Glu Tyr Pro Val Gly Ala Lys Leu Pro Asn Glu Tyr
20 25 30

Glu Leu Ala Glu Asp Leu Asp Val Gly Arg Ser Thr Ile Arg Glu Ala
35 40 45

Val Arg Ser Leu Ala Thr Arg Asn Ile Leu Glu Val Arg Gln Gly Ser
50 55 60

Gly Thr Tyr Ile Ser Ser Lys Lys Gly Val Ser Glu Asp Pro Leu Gly
65 70 75 80

Phe Ser Leu Ile Lys Asp Thr Asp Arg Leu Thr Ser Asp Leu Phe Glu
85 90 95

Leu Arg Leu Leu Leu Glu Pro Arg Ile Ala Glu Leu Val Ala Tyr Arg
100 105 110

Ile Thr Asp Asp Gln Leu Gln Leu Leu Glu Lys Leu Val Gly Asp Ile
115 120 125

Glu Asp Ala Val His Ala Gly Asp Pro Lys His Leu Leu Leu Asp Val
130 135 140

Glu Phe His Ser Met Leu Ala Lys Tyr Ser Gly Asn Ile Ala Met Asp
145 150 155 160

Ser Leu Leu Pro Val Ile Asn Gln Ser Ile His Leu Ile Asn Ala Asn
165 170 175

Tyr Thr Asn Arg Gln Met Lys Ser Asp Ser Leu Glu Ala His Arg Glu
180 185 190

Ile Ile Lys Ala Ile Arg Glu Lys Asn Pro Val Ala Ala His Asp Ala
195 200 205

Met Leu Met His Ile Met Ser Val Arg Arg Ser Ala Leu Lys Ala
210 215 220

<210> 259

<211> 188

<212> PRT

<213> Streptococcus agalactiae

<400> 259

Met Ile Lys Lys Asn Lys Val Phe Leu Gly Val Leu Leu Val Leu Val
1 5 10 15

Val Ile Leu Gly Gly Gly Val Leu Phe Tyr Gln Ser Gln Phe Gln Lys
20 25 30

Thr Thr Asn Gln Ala Leu Ala Ile Ala Tyr Lys Asp Ala Lys Val Ala
35 40 45

Lys Lys Asp Val Ile His Gln Lys Ile Asp Lys Glu Phe Glu Asn Phe
50 55 60

Arg Gly Ser Tyr Glu Ile Glu Phe Asn Thr Lys Ser Ala Glu Tyr Ser
65 70 75 80

Tyr His Val Asp Ala Lys Thr Gly Gln Ile Leu Glu Arg Asp Met Asp
85 90 95

Asn Asn Gly Phe Ser Lys Ser Thr Ser Gln Ser Ser Ser Ser Ser Ser
100 105 110

Gln Lys Ser His Lys Ile Ser Gln Glu Glu Ala Lys Lys Ile Ala Phe
115 120 125

Lys Asp Ala Asn Ile Glu Glu Ser Glu Val Ser Asn Leu Lys Ile Lys
130 135 140

Glu Glu Ile Glu Asn Gly Lys Ser Val Tyr Asp Ile Asp Phe Val Asp
145 150 155 160

Leu Lys Asn Lys Asn Glu Val Asp Tyr Gln Ile Asp Ala Glu Thr Gly
165 170 175

Lys Ile Ile Glu Arg Ser Arg Asp His Met Asn Asp
180 185

<210> 260

<211> 680

<212> PRT

<213> Streptococcus agalactiae

<400> 260

Leu Asn Arg Lys Lys Arg Tyr Arg Leu Thr Val Lys Lys Gln Asn Ala
1 5 10 15

Ser Ile Pro Arg Arg Leu Asn Leu Leu Phe Phe Ile Ile Val Leu Leu
20 25 30

Phe Thr Val Leu Ile Leu Arg Leu Glu Gln Met Gln Ile Gly Gln Gln
35 40 45

Ser Phe Tyr Met Lys Lys Leu Thr Ala Leu Thr Ser Tyr Thr Val Lys
50 55 60

Glu Ser Lys Ala Arg Gly Gln Ile Phe Asp Ala Lys Gly Val Val Leu
65 70 75 80

Val Glu Asn Asp Glu Arg Pro Thr Val Ala Phe Ser Arg Gly Asn Asn
85 90 95

Ile Ser Ser Gln Ser Ile Lys Glu Leu Ala Asn Lys Leu Ser His Tyr
100 105 110

Ile Thr Leu Thr Glu Val Ala Ser Ser Asp Arg Ala Lys Arg Asp Tyr
115 120 125

Tyr Leu Ala Asp Lys Ala Asn Tyr Lys Lys Val Val Glu Ser Leu Pro
130 135 140

Asp Ser Lys Arg Tyr Asp Lys Phe Gly Asn His Leu Ala Glu Ser Thr
145 150 155 160

Val Tyr Ala Asn Ala Val Ala Ala Val Pro Val Ser Ala Ile Asn Tyr
165 170 175

Ser Glu Asp Glu Leu Lys Val Val Ala Leu Phe Asn Gln Met Asn Ala
180 185 190

Thr Pro Thr Phe Gly Ser Val Lys Leu Ser Thr Gly Glu Leu Ser Asp
195 200 205

Asp Gln Ile Lys Lys Leu Asp Ala Asp Lys Lys Glu Leu Leu Gly Ile
210 215 220

Ser Val Thr Ser Asn Trp His Arg Arg Lys Lys Gly Thr Ser Leu Ser
225 230 235 240

Asp Ile Leu Gly Thr Ile Ser Thr Glu Lys Ala Gly Leu Pro Arg Glu
245 250 255

Glu Val Lys Lys Tyr Leu Lys Lys Gly Tyr Ser Leu Asn Asp Arg Val
260 265 270

Gly Thr Ser Tyr Leu Glu Lys Gln Tyr Glu Asp Asp Leu Gln Gly Ile
275 280 285

Arg Gln Ile Arg Lys Val Val Val Asn Lys Lys Gly Lys Val Val Ser
290 295 300

Asp Asn Ile Thr Gln Glu Gly Lys Ser Gly Arg Asn Leu Lys Leu Thr
305 310 315 320

Ile Asp Leu Asn Tyr Gln Asn Lys Val Glu Ser Ile Leu Lys Gln Tyr
325 330 335

Tyr Gly Ser Glu Leu Ser Ser Gly Arg Ala Ser Phe Ser Glu Gly Met
340 345 350

Tyr Ala Val Ala Ile Glu Pro Ser Thr Gly Lys Val Leu Ala Met Ala
355 360 365

Gly Leu Lys Asn Asp His Gly Asn Leu Val Asp Asp Ser Leu Gly Thr
370 375 380

Ile Ala Lys Asn Phe Thr Pro Gly Ser Val Val Lys Gly Ala Thr Leu
385 390 395 400

Ser Ser Gly Trp Glu Asn Lys Val Leu Arg Gly Asn Glu Val Leu Tyr
405 410 415

Asp Gln Glu Ile Ala Asn Ile Arg Ser Trp Phe Thr Arg Gly Leu Thr
420 425 430

Pro Ile Ser Ala Ala Gln Ala Leu Glu Tyr Ser Ser Asn Thr Tyr Met
435 440 445

Val Gln Val Ala Leu Arg Leu Met Gly Gln Asp Tyr Asn Thr Gly Asp
450 455 460

Ala Leu Thr Asp Arg Gly Tyr Gln Glu Ala Met Ala Lys Leu Arg Lys
465 470 475 480

Thr Tyr Gly Glu Tyr Gly Leu Gly Val Ser Thr Gly Leu Asp Leu Pro
485 490 495

Glu Ser Glu Gly Tyr Val Pro Gly Lys Tyr Ser Leu Gly Thr Thr Leu
500 505 510

Met Glu Ser Phe Gly Gln Tyr Asp Ala Tyr Thr Pro Met Gln Leu Gly
515 520 525

Gln Tyr Ile Ser Thr Ile Ala Asn Asn Gly Asn Arg Leu Ala Pro His
530 535 540

Val Val Ser Asp Ile Tyr Glu Gly Asn Asp Ser Asn Lys Phe Ala Gln
545 550 555 560

Leu Val Arg Ser Ile Thr Pro Lys Thr Leu Asn Lys Ile Ala Ile Ser
565 570 575

Asp Gln Glu Leu Ala Ile Ile Gln Glu Gly Phe Tyr Asn Val Val Asn
580 585 590

Ser Gly Ser Gly Tyr Ala Thr Gly Thr Ser Met Arg Gly Asn Val Thr
595 600 605

Thr Ile Ser Gly Lys Thr Gly Thr Ala Glu Thr Phe Ala Lys Asn Val
610 615 620

Asn Gly Gln Thr Val Ser Thr Tyr Asn Leu Asn Ala Ile Ala Tyr Asp
625 630 635 640

Thr Asn Arg Lys Ile Ala Val Ala Val Met Tyr Pro His Val Thr Thr
645 650 655

Asp Thr Thr Lys Ser His Gln Leu Val Ala Arg Asp Met Ile Asp Gln
660 665 670

Tyr Ile Ser Gln Phe Thr Gly Gln
675 680

<210> 261

<211> 475

<212> PRT

<213> Streptococcus agalactiae

<400> 261

Met Thr Val Phe Pro Lys His Phe Leu Trp Gly Gly Ala Val Ala Ala
1 5 10 15

Asn Gln Val Glu Gly Ala Phe Arg Thr Asp Gly Lys Gly Leu Ser Val
20 25 30

Gln Asp Val Leu Pro Asn Gly Gly Leu Gly Asp Phe Thr Ala Lys Pro
35 40 45

Thr Pro Asp Asn Leu Lys Leu Glu Ala Ile Asp Phe Tyr His Asn Tyr
50 55 60

Lys Asn Asp Ile Lys Leu Phe Ala Glu Met Gly Phe Lys Val Phe Arg
65 70 75 80

Thr Ser Ile Ala Trp Ser Arg Ile Phe Pro Asn Gly Asp Asp Ser Ala
85 90 95

Pro Asn Glu Ala Gly Leu Gln Phe Tyr Asp Asn Leu Phe Asp Glu Leu
100 105 110

Leu Lys Tyr Asn Ile Glu Pro Leu Val Thr Leu Ser His Tyr Glu Thr
115 120 125

Pro Leu His Leu Ala Lys Thr Tyr Asn Gly Trp Ala Asp Arg Arg Leu
130 135 140

Ile Ala Phe Phe Glu Lys Phe Ala Gln Thr Val Met Glu Arg Tyr Lys
145 150 155 160

Asp Lys Val Lys Tyr Trp Leu Thr Phe Asn Glu Val Asn Ser Ile Leu
165 170 175

His Met Pro Phe Thr Ser Gly Ala Ile Met Thr Asp Lys Ser Gln Leu
180 185 190

Ser Pro Gln Glu Leu Tyr Gln Ala Ile His His Glu Leu Val Ala Ser
195 200 205

Ala Arg Val Thr Lys Leu Gly Arg Ser Ile Asn Pro Asn Phe Lys Ile
210 215 220

Gly Cys Met Ile Leu Ala Met Pro Ala Tyr Pro Met Thr Ser Asp Pro
225 230 235 240

Arg Asp Val Leu Ala Ala Arg Gln Phe Glu Gln His Asn Leu Leu Phe
245 250 255

Ser Asp Ile His Val Arg Gly Lys Tyr Pro Thr Tyr Ile Gln Ser Tyr
260 265 270

Phe Lys Asn Asn Gly Ile Lys Ile Lys Phe Glu Glu Gly Asp Glu Glu
275 280 285

Val Leu Ala Gln Asn Thr Val Asp Phe Leu Ser Phe Ser Tyr Tyr Met
290 295 300

Ser Val Thr Gln Ala Tyr Asp Phe Glu Asn Tyr Gln Ser Gly Gln Gly
305 310 315 320

Asn Ile Leu Gly Gly Leu Thr Asn Pro His Leu Thr Thr Ser Glu Trp
325 330 335

Gly Trp Gln Ile Asp Pro Ile Gly Leu Arg Leu Val Leu Asn Gln Tyr
340 345 350

Tyr Glu Arg Tyr Gln Ile Pro Leu Phe Ile Val Glu Asn Gly Leu Gly
355 360 365

Ala Lys Asp Gln Leu Ile Glu Thr Leu Asp Gly Asp Tyr Thr Val Glu
370 375 380

Asp Asp Tyr Arg Ile Asp Tyr Met Asn Gln His Leu Val Gln Val Ala
385 390 395 400

Lys Ala Ile Glu Asp Gly Val Glu Ile Met Gly Tyr Thr Ser Trp Gly
405 410 415

Cys Ile Asp Cys Val Ser Met Ser Thr Ala Gln Leu Ser Lys Arg Tyr
420 425 430

Gly Leu Ile Tyr Val Asp Arg Asn Asp Asp Gly Thr Gly Ser Leu Gln
435 440 445

Arg Tyr Lys Lys Lys Ser Phe Gly Trp Tyr Gln Lys Val Ile Lys Thr
450 455 460

Asn Gly Gln Ser Leu Phe Glu His His Asn Arg
465 470 475

<210> 262

<211> 161

<212> PRT

<213> Streptococcus agalactiae

<400> 262

Met Ala Thr Phe Gln Ile Lys Glu Lys Met Phe Ser Leu Gly Gly Lys
1 5 10 15

Phe Thr Ile Thr Asp Gln Thr Gly Leu Pro Cys Tyr His Val Glu Gly
20 25 30

Ser Leu Phe Pro Leu Pro Lys Thr Phe Lys Val Phe Asp Glu Glu Gly
35 40 45

His Leu Ile Ser Gln Ile Glu Lys Lys Val Leu Ser Phe Leu Pro Lys
50 55 60

Phe Asn Val Thr Leu Ala Asn Gly Asn His Phe Thr Ile Lys Lys Asp
65 70 75 80

Phe Ser Phe Leu Lys Pro His Tyr Thr Ile Glu Asp Leu Asp Met Glu
85 90 95

Val Lys Gly Asn Phe Trp Asp Ile Asp Phe Gln Leu Leu Lys Asp Asn
100 105 110

Gln Val Ile Ala Asn Ile Ser Gln Gln Trp Phe Arg Met Thr Ser Thr
115 120 125

Tyr Gln Val Glu Val Tyr Asn Glu Thr Tyr Asn Asp Leu Thr Ile Ser
130 135 140

Leu Val Ile Ala Ile Asp Tyr Val Lys Glu Leu Glu Lys Asn Ala Ser
145 150 155 160

Asn

<210> 263

<211> 181

<212> PRT

<213> Streptococcus agalactiae

<400> 263

Met Lys Lys Ile Thr Thr Leu Ile Leu Ala Ser Ser Leu Leu Leu Val
1 5 10 15

Ala Thr Thr Ser Val Lys Ala Asp Asp Asn Phe Glu Met Pro Thr Arg
20 25 30

Tyr Val Lys Met Ser Glu Lys Ser Lys Ala Phe Tyr Gln Arg Leu Gln
35 40 45

Glu Lys Gln Arg Lys Ala His Thr Thr Val Lys Thr Phe Asn Asn Ser
50 55 60

Glu Ile Arg His Gln Leu Pro Leu Lys Gln Glu Lys Ala Arg Asn Asp
65 70 75 80

Ile Tyr Asn Leu Gly Ile Leu Ile Ser Gln Glu Ser Lys Gly Phe Ile
85 90 95

Gln Arg Ile Asp Asn Ala Tyr Ser Leu Glu Asn Val Ser Asp Ile Val
100 105 110

Asn Glu Ala Gln Ala Leu Tyr Lys Arg Asn Tyr Asp Leu Phe Glu Lys
115 120 125

Ile Lys Ser Thr Arg Asp Lys Val Gln Val Leu Leu Ala Ser His Gln
130 135 140

Asp Asn Thr Asp Leu Lys Asn Phe Tyr Ala Glu Leu Asp Asp Met Tyr
145 150 155 160

Glu His Val Tyr Leu Asn Glu Ser Arg Val Glu Ala Ile Asn Arg Asn
165 170 175

Ile Gln Lys Tyr Asn
180

<210> 264

<211> 306

<212> PRT

<213> Streptococcus agalactiae

<400> 264

Met Lys Leu Lys Lys Phe Phe Glu Asp Leu Leu Ala Lys Leu Glu Tyr
1               5                   10                  15

Arg Pro Ile Gln Val Phe Met Arg His Phe Gln Ser Ala Glu Met Asp
            20                  25                  30

Leu Ser Ala Ile Ala Val Ala Tyr Tyr Leu Leu Val Thr Ala Phe Pro
        35                  40                  45

Leu Leu Val Ile Ala Ala Asn Ile Phe Pro Tyr Phe His Ile Asn Val
    50                  55                  60

Ser Asp Leu Leu Ser Leu Met Gln Lys Asn Leu Pro Lys Asn Ile Tyr
65                  70                  75                  80

Glu Pro Ala Ser Arg Leu Ala Val Asp Ala Phe Ser Lys Pro Ser Thr
                85                  90                  95

Gly Ile Leu Gly Phe Ala Ser Leu Thr Ala Phe Trp Thr Met Ser Lys
            100                 105                 110

Ser Leu Thr Ser Leu Gln Lys Ala Ile Asn Lys Ala Tyr Gly Val Asp
        115                 120                 125

Gln His Arg Asp Phe Val Ile Ser Arg Leu Val Gly Val Gly Thr Gly
    130                 135                 140

Leu Ile Ile Leu Phe Leu Leu Thr Phe Val Leu Ile Phe Ser Thr Phe
145                 150                 155                 160

Ser Lys Pro Val Leu Gln Ile Ile Val Asn Met Tyr Asp Leu Gly Asp
                165                 170                 175

Thr Leu Thr Ala Trp Leu Leu Asn Leu Ala Gln Pro Val Thr Phe Leu
            180                 185                 190

Thr Ile Phe Leu Gly Ile Gly Ile Leu Tyr Phe Ile Leu Pro Asn Ala
        195                 200                 205

Arg Ile Arg Lys Val Arg Tyr Val Ile Pro Gly Thr Leu Phe Ser Thr
    210                 215                 220

Phe Val Ile Gly Phe Phe Ser Asn Leu Ile Ser Gln Tyr Val Leu Asn
225                 230                 235                 240

Arg Val Glu Lys Met Val Asp Ile Lys Thr Phe Gly Ser Val Val Ile
245 250 255

Phe Ile Leu Met Leu Trp Phe Ile Phe Leu Ala His Ile Met Ile Leu
260 265 270

Gly Ala Ile Leu Asn Ala Ser Val Gln Glu Ile Ala Thr Gly Lys Ile
275 280 285

Glu Ser Arg Arg Gly Asp Ile Met Ser Leu Ile Gln Lys Ser Lys Glu
290 295 300

Glu Lys
305

<210> 265

<211> 1077

<212> PRT

<213> Streptococcus agalactiae

<400> 265

Met Lys Leu Leu Tyr Thr Asp Ile Asn His Asp Met Thr Glu Ile Leu
1 5 10 15

Val Asn Gln Ala Ala His Ala Ala Glu Ala Gly Trp Arg Ile Phe Tyr
20 25 30

Ile Ala Pro Asn Ser Leu Ser Phe Glu Lys Glu Arg Ala Val Leu Glu
35 40 45

Asn Leu Pro Gln Glu Ala Ser Phe Ala Ile Thr Ile Thr Arg Phe Ala
50 55 60

Gln Leu Ala Arg Tyr Phe Thr Leu Asn Gln Pro Asn Gln Lys Glu Ser
65 70 75 80

Leu Asn Asp Ile Gly Leu Ala Met Ile Phe Tyr Arg Ala Leu Ala Ser
85 90 95

Phe Glu Asp Gly Gln Leu Lys Val Phe Gly Arg Leu Lys Gln Asp Ala
100 105 110

Ser Phe Ile Ser Gln Leu Val Asp Leu Tyr Lys Glu Leu Gln Thr Ala
115 120 125

Asn Leu Ser Ile Leu Asp Leu Lys Tyr Leu His Ser Pro Glu Lys Phe
130 135 140

Glu Asp Leu Leu Ala Ile Phe Leu Val Val Ser Asp Leu Leu Arg Glu
145 150 155 160

Gly Glu Tyr Asp Asn Gln Ser Lys Ile Ala Phe Phe Thr Glu Gln Val
165 170 175

Arg Ser Gly Gln Leu Asp Val Asp Leu Lys Asn Thr Ile Leu Ile Val
180 185 190

Asp Gly Phe Thr Arg Phe Ser Ala Glu Glu Glu Ala Leu Ile Lys Ser
195 200 205

Leu Ser Ser Arg Cys Gln Glu Ile Ile Ile Gly Ala Tyr Ala Ser Gln
210 215 220

Lys Ala Tyr Lys Ala Asn Phe Thr Asn Gly Asn Ile Tyr Ser Ala Gly
225 230 235 240

Val Asp Phe Leu Arg Tyr Leu Ala Thr Thr Phe Gln Thr Lys Pro Glu
245 250 255

Phe Ile Leu Ser Lys Trp Glu Ser Lys Ser Gly Phe Glu Met Ile Ser
260 265 270

Lys Asn Ile Glu Gly Lys His Asp Phe Thr Asn Ser Ser His Ile Leu
275 280 285

Asp Asp Thr Ala Lys Asp Cys Ile Thr Ile Trp Glu Cys Ile Asn Gln
290 295 300

Lys Asp Glu Val Glu His Val Ala Arg Ala Ile Arg Gln Lys Leu Tyr
305 310 315 320

Gln Gly Tyr Arg Tyr Lys Asp Ile Leu Val Leu Leu Gly Asp Val Asp
325 330 335

Ser Tyr Lys Leu Gln Leu Ser Lys Ile Phe Glu Gln Tyr Asp Ile Pro
340 345 350

Tyr Tyr Phe Gly Lys Ala Glu Thr Met Ala Ala His Pro Leu Val His
355 360 365

Phe Met Asp Ser Leu Ser Arg Ile Lys Arg Tyr Arg Phe Arg Ala Glu
370 375 380

Asp Val Leu Asn Leu Phe Lys Thr Gly Ile Tyr Gly Glu Ile Ser Gln
385 390 395 400

Asp Asp Leu Asp Tyr Phe Glu Ala Tyr Ile Ser Tyr Ala Asp Ile Lys
405 410 415

Gly Pro Lys Lys Phe Phe Thr Asp Phe Val Val Gly Ala Lys Lys Phe
420 425 430

Asp Leu Gly Arg Leu Asn Thr Ile Arg Gln Ser Leu Leu Ala Pro Leu
435 440 445

Glu Ser Phe Val Lys Thr Lys Lys Gln Asp Gly Ile Lys Thr Leu Asn
450 455 460

Gln Phe Met Phe Phe Leu Thr Gln Val Gly Leu Ser Asp Asn Leu Ser
465 470 475 480

Arg Leu Val Gly Gln Met Ser Glu Asn Glu Gln Glu Lys His Gln Glu
485 490 495

Val Trp Lys Thr Phe Thr Asp Ile Leu Glu Gln Phe Gln Thr Ile Phe
500 505 510

Gly Gln Glu Lys Leu Asn Leu Asp Glu Phe Leu Ser Leu Leu Asn Ser
515 520 525

Gly Met Met Gln Ala Glu Tyr Arg Met Val Pro Ala Thr Val Asp Val
530 535 540

Val Thr Val Lys Ser Tyr Asp Leu Val Glu Pro His Ser Asn Gln Phe
545 550 555 560

Val Tyr Ala Leu Gly Met Thr Gln Ser His Phe Pro Lys Ile Ala Gln
565 570 575

Asn Lys Ser Leu Ile Ser Asp Ile Glu Arg Gln Leu Ile Asn Asp Ala
580 585 590

Asn Asp Thr Asp Gly His Phe Asp Ile Met Thr Arg Glu Asn Leu Lys
595 600 605

Lys Asn His Phe Ala Ala Leu Ser Leu Phe Asn Ala Ala Lys Gln Ala
610 615 620

Leu Val Leu Thr Ile Pro Gln Leu Leu Asn Glu Ser Glu Asp Gln Met
625 630 635 640

Ser Pro Tyr Leu Ile Glu Leu Arg Asp Ile Gly Val Pro Phe Asn His
645 650 655

Lys Gly Arg Gln Ser Leu Lys Glu Glu Ala Asp Asn Ile Gly Asn Tyr
660 665 670

Lys Ala Leu Leu Ser Arg Val Val Asp Leu Tyr Arg Ser Ala Ile Asp
675 680 685

Lys Glu Met Thr Lys Glu Glu Gln Thr Phe Trp Ser Val Ala Val Arg
    690                 695                 700

Tyr Leu Arg Arg Gln Leu Thr Ser Lys Gly Ile Glu Ile Pro Ile Ile
705                 710                 715                 720

Thr Asp Ser Leu Asp Thr Val Thr Val Ser Ser Asp Val Met Thr Arg
                725                 730                 735

Arg Phe Pro Glu Asp Asp Pro Leu Lys Leu Ser Ser Ser Ala Leu Thr
            740                 745                 750

Thr Phe Tyr Asn Asn Gln Tyr Lys Tyr Phe Leu Gln Tyr Val Leu Gly
        755                 760                 765

Leu Glu Glu Gln Asp Ser Ile His Pro Asp Met Arg His His Gly Thr
    770                 775                 780

Tyr Leu His Arg Val Phe Glu Ile Leu Met Lys Asn Gln Gly Ile Glu
785                 790                 795                 800

Ser Phe Glu Glu Lys Leu Asn Ser Ala Ile Asn Lys Thr Asn Gln Glu
                805                 810                 815

Asp Val Phe Lys Ser Leu Tyr Ser Glu Asp Ala Glu Ser Arg Tyr Ser
            820                 825                 830

Leu Glu Ile Leu Glu Asp Ile Ala Arg Ala Thr Ala Thr Ile Leu Arg
        835                 840                 845

Gln Asp Ser Gln Met Thr Val Glu Ser Glu Glu Glu Arg Phe Glu Leu
    850                 855                 860

Met Ile Asp Asn Thr Ile Lys Ile Asn Gly Ile Ile Asp Arg Ile Asp
865                 870                 875                 880

Arg Leu Ser Asp Gly Ser Leu Gly Val Val Asp Tyr Lys Ser Ser Ala
                885                 890                 895

Gln Lys Phe Asp Ile Gln Lys Phe Tyr Asn Gly Leu Ser Pro Gln Leu
            900                 905                 910

Val Thr Tyr Ile Asp Ala Ile Ser Arg Asp Lys Glu Val Glu Gln Lys
        915                 920                 925

Pro Pro Ile Phe Gly Ala Met Tyr Leu His Met Gln Glu Pro Lys Gln
    930                 935                 940

Asp Leu Ser Lys Ile Lys Asn Leu Asp Asp Leu Val Thr Lys Asn His
945                 950                 955                 960

Gln Ala Leu Thr Tyr Lys Gly Leu Phe Ser Glu Ala Glu Lys Glu Phe
965 970 975

Leu Ala Asn Gly Lys Tyr His Leu Lys Asp Ser Leu Tyr Ser Glu Ala
980 985 990

Glu Ile Ala Ile Leu Gln Ala His Asn Gln Leu Leu Tyr Lys Lys Ala
995 1000 1005

Ser Glu Thr Ile Lys Ser Gly Lys Phe Leu Ile Asn Pro Tyr Thr
1010 1015 1020

Glu Asp Ala Lys Thr Val Asp Gly Asp Gln Phe Lys Ser Ile Thr
1025 1030 1035

Gly Phe Glu Ala Asp Arg His Met Ala Arg Ala Arg Ala Leu Tyr
1040 1045 1050

Lys Leu Pro Ala Lys Glu Lys Arg Gln Gly Phe Leu Thr Leu Met
1055 1060 1065

Gln Gln Glu Glu Glu Asn Asp Asp Leu
1070 1075

<210> 266

<211> 332

<212> PRT

<213> Streptococcus agalactiae

<400> 266

Met Ser Glu Thr Lys Val Met Ala Leu Arg Glu Ala Ile Asn Val Ala
1 5 10 15

Met Ser Glu Glu Met Arg Lys Asp Glu Lys Val Phe Leu Met Gly Glu
20 25 30

Asp Val Gly Val Tyr Gly Gly Asp Phe Gly Thr Ser Val Gly Met Leu
35 40 45

Glu Glu Phe Gly Ala Lys Arg Val Arg Asp Thr Pro Ile Ser Glu Ala
50 55 60

Ala Ile Ala Gly Ser Ala Ile Gly Ala Ala Gln Thr Gly Leu Arg Pro
65 70 75 80

Ile Val Asp Leu Thr Phe Met Asp Phe Val Thr Ile Ala Met Asp Ala
85 90 95

Ile Val Asn Gln Gly Ala Lys Thr Asn Tyr Met Phe Gly Gly Gly Leu
100 105 110

Ser Thr Pro Val Thr Phe Arg Val Ala Ser Gly Ser Gly Ile Gly Ser
115 120 125

Ala Ala Gln His Ser Gln Ser Leu Glu Ala Trp Leu Thr His Ile Pro
130 135 140

Gly Leu Lys Val Val Ala Pro Gly Thr Val Asn Glu Ser Lys Ala Leu
145 150 155 160

Leu Lys Ser Ser Ile Leu Asp Asn Asn Pro Val Ile Phe Leu Glu Pro
165 170 175

Lys Ala Leu Tyr Gly Lys Lys Glu Glu Val Asn Met Asp Pro Asp Phe
180 185 190

Tyr Ile Pro Leu Gly Lys Gly Asp Ile Lys Arg Glu Gly Thr Asp Leu
195 200 205

Thr Ile Val Ser Tyr Gly Arg Met Leu Glu Arg Val Met Gln Ala Ala
210 215 220

Glu Glu Val Ala Glu Glu Gly Ile Asn Val Glu Val Val Asp Pro Arg
225 230 235 240

Thr Leu Ile Pro Leu Asp Lys Glu Leu Ile Ile Asp Ser Val Lys Lys
245 250 255

Thr Gly Lys Leu Ile Leu Val Asn Asp Ala Tyr Lys Thr Gly Gly Phe
260 265 270

Thr Gly Glu Ile Ala Thr Met Val Ala Glu Ser Glu Ala Phe Asp Tyr
275 280 285

Leu Asp His Pro Ile Val Arg Leu Ala Ser Glu Asp Val Pro Val Pro
290 295 300

Tyr Ser Arg Val Leu Glu Gln Gly Ile Leu Pro Asp Val Ala Lys Ile
305 310 315 320

Lys Asp Ala Ile Tyr Lys Val Val Asn Lys Gly Lys
325 330

<210> 267

<211> 585

<212> PRT

<213> Streptococcus agalactiae

<400> 267

Met Ala Phe Asp Val Ile Met Pro Lys Leu Gly Val Asp Met Gln Glu
1               5                   10                  15

Gly Glu Ile Leu Glu Trp Lys Lys Asn Glu Gly Asp Thr Val Asn Glu
            20                  25                  30

Gly Asp Val Leu Leu Glu Ile Met Ser Asp Lys Thr Asn Met Glu Ile
        35                  40                  45

Glu Ala Glu Asp Thr Gly Val Leu Leu Lys Ile Val His Gln Ala Gly
    50                  55                  60

Asp Val Val Pro Val Thr Glu Val Ile Ala Tyr Ile Gly Glu Glu Gly
65                  70                  75                  80

Glu Glu Val Gly Thr Ser Ser Pro Ser Ala Asp Ala Thr Ile Thr Ala
                85                  90                  95

Glu Asp Gly Gln Ser Val Ser Gly Pro Ala Ala Pro Ser Gln Glu Thr
            100                 105                 110

Val Ala Ala Ala Thr Pro Lys Glu Glu Leu Ala Ala Asp Glu Tyr Asp
        115                 120                 125

Ile Val Val Val Gly Gly Gly Pro Ala Gly Tyr Tyr Ala Ala Ile Arg
    130                 135                 140

Gly Ala Gln Leu Gly Gly Lys Ile Ala Ile Val Glu Lys Thr Glu Phe
145                 150                 155                 160

Gly Gly Thr Cys Leu Asn Val Gly Cys Ile Pro Thr Lys Thr Tyr Leu
                165                 170                 175

Lys Asn Ala Glu Ile Leu Asp Gly Leu Lys Val Ala Ala Gly Arg Gly
            180                 185                 190

Ile Asn Leu Ala Ser Thr Asn Tyr Ala Ile Asp Met Asp Lys Thr Val
        195                 200                 205

Ala Phe Lys Asn Ser Val Val Lys Thr Leu Thr Gly Gly Val Arg Gly
    210                 215                 220

Leu Leu Lys Ala Asn Lys Val Glu Ile Phe Asn Gly Leu Gly Gln Val
225                 230                 235                 240

Asn Pro Asp Lys Ser Val Val Ile Gly Asp Lys Val Ile Lys Gly Arg
                245                 250                 255

Asn Val Val Leu Ala Thr Gly Ser Lys Val Ser Arg Ile Asn Ile Pro
260 265 270

Gly Ile Glu Ser Pro Leu Val Leu Thr Ser Asp Asp Ile Leu Asp Leu
275 280 285

Arg Glu Ile Pro Lys Ser Leu Ala Val Met Gly Gly Gly Val Val Gly
290 295 300

Ile Glu Leu Gly Leu Val Trp Ala Ser Tyr Gly Val Asp Val Thr Val
305 310 315 320

Ile Glu Met Ala Asp Arg Ile Ile Pro Ala Met Asp Lys Glu Val Ser
325 330 335

Leu Glu Leu Gln Lys Ile Leu Ala Lys Lys Gly Met Lys Ile Lys Thr
340 345 350

Ser Val Gly Val Ser Glu Ile Val Glu Ala Asn Asn Gln Leu Thr Leu
355 360 365

Lys Leu Asn Asn Gly Glu Glu Val Val Ala Asp Lys Ala Leu Leu Ser
370 375 380

Ile Gly Arg Val Pro Gln Met Asn Gly Leu Glu Asn Leu Glu Pro Glu
385 390 395 400

Leu Glu Met Glu Arg Gly Arg Ile Lys Val Asn Ala Tyr Gln Glu Thr
405 410 415

Ser Ile Pro Gly Ile Tyr Ala Pro Gly Asp Val Asn Gly Thr Arg Met
420 425 430

Leu Ala His Ala Ala Tyr Arg Met Gly Glu Val Ala Ala Glu Asn Ala
435 440 445

Leu Gly Gly Asn Lys Arg Lys Ala His Leu Asp Phe Thr Pro Ala Ala
450 455 460

Val Tyr Thr His Pro Glu Val Ala Met Val Gly Met Thr Glu Glu Gln
465 470 475 480

Ala Arg Glu Gln Tyr Gly Asp Ile Leu Val Gly Lys Asn Ser Phe Thr
485 490 495

Gly Asn Gly Arg Ala Ile Ala Ser Asn Glu Ala His Gly Phe Val Lys
500 505 510

Val Ile Ala Glu Pro Lys Tyr Lys Glu Ile Leu Gly Val His Ile Ile
515 520 525

Gly Pro Ala Ala Ala Glu Leu Ile Asn Glu Ala Ser Thr Ile Met Glu
530 535 540

Asn Glu Leu Thr Val Tyr Asp Val Ala Gln Ser Ile His Gly His Pro
545 550 555 560

Thr Phe Ser Glu Val Met Tyr Glu Ala Phe Leu Asp Val Leu Gly Glu
565 570 575

Ala Ile His Asn Pro Pro Lys Arg Lys
580 585

<210> 268

<211> 450

<212> PRT

<213> Streptococcus agalactiae

<400> 268

Met Gly Lys Tyr Phe Gly Thr Asp Gly Val Arg Gly Glu Ala Asn Val
1 5 10 15

Glu Leu Thr Pro Glu Leu Ala Phe Lys Leu Gly Arg Phe Gly Gly Tyr
20 25 30

Val Leu Ser Gln His Glu Thr Asp Arg Pro Arg Val Phe Val Ala Arg
35 40 45

Asp Thr Arg Ile Ser Gly Glu Met Leu Glu Ser Ala Leu Ile Ala Gly
50 55 60

Leu Leu Ser Val Gly Ile Glu Val Tyr Lys Leu Gly Val Leu Ala Thr
65 70 75 80

Pro Gly Val Ser Tyr Leu Val Arg Thr Glu Lys Ala Ser Ala Gly Val
85 90 95

Met Ile Ser Ala Ser His Asn Pro Ala Leu Asp Asn Gly Ile Lys Phe
100 105 110

Phe Gly Ser Asp Gly Phe Lys Leu Asp Asp Asp Arg Glu Leu Glu Ile
115 120 125

Glu Ala Leu Leu Asp Ala Lys Glu Asp Thr Leu Pro Arg Pro Ser Ala
130 135 140

Gln Gly Leu Gly Thr Leu Val Asp Tyr Pro Glu Gly Leu Arg Lys Tyr
145 150 155 160

Glu Lys Phe Met Glu Ser Thr Gly Ile Asp Leu Glu Gly Met Lys Val
165 170 175

Ala Leu Asp Thr Ala Asn Gly Ala Ala Thr Ala Ser Ala Arg Asn Ile
180 185 190

Phe Leu Asp Leu Asn Ala Asp Ile Ser Val Ile Gly Asp Gln Pro Asp
195 200 205

Gly Leu Asn Ile Asn Asp Gly Val Gly Ser Thr His Pro Glu Gln Leu
210 215 220

Gln Ser Leu Val Arg Glu Asn Gly Ser Asp Ile Gly Leu Ala Phe Asp
225 230 235 240

Gly Asp Ser Asp Arg Leu Ile Ala Val Asp Glu Asn Gly Glu Ile Val
245 250 255

Asp Gly Asp Lys Ile Met Phe Ile Ile Gly Lys Tyr Leu Ser Asp Lys
260 265 270

Gly Gln Leu Ala Gln Asn Thr Ile Val Thr Thr Val Met Ser Asn Leu
275 280 285

Gly Phe His Lys Ala Leu Asp Arg Glu Gly Ile His Lys Ala Ile Thr
290 295 300

Ala Val Gly Asp Arg Tyr Val Val Glu Glu Met Arg Lys Ser Gly Tyr
305 310 315 320

Asn Leu Gly Gly Glu Gln Ser Gly His Val Ile Ile Met Asp Tyr Asn
325 330 335

Thr Thr Gly Asp Gly Gln Leu Thr Ala Ile Gln Leu Thr Lys Val Met
340 345 350

Lys Glu Thr Gly Lys Lys Leu Ser Glu Leu Ala Ser Glu Val Thr Ile
355 360 365

Tyr Pro Gln Lys Leu Val Asn Ile Arg Val Glu Asn Asn Met Lys Asp
370 375 380

Lys Ala Met Glu Val Pro Ala Ile Ala Glu Ile Ile Ala Lys Met Glu
385 390 395 400

Glu Glu Met Asp Gly Asn Gly Arg Ile Leu Val Arg Pro Ser Gly Thr
405 410 415

Glu Pro Leu Leu Arg Val Met Ala Glu Ala Pro Thr Asn Glu Ala Val
420 425 430

Asp Tyr Tyr Val Asp Thr Ile Ala Asp Val Val Arg Thr Glu Ile Gly
435 440 445

Leu Asp
450

<210> 269

<211> 877

<212> PRT

<213> Streptococcus agalactiae

<400> 269

Met Lys Gly Gln Lys Ile Ile Ala Leu Ala Gly Leu Val Leu Ser Cys
1 5 10 15

His Phe Ala Leu Thr Ala Cys His Thr Gln Glu His Lys Asn Ser His
20 25 30

His Ile Lys Thr Lys Gln Val Ala Lys Lys Lys Ala Asn Lys Lys Lys
35 40 45

Val Ser Val Lys Glu Ser His Lys Lys Arg Lys Gly Val Ala Gly Val
50 55 60

Asp Phe Pro Thr Asp Asp Gly Phe Leu Leu Thr Lys Asp Ser Lys Ile
65 70 75 80

Leu Ser His Pro Asp Ser Gly Ile Val Val Ala His Gly Asn His Ser
85 90 95

His Phe Ile Phe Tyr Ser Asp Leu Lys Gly Ser Lys Phe Ser Tyr Leu
100 105 110

Ile Pro Asn Ala Asn Ala Lys Thr Asn Lys Lys Gln Ala Val Arg Asn
115 120 125

Phe Lys Ala Gly Ala Val Ala Val Asn Thr Leu Asn Asp Gly Tyr Val
130 135 140

Phe Asn Pro Ala Asp Ile Val Ser Glu Asp Ala Asn Gly Tyr Val Val
145 150 155 160

Arg His Gly Asp His Phe His Tyr Ile Pro Lys Ala Ser Leu Ser Gln
165 170 175

Gln Lys Gln Val Gln Ala Ser Arg Ala Val Ser Arg Leu Gly Asn Gln
180 185 190

Asn Asn Ser His Tyr Arg Val Asn Ser Ser Lys Ile Ala Gly Leu His
195 200 205

His Pro Thr Ser Asp Gly Phe Leu Phe Asn Gly Gln Gly Ile Lys Gly
210 215 220

Thr Thr Pro Thr Gly Ile Leu Val Glu His His Asn His Leu His Phe
225 230 235 240

Ile Ser Phe Ala Asp Leu Arg Lys Gly Gly Trp Gly Ser Ile Ala Asp
245 250 255

Arg Tyr Gln Pro Gln Lys Lys Val Asp Ser Lys Lys Gln Ser Pro Ser
260 265 270

Ser Lys Lys Pro Arg Thr Glu Asn Thr Leu Pro Lys Asp Ile Lys Asp
275 280 285

Lys Leu Ala Tyr Leu Ala Arg Glu Leu His Leu Asp Ile Ser Arg Ile
290 295 300

Arg Val Leu Lys Thr Leu Asn Gly Glu Ile Gly Phe Glu Tyr Pro His
305 310 315 320

Asp Asp His Thr His Val Ile Met Ala Lys Asp Ile Asp Leu Ser Lys
325 330 335

Pro Ile Pro Asn Pro His His Asp Asp Glu Asp His His Lys Gly His
340 345 350

His His Asp Glu Ser Asp His Lys His Glu Glu His Glu His Thr Lys
355 360 365

Ser Asn Lys Leu Ser Asp Glu Asp Gln Lys Lys Leu Ile Tyr Leu Ala
370 375 380

Glu Lys Leu Gly Leu Asn Pro Asn Gln Ile Glu Val Leu Thr Ser Glu
385 390 395 400

Asp Gly Ser Ile Ile Phe Lys Tyr Pro His Asp Asp His Ser His Thr
405 410 415

Ile Ala Ser Lys Asp Ile Glu Ile Gly Lys Pro Ile Pro Asp Gly His
420 425 430

His Asp His Ser His Ala Lys Asp Lys Val Gly Met Ala Thr Leu Lys
435 440 445

Gln Ile Gly Phe Asp Asp Glu Ile Ile Gln Asp Ile Leu His Ala Asp
450 455 460

Ala Pro Thr Pro Phe Pro Ser Asn Glu Thr Asn Pro Glu Lys Met Arg
465 470 475 480

Gln Trp Leu Ala Thr Val Thr Lys Ile Asn Ile Gly Gln Arg Thr Asn
485 490 495

Pro Phe Gln Arg Phe Gly Leu Ser Leu Met Pro Asn Ile Glu Val Leu
500 505 510

Gly Ile Gly Phe Thr Pro Ile Asn Asp Met Thr Pro Val Leu Gln Phe
515 520 525

Lys Lys Leu Lys Gln Leu Trp Met Thr Asn Thr Gly Ile Thr Asp Tyr
530 535 540

Ser Phe Leu Asp Lys Met Pro Leu Leu Glu Gly Leu Asp Ile Ser Gln
545 550 555 560

Asn Gly Ile Lys Asp Leu Ser Phe Leu Thr Lys Tyr Lys Gln Leu Ser
565 570 575

Leu Ile Ala Ala Ala Asn Asn Gly Ile Thr Ser Leu Lys Pro Leu Ala
580 585 590

Glu Leu Pro Asn Leu Gln Phe Leu Val Leu Ser His Asn Asn Ile Ser
595 600 605

Asp Leu Thr Pro Leu Ser Asn Leu Thr Lys Leu Gln Glu Leu His Leu
610 615 620

Asp His Asn Asn Val Lys Asn Leu Ser Ala Leu Ser Gly Lys Lys Asp
625 630 635 640

Leu Lys Val Leu Asp Leu Ser Asn Asn Lys Ser Ala Asp Leu Ser Thr
645 650 655

Leu Lys Thr Thr Ser Leu Glu Thr Leu Leu Leu Asn Glu Thr Asn Thr
660 665 670

Ser Asn Leu Ser Phe Leu Lys Gln Asn Pro Lys Val Ser Asn Leu Thr
675 680 685

Ile Asn Asn Ala Lys Leu Ala Ser Leu Asp Gly Ile Glu Glu Ser Asp
690 695 700

Glu Ile Val Lys Val Glu Ala Glu Gly Asn Gln Ile Lys Ser Leu Val
705 710 715 720

Leu Lys Asn Lys Gln Gly Ser Leu Lys Phe Leu Asn Val Thr Asn Asn
725 730 735

Gln Leu Thr Ser Leu Glu Gly Val Asn Asn Tyr Thr Ser Leu Glu Thr
740 745 750

Leu Ser Val Ser Lys Asn Lys Leu Glu Ser Leu Asp Ile Lys Thr Pro
755 760 765

Asn Lys Thr Val Thr Asn Leu Asp Phe Ser His Asn Asn Val Pro Thr
770 775 780

Ser Gln Leu Lys Leu Asn Glu Lys Asn Ile Pro Glu Ala Val Ala Lys
785 790 795 800

Asn Phe Pro Ala Val Val Glu Gly Ser Met Val Gly Asn Gly Ser Leu
805 810 815

Ala Glu Lys Ala Ala Met Ala Ser Lys Glu Asp Lys Gln Val Ser Asp
820 825 830

Asn Thr Asn His Gln Lys Asn Thr Glu Lys Ser Ala Gln Ala Asn Ala
835 840 845

Asp Ser Lys Lys Glu Asn Pro Lys Thr His Asp Glu His His Asp His
850 855 860

Glu Glu Thr Asp His Ala His Val Gly His His His His
865 870 875

<210> 270

<211> 500

<212> PRT

<213> Streptococcus agalactiae

<400> 270

Met Asn Lys Arg Val Lys Ile Val Ala Thr Leu Gly Pro Ala Val Glu
1 5 10 15

Phe Arg Gly Gly Lys Lys Phe Gly Glu Ser Gly Tyr Trp Gly Glu Ser
20 25 30

Leu Asp Val Glu Ala Ser Ala Glu Lys Ile Ala Gln Leu Ile Lys Glu
35 40 45

Gly Ala Asn Val Phe Arg Phe Asn Phe Ser His Gly Asp His Ala Glu
50 55 60

Gln Gly Ala Arg Met Ala Thr Val Arg Lys Ala Glu Glu Ile Ala Gly
65 70 75 80

Gln Lys Val Gly Phe Leu Leu Asp Thr Lys Gly Pro Glu Ile Arg Thr
85 90 95

Glu Leu Phe Glu Asp Gly Ser Asp Phe His Ser Tyr Thr Thr Gly Thr
100 105 110

Lys Leu Arg Val Ala Thr Lys Gln Gly Ile Lys Ser Thr Pro Glu Val
115 120 125

Ile Ala Leu Asn Val Ala Gly Gly Leu Asp Ile Phe Asp Asp Val Glu
130 135 140

Val Gly Lys Gln Ile Leu Val Asp Asp Gly Lys Leu Gly Leu Thr Val
145 150 155 160

Phe Ala Lys Asp Lys Asp Thr Arg Glu Phe Glu Val Val Val Glu Asn
165 170 175

Asp Gly Leu Ile Gly Lys Gln Lys Gly Val Asn Ile Pro Tyr Thr Lys
180 185 190

Ile Pro Phe Pro Ala Leu Ala Glu Arg Asp Asn Ala Asp Ile Arg Phe
195 200 205

Gly Leu Glu Gln Gly Leu Asn Phe Ile Ala Ile Ser Phe Val Arg Thr
210 215 220

Ala Lys Asp Val Asn Glu Val Arg Ala Ile Cys Glu Glu Thr Gly Asn
225 230 235 240

Gly His Val Lys Leu Phe Ala Lys Ile Glu Asn Gln Gln Gly Ile Asp
245 250 255

Asn Ile Asp Glu Ile Ile Glu Ala Ala Asp Gly Ile Met Ile Ala Arg
260 265 270

Gly Asp Met Gly Ile Glu Val Pro Phe Glu Met Val Pro Val Tyr Gln
275 280 285

Lys Met Ile Ile Thr Lys Val Asn Ala Ala Gly Lys Ala Val Ile Thr
290 295 300

Ala Thr Asn Met Leu Glu Thr Met Thr Asp Lys Pro Arg Ala Thr Arg
305 310 315 320

Ser Glu Val Ser Asp Val Phe Asn Ala Val Ile Asp Gly Thr Asp Ala
325 330 335

Thr Met Leu Ser Gly Glu Ser Ala Asn Gly Lys Tyr Pro Val Glu Ser
340 345 350

Val Arg Thr Met Ala Thr Ile Asp Lys Asn Ala Gln Thr Leu Leu Asn
355 360 365

Glu Tyr Gly Arg Leu Asp Ser Ser Ala Phe Pro Arg Asn Asn Lys Thr
370 375 380

Asp Val Ile Ala Ser Ala Val Lys Asp Ala Thr His Ser Met Asp Ile
385 390 395 400

Lys Leu Val Val Thr Ile Thr Glu Thr Gly Asn Thr Ala Arg Ala Ile
405 410 415

Ser Lys Phe Arg Pro Asp Ala Asp Ile Leu Ala Val Thr Phe Asp Glu
420 425 430

Lys Val Gln Arg Ser Leu Met Ile Asn Trp Gly Val Ile Pro Val Leu
435 440 445

Ala Asp Lys Pro Ala Ser Thr Asp Asp Met Phe Glu Val Ala Glu Arg
450 455 460

Val Ala Leu Glu Ala Gly Leu Val Glu Ser Gly Asp Asn Ile Val Ile
465 470 475 480

Val Ala Gly Val Pro Val Gly Thr Gly Gly Thr Asn Thr Met Arg Val
485 490 495

Arg Thr Val Lys
500

<210> 271

<211> 329

<212> PRT

<213> Streptococcus agalactiae

<400> 271

Met Thr Ala Thr Lys Gln His Lys Lys Val Ile Leu Val Gly Asp Gly
1 5 10 15

Ala Val Gly Ser Ser Tyr Ala Phe Ala Leu Val Asn Gln Gly Ile Ala
20 25 30

Gln Glu Leu Gly Ile Ile Glu Ile Pro Ala Leu Phe Asp Lys Ala Val
35 40 45

Gly Asp Ala Glu Asp Leu Ser His Ala Leu Ala Phe Thr Ser Pro Lys
50 55 60

Lys Ile Tyr Ala Ala Thr Tyr Ala Asp Cys Ala Asp Ala Asp Leu Val
65 70 75 80

Val Ile Thr Ala Gly Ala Pro Gln Lys Pro Gly Glu Thr Arg Leu Asp
85 90 95

Leu Val Gly Lys Asn Leu Ala Ile Asn Lys Ser Ile Val Thr Gln Val
100 105 110

Val Glu Ser Gly Phe Asn Gly Ile Phe Leu Val Ala Ala Asn Pro Val
115 120 125

Asp Val Leu Thr Tyr Ser Thr Trp Lys Phe Ser Gly Phe Pro Lys Glu
130 135 140

Arg Val Ile Gly Ser Gly Thr Ser Leu Asp Ser Ala Arg Phe Arg Gln
145 150 155 160

Ala Leu Ala Asp Lys Ile Gly Val Asp Ala Arg Ser Val His Ala Tyr
165 170 175

Ile Met Gly Glu His Gly Asp Ser Glu Phe Ala Val Trp Ser His Ala
180 185 190

Asn Val Ala Gly Val Gln Leu Glu Gln Trp Leu Gln Glu Asn Arg Asp
195 200 205

Ile Asp Glu Gln Gly Leu Val Asp Leu Phe Ile Ser Val Arg Asp Ala
210 215 220

Ala Tyr Ser Ile Ile Asn Lys Lys Gly Ala Thr Tyr Tyr Gly Ile Ala
225 230 235 240

Val Ala Leu Ala Arg Ile Thr Lys Ala Ile Leu Asp Asp Glu Asn Ala
245 250 255

Val Leu Pro Leu Ser Val Tyr Gln Glu Gly Gln Tyr Gly Asp Val Lys
260 265 270

Asp Val Phe Ile Gly Gln Pro Ala Ile Val Gly Ala His Gly Ile Val
275 280 285

Arg Pro Val Asn Ile Pro Leu Asn Asp Ala Glu Leu Gln Lys Met Gln
290 295 300

Ala Ser Ala Glu Gln Leu Lys Asp Ile Ile Asp Glu Ala Trp Lys Asn
305 310 315 320

Pro Glu Phe Gln Glu Ala Ser Lys Asn
325

<210> 272

<211> 819

<212> PRT

<213> Streptococcus agalactiae

<400> 272

Met Gln Asp Lys Asn Leu Val Asp Val Asn Leu Thr Ser Glu Met Lys
1               5                   10                  15

Thr Ser Phe Ile Asp Tyr Ala Met Ser Val Ile Val Ala Arg Ala Leu
            20                  25                  30

Pro Asp Val Arg Asp Gly Leu Lys Pro Val His Arg Arg Ile Leu Tyr
        35                  40                  45

Gly Met Asn Glu Leu Gly Val Thr Pro Asp Lys Pro His Lys Lys Ser
    50                  55                  60

Ala Arg Ile Thr Gly Asp Val Met Gly Lys Tyr His Pro His Gly Asp
65                  70                  75                  80

Ser Ser Ile Tyr Glu Ala Met Val Arg Met Ala Gln Trp Trp Ser Tyr
                85                  90                  95

Arg His Met Leu Val Asp Gly His Gly Asn Phe Gly Ser Met Asp Gly
            100                 105                 110

Asp Gly Ala Ala Ala Gln Arg Tyr Thr Glu Ala Arg Met Ser Lys Ile
        115                 120                 125

Ala Leu Glu Met Leu Arg Asp Ile Asn Lys Asn Thr Val Asp Phe Gln
    130                 135                 140

Asp Asn Tyr Asp Gly Ser Glu Arg Glu Pro Leu Val Leu Pro Ala Arg
145                 150                 155                 160

Phe Pro Asn Leu Leu Val Asn Gly Ala Thr Gly Ile Ala Val Gly Met
                165                 170                 175

Ala Thr Asn Ile Pro Pro His Asn Leu Gly Glu Ser Ile Asp Ala Val
            180                 185                 190

Lys Leu Val Met Asp Asn Pro Asp Val Thr Thr Arg Glu Leu Met Glu
        195                 200                 205

Val Ile Pro Gly Pro Asp Phe Pro Thr Gly Ala Leu Val Met Gly Arg
    210                 215                 220

Ser Gly Ile His Arg Ala Tyr Glu Thr Gly Lys Gly Ser Ile Val Leu
225                 230                 235                 240

Arg Ser Arg Thr Glu Ile Glu Thr Thr Ser Asn Gly Lys Glu Arg Ile
                245                 250                 255

Val Val Thr Glu Phe Pro Tyr Gly Val Asn Lys Thr Lys Val His Glu
            260                 265                 270

His Ile Val Arg Leu Ala Gln Glu Lys Arg Ile Glu Gly Ile Thr Ala
        275                 280                 285

Val Arg Asp Glu Ser Ser Arg Glu Gly Val Arg Phe Val Ile Glu Val
    290                 295                 300

Arg Arg Asp Ala Ser Ala Asn Val Ile Leu Asn Asn Leu Phe Lys Leu
305                 310                 315                 320

Thr Ser Leu Gln Thr Asn Phe Ser Phe Asn Met Leu Ala Ile Glu Lys
                325                 330                 335

Gly Val Pro Lys Ile Leu Ser Leu Arg Gln Ile Ile Asp Asn Tyr Ile
            340                 345                 350

Glu His Gln Lys Glu Val Ile Val Arg Arg Thr Gln Phe Asp Lys Ala
        355                 360                 365

Lys Ala Glu Ala Arg Ala His Ile Leu Glu Gly Leu Leu Val Ala Leu
    370                 375                 380

Asp His Leu Asp Glu Val Ile Thr Ile Ile Arg Asn Ser Glu Thr Asp
385                 390                 395                 400

Thr Ile Ala Gln Ala Glu Leu Met Ser Arg Phe Glu Leu Ser Glu Arg
                405                 410                 415

Gln Ser Gln Ala Ile Leu Asp Met Arg Leu Arg Arg Leu Thr Gly Leu
            420                 425                 430

Glu Arg Asp Lys Ile Gln Ser Glu Tyr Asn Asp Leu Leu Ala Leu Ile
        435                 440                 445

Ala Asp Leu Ala Asp Ile Leu Ala Lys Pro Glu Arg Val Val Thr Ile
    450                 455                 460

Ile Lys Glu Glu Met Asp Glu Val Lys Arg Lys Tyr Ala Asp Ala Arg
465                 470                 475                 480

Arg Thr Glu Leu Met Ile Gly Glu Val Leu Ser Leu Glu Asp Glu Asp
                485                 490                 495

Leu Ile Glu Glu Glu Asp Val Leu Ile Thr Leu Ser Asn Lys Gly Tyr
500 505 510

Ile Lys Arg Leu Ala Gln Asp Glu Phe Arg Ala Gln Lys Arg Gly Gly
515 520 525

Arg Gly Ile Gln Gly Thr Gly Val Asn Asn Asp Asp Phe Val Arg Glu
530 535 540

Leu Val Ser Thr Ser Thr His Asp Thr Val Leu Phe Phe Thr Asn Leu
545 550 555 560

Gly Arg Val Tyr Arg Leu Lys Ala Tyr Glu Ile Pro Glu Tyr Gly Arg
565 570 575

Thr Ala Lys Gly Leu Pro Ile Val Asn Leu Leu Lys Leu Asp Glu Gly
580 585 590

Glu Thr Ile Gln Thr Ile Ile Asn Ala Arg Lys Glu Asp Val Ala Asn
595 600 605

Lys Tyr Phe Phe Phe Thr Thr Gln Gln Gly Ile Val Lys Arg Thr Ser
610 615 620

Val Ser Glu Phe Ser Asn Ile Arg Gln Asn Gly Leu Arg Ala Ile Asn
625 630 635 640

Leu Lys Glu Asn Asp Glu Leu Ile Asn Val Leu Leu Ile Asp Glu Asn
645 650 655

Glu Asp Val Ile Ile Gly Thr Arg Thr Gly Tyr Ser Val Arg Phe Lys
660 665 670

Val Asn Ala Val Arg Asn Met Gly Arg Thr Ala Thr Gly Val Arg Gly
675 680 685

Val Asn Leu Arg Glu Gly Asp Lys Val Val Gly Ala Ser Arg Ile Val
690 695 700

Asn Gly Gln Glu Val Leu Ile Ile Thr Glu Lys Gly Tyr Gly Lys Arg
705 710 715 720

Thr Glu Ala Ser Glu Tyr Pro Thr Lys Gly Arg Gly Gly Lys Gly Ile
725 730 735

Lys Thr Ala Asn Ile Thr Ala Lys Asn Gly Pro Leu Ala Arg Leu Val
740 745 750

Thr Ile Asn Gly Asn Glu Asp Ile Met Val Ile Thr Asp Thr Gly Val
755 760 765

Ile Ile Arg Thr Asn Val Ala Asn Ile Ser Gln Thr Gly Arg Ser Thr
770 775 780

Met Gly Val Lys Val Met Arg Leu Asp Gln Glu Ala Lys Ile Val Thr
785 790 795 800

Val Ala Leu Val Glu Gln Glu Ile Glu Asp Lys Ser Asn Ile Glu Asp
805 810 815

Thr Lys Glu

<210> 273

<211> 442

<212> PRT

<213> Streptococcus agalactiae

<400> 273

Met Thr Ile Phe Asp Glu Arg Glu Leu Lys Glu Arg Phe Thr His Glu
1 5 10 15

Asn Arg Val Ser Phe Tyr Glu Phe Val Ala Lys Tyr Asp Ala Gln Met
20 25 30

Val Pro Val Met Lys Ala Lys Gly Tyr Arg Cys Ile His Ser Met Glu
35 40 45

Arg Thr Val Val Phe Thr Phe Gly Glu Phe Thr Ile Arg Arg Arg Arg
50 55 60

Trp Gln Lys Gly Glu His Trp Val Val Pro Val Asp Glu Lys Leu Gly
65 70 75 80

Leu Lys Lys Asn Val Arg Tyr Ser Leu Glu Phe Met Tyr Gln Ile Ala
85 90 95

Ser Leu Ala Thr Met Met Pro Tyr Glu Lys Val Ile Lys Val Val Gln
100 105 110

Met Met Tyr Cys Ile Val Ile Thr Lys Pro Thr Val Val Lys Ala Val
115 120 125

Lys Ile Ser Arg Glu Leu Leu Lys Glu Lys Glu Ala Tyr Arg Phe Phe
130 135 140

Asp Glu Asp Ile Pro Val Asp Lys Glu Pro Val Asp Met Ile Tyr Leu
145 150 155 160

Glu Gly Asp Gly Val Met Val Lys Ala Arg Glu Glu Gly Leu Asp Asn
165 170 175

Arg Asn Val Asp Leu Ser His Phe Val Val His Thr Gly Ser Gln Lys
180 185 190

Val Gly Ser Asn Arg Phe Val Leu Gln Asn Lys Lys Glu Phe Val Ser
195 200 205

Leu Asp Asn Arg Gln Thr Arg Gln Lys Ile Leu Asp Tyr Leu Tyr Asn
210 215 220

His Phe Tyr Ile Ala Pro Asn Thr Leu Leu Ile Thr Asn Ser Asp Gly
225 230 235 240

Gly His Gly Tyr Thr Pro Tyr Val Phe Lys Glu Ile Ala Lys Ala Leu
245 250 255

Lys Val Lys Gln His Glu His Phe Trp Asp Arg Tyr His Val Asn Glu
260 265 270

Lys Ile Lys Ser Phe Phe Lys Leu Tyr Pro Val Glu Leu Met Thr Gly
275 280 285

Ala Phe Gln Ser Ile Lys Gln His Asp Lys Glu Lys Leu Arg Thr Val
290 295 300

Leu Asp Thr Thr Glu Ala Leu Ile Leu Met Glu Glu Glu Met Glu Gly
305 310 315 320

Phe Asn Gln Phe Lys Arg Lys Leu Leu Asn Asn Phe Gln Tyr Thr Lys
325 330 335

Ser Ala Glu Leu Arg Gly Phe Ser Arg Ala Gly Ile Gly Val Met Glu
340 345 350

Ser Gln His Arg Lys Ile Thr Tyr Arg Met Lys Lys Arg Gly Met Tyr
355 360 365

Trp Thr Ile Gln Gly Ala Glu Thr Met Ser Gln Leu Ile Val Leu Ser
370 375 380

Tyr Glu Gly Gln Leu Arg Asp Leu Phe Phe Gly Ser Trp Arg Glu Asp
385 390 395 400

Tyr Gln Lys Tyr Gln Glu Leu Glu Asn Leu Ser Ala Gly Lys Ile Lys
405 410 415

His Glu Gln Asn Lys Ile Asn Lys Arg Tyr Asp Leu Gln Thr Leu Gly
420 425 430

Arg Leu Arg Tyr Gly Arg His Arg Asn Leu
        435                 440

<210>  274

<211>  127

<212>  PRT

<213>  Streptococcus agalactiae

<400>  274

Met Ala Tyr Leu Ser Lys Leu Ser Asp Leu Asp Pro Ser Leu Met Asp
1               5                   10                  15

Ala Asp Ser Glu Gln Ile Tyr Ile Pro Lys Val Leu Phe Glu His Asn
            20                  25                  30

Asp Phe Lys Gly Leu Thr Tyr Lys Glu Ile Leu Leu Tyr Ser Phe Leu
        35                  40                  45

Leu Asn Arg Leu Arg Glu Pro Leu Asp Phe Ile Gln Lys Gly Tyr Asp
    50                  55                  60

Asp Asn Glu Asp Thr Tyr Val His Phe Lys Val Glu Asp Leu Cys Glu
65                  70                  75                  80

Leu Leu Asn Gln Ser Lys Thr Thr Val Ile Ser Leu Lys Lys Arg Leu
                85                  90                  95

Ala Gln Tyr Gly Leu Ile Glu Glu Val Lys Ala Gly Ser His Gln Pro
            100                 105                 110

Asn Arg Ile Tyr Leu Thr Asp Lys Leu Val Pro Tyr Ile Lys Gly
        115                 120                 125

<210>  275

<211>  92

<212>  PRT

<213>  Streptococcus agalactiae

<400>  275

Met Thr Asp Asn Arg Phe Ala Gln Leu Lys Glu Asn Phe Glu Lys Gly
1               5                   10                  15

Ser Pro Lys Arg Arg Val Pro Thr Ser Arg Pro Ile Ala Ala Gln Lys
            20                  25                  30

Ala Pro Glu Ser Tyr Asn Lys Lys Gly Arg Tyr Pro Phe Ser Leu His
        35                  40                  45

Gln Asp Val Arg Tyr Asp Lys Leu Glu Ala Leu Val Ala Tyr His Gly
    50                  55                  60

Ala Lys Ser Ala Ser Asp Tyr Leu Glu Arg Leu Ile Val Gln Glu Trp
65                  70                  75                  80

Glu Lys Met Gln Arg Lys Leu Lys Asn Lys Glu Lys
                85                  90

<210> 276

<211> 1049

<212> PRT

<213> Streptococcus agalactiae

<400> 276

Met Phe Ser Trp Leu Glu Ala Leu Tyr Tyr Thr Leu Ile Gln Leu Ala
1               5                   10                  15

Lys Val Asn Arg Leu Asn Ala Leu Phe Leu Val Ser Val Val Gly Tyr
            20                  25                  30

Leu Cys Tyr Gln Gly Ile Lys Leu Val Arg Lys Thr Ile Arg Asn Phe
        35                  40                  45

Phe Gln Leu Met Lys Gly Phe Ile Gly Asp Arg Glu Asn Ile Lys Lys
    50                  55                  60

Cys Ile Lys Asn Lys Lys Glu Ala Leu Val His Ser Trp Lys His Arg
65                  70                  75                  80

Gln Asp Ile Asp Trp Lys Ser Thr Gly Lys Asp Lys Ser Lys Gln Leu
                85                  90                  95

Trp Asn Leu Met Lys Arg Leu Ala Thr Val Ala Pro Ser Phe Leu Phe
            100                 105                 110

Leu Leu Leu Gly Asn Val Leu Phe Arg Leu Ile Tyr Gln Leu Pro Phe
        115                 120                 125

Val Lys Gln Asp Arg Lys Arg Phe Asp Lys Glu Met Lys Pro Leu Leu
    130                 135                 140

Tyr Phe Lys Asn Tyr Arg Ser Phe Val Phe Met Gly Ile Gly Phe Ser
145                 150                 155                 160

Phe Ile Ala Phe Ile Leu Thr Asn Tyr Phe Val Thr Val Leu Arg Ala
165 170 175

Ala Ile Arg Phe Leu Tyr Phe Ser Ile Met Thr Leu Arg Asp Asn Ser
180 185 190

Gln Val Val Ser Phe Asn Val Asp Ser Leu Leu Ile Gln Asn Leu Phe
195 200 205

Asn Ala Arg Val Phe Val Ile Ala Pro Ile Leu Ala Val Pro Ile Phe
210 215 220

Leu Ile Gly Leu Val Val Ala Trp Arg Ser Ala Trp Val Asn Phe Glu
225 230 235 240

Gln Tyr Arg Asp Tyr Asn His Asn Glu Glu Gly Asp Asp Arg Phe Ala
245 250 255

Thr Val Lys Glu Ile His Gln Gln Tyr Lys Lys Val Pro Asn Lys Thr
260 265 270

Glu Thr Tyr Pro Gly Glu Gly Gly Val Pro Val Leu His Glu Thr Arg
275 280 285

Lys Asn Leu Thr Gly Leu Thr Leu Lys Ser Gln Met Leu Trp Gln Asn
290 295 300

Arg Thr Phe Ser Arg Tyr Leu Thr Asn Ala Glu Arg Ile Leu Gly Leu
305 310 315 320

Leu Ser Thr Pro Ser Gly Asp Tyr Tyr Ile Asp Asp Ser Thr Thr Asn
325 330 335

Leu Ile Thr Met Gly Ile Thr Arg Ser Gly Lys Gly Glu Ala His Ile
340 345 350

Ala Pro Ile Ile Asp Ile Asn Ser Arg Ala Glu Ile Gln Pro Ser Leu
355 360 365

Ile Ile Ala Asp Pro Lys Gly Glu His Tyr Gln Ser Ser Tyr Lys Thr
370 375 380

Met Arg Arg Arg Gly Tyr Asp Val Asn Val Leu Ser Phe Gln Asn Met
385 390 395 400

Asp Trp Ser Met Ser Tyr Asn Pro Leu Ala Leu Ala Ile Ala Ala Ala
405 410 415

Lys Lys Gly Tyr Tyr Glu Met Thr Gln Thr Arg Val Asn Ala Val Ala
420 425 430

Glu Ala Ile Tyr Arg Lys Thr Lys Pro Gly Ser Gly Asn Gly Asn Ala
        435                 440                 445

Lys Tyr Trp Glu Asp Thr Ser Ile Ser Leu Phe Asn Ala Ile Ala Met
    450                 455                 460

Ala Leu Met Asp Arg Ala Asn Glu Thr Val Arg Asn Gly Glu Thr Asp
465                 470                 475                 480

Ala Trp Asp Thr Val Thr Val Arg Asn Ile Ala Lys Phe Leu Thr Asp
                485                 490                 495

Leu Gly Ser Glu Glu Val Phe Val Asn Asp Phe Gly Glu Ile Val Glu
            500                 505                 510

Asn Pro Asp Lys Asn Gln Gln Val Lys Lys Lys Ser Lys Ile Thr Val
        515                 520                 525

Tyr Phe Asp Asn Leu Arg Lys Ile Asn Gln Glu Gln Phe Ser Lys Phe
    530                 535                 540

Arg Asp Met Ala Asp Leu Asn Phe Arg Ser Ser Asp Phe Ala Ser Glu
545                 550                 555                 560

Glu Thr Lys Gly Asn Val Phe Ser Ser Met Met Ser Gly Ile Asn Leu
                565                 570                 575

Phe Leu Gln Asp Asn Ile Ala Lys Leu Thr Ser Lys Asn Ser Ile Asp
            580                 585                 590

Leu Glu Ser Val Gly Phe Pro Arg Arg Leu Ser Ile Lys Phe Arg Ser
        595                 600                 605

Ser Ser Asn Val Ala Met Arg Asn Glu Tyr Thr His Lys Thr Ala Lys
    610                 615                 620

Val Thr Ile Thr Ser Gln Ala Val Trp Gly Lys Thr Thr Lys Gln Val
625                 630                 635                 640

Ile His Val Asp Ala Ala Thr Ala Leu Ile Asp Gly Glu Gly Tyr Leu
                645                 650                 655

Thr Tyr Val Ile Glu Pro Gln Leu Pro Asp Gln Phe Leu Val Thr Ile
            660                 665                 670

Asp Phe Asn His Glu Asn Asn Gly Gly Ser Ala Ile Arg His Lys Thr
        675                 680                 685

Phe Gln Phe Ser Ala Glu Lys Val Tyr Lys Lys Arg Gly Asn Val Ile
    690                 695                 700

Thr Leu Asp Asp Tyr Thr Lys Lys Pro Val Leu Asp His Ile Lys Val
705 710 715 720

Thr Val Leu Asn Lys Gln Asp Asp Asn Leu Leu Gln Lys Glu Asp Ile
725 730 735

Asp Leu Ile Tyr Ser Asp Asn Pro Lys Val Ile Tyr Leu Val Thr Pro
740 745 750

Pro Asn Arg Thr Glu Tyr Asn Ser Ile Val Ser Leu Phe Leu Asp Gln
755 760 765

Leu Phe Asn Ala Asn Tyr Glu Leu Ala Leu Ser Asn Gly Arg Lys Cys
770 775 780

Val Asn Arg Ile Leu His Ile Leu Asp Glu Phe Thr Asn Ile Pro Ala
785 790 795 800

Ile Pro His Met Asp Thr Lys Ile Ser Ile Gly Leu Gly Gln Asn Ile
805 810 815

Leu Tyr Tyr Leu Trp Ile Gln Asn Leu Lys Gln Leu Val Ser Glu Tyr
820 825 830

Gly Glu Asn Thr Ala Glu Thr Ile Arg Glu Asn Cys Ser Leu Lys Val
835 840 845

Tyr Ile Lys Ser Thr Ala Pro Ala Thr Asn Glu Tyr Phe Ser Lys Glu
850 855 860

Leu Gly Thr Arg Thr Ile Thr Arg Arg Arg Arg Ser Ser Asn Ile Leu
865 870 875 880

Asp Glu Ala Asn Pro Asn Val Ser Ile Glu Asn Pro Arg Gln Glu Leu
885 890 895

Leu Thr Pro Thr Gln Leu Ser Lys Leu Gln Glu Gly Glu Ala Val Ile
900 905 910

Leu Arg Gly Val Lys Gly Arg Asp Asn Ala Gly Arg Lys Ile Thr Thr
915 920 925

Asp Pro Ile Phe Leu His Glu Lys Thr Ser Leu Pro Tyr Arg Tyr Met
930 935 940

Phe Leu Gln Glu Glu Phe Asp Gln Ser Met Ala Leu Ala Asp Ile Pro
945 950 955 960

Val Glu Ser Gly His Arg Asp Leu Asp Leu Gln Asp Ile Ala Val Gly
965 970 975

Ala Gln Ser Thr Phe Asn Lys Ile Ile Asp Trp Arg Met Ala Leu Thr
980 985 990

Asp Arg Met Arg Thr Asn Gly Lys Ile Pro Gln Leu Ala Ser Arg Lys
995 1000 1005

Gln Thr Ile Lys Ala Leu Ser Gln Ser Gln Phe Thr Ser Pro Ala
1010 1015 1020

Asp Leu Thr Gln Ala Val Ile Ala Glu Val Phe Asp Glu Glu Asp
1025 1030 1035

Asp Asp Asp Leu Phe Phe Val Asp Asp Val Met
1040 1045

<210> 277

<211> 933

<212> PRT

<213> Streptococcus agalactiae

<400> 277

Met Asn Ser Asn Thr Lys Gly His Gly Phe Phe Arg Lys Ser Lys Ala
1 5 10 15

Tyr Gly Leu Val Cys Ala Ile Ala Leu Ala Gly Ala Phe Thr Leu Ala
20 25 30

Thr Ser Gln Val Ser Ala Asp Gln Val Thr Thr Gln Ala Thr Thr Gln
35 40 45

Thr Val Thr Gln Asn Gln Ala Glu Thr Val Thr Ser Thr Gln Leu Asp
50 55 60

Lys Ala Val Ala Thr Ala Lys Lys Ala Ala Val Ala Val Thr Thr Thr
65 70 75 80

Pro Ala Val Asn His Ala Thr Thr Thr Asp Ala Gln Ala Asp Leu Ala
85 90 95

Asn Gln Thr Gln Ala Val Lys Asp Val Thr Ala Lys Ala Gln Ala Asn
100 105 110

Thr Gln Ala Ile Lys Asp Ala Thr Ala Glu Asn Ala Lys Ile Asp Ala
115 120 125

Glu Asn Lys Ala Glu Ala Glu Arg Val Ala Lys Glu Asn Lys Glu Gly
130 135 140

Gln Ala Ala Val Asp Ala Arg Asn Lys Ala Gly Gln Ala Ala Val Asp
145 150 155 160

Ala Arg Asn Lys Ala Lys Gln Gln Ala Gln Asp Asp Gln Lys Ala Lys
165 170 175

Ile Asp Ala Glu Asn Lys Ala Glu Ser Gln Arg Val Ser Gln Leu Asn
180 185 190

Ala Gln Asn Lys Ala Lys Ile Asp Ala Glu Asn Lys Asp Ala Gln Ala
195 200 205

Lys Ala Asn Ala Thr Asn Ala Gln Leu Gln Lys Asp Tyr Gln Ala Lys
210 215 220

Leu Ala Glu Ile Lys Ser Val Glu Ala Tyr Asn Ala Gly Val Arg Gln
225 230 235 240

Arg Asn Lys Asp Ala Gln Ala Lys Ala Asp Ala Thr Asn Ala Gln Leu
245 250 255

Gln Lys Asp Tyr Gln Ala Lys Leu Ala Leu Tyr Asn Gln Ala Leu Lys
260 265 270

Ala Lys Ala Glu Ala Asp Lys Gln Ser Ile Asn Asn Val Ala Phe Asp
275 280 285

Ile Lys Ala Gln Ala Lys Gly Val Asp Asn Ala Glu Tyr Gly Asn Ser
290 295 300

Ile Met Thr Ala Lys Thr Lys Pro Asp Gly Ser Phe Glu Phe Asn His
305 310 315 320

Asp Met Ile Asp Gly Val Lys Thr Ile Gly Tyr Gly Lys Leu Thr Gly
325 330 335

Lys Val Asn His His Tyr Val Ala Asn Lys Asp Gly Ser Val Thr Ala
340 345 350

Phe Val Asp Ser Val Thr Leu Tyr Lys Tyr Glu Tyr Arg Asn Val Ala
355 360 365

Gln Asn Ala Ala Val Asn Gln Asn Ile Val Phe Arg Val Leu Thr Lys
370 375 380

Asp Gly Arg Pro Ile Phe Glu Lys Ala His Asn Gly Asn Lys Thr Phe
385 390 395 400

Ala Glu Thr Leu Asn Lys Thr Leu Gln Leu Asn Leu Lys Tyr Glu Leu
405 410 415

Lys Pro His Ala Ser Ser Gly Asn Val Glu Val Phe Lys Ile His Asp
420 425 430

Asp Trp Val His Asp Thr His Gly Ser Ala Leu Val Ser Tyr Val Asn
435 440 445

Asn Asn Asp Ala Val Pro Asn Val Val Ile Pro Glu Arg Pro Thr Pro
450 455 460

Pro Lys Pro Val Lys Val Thr Pro Glu Ala Glu Lys Pro Val Pro Glu
465 470 475 480

Lys Pro Val Glu Pro Lys Leu Val Thr Pro Thr Leu Lys Thr Tyr Thr
485 490 495

Pro Val Lys Phe Ile Pro Arg Glu Tyr Lys Pro Glu Pro Ile Thr Pro
500 505 510

Glu Thr Phe Thr Pro Glu Lys Phe Thr Pro Ala Gln Pro Lys Val Lys
515 520 525

Pro His Val Ser Ile Pro Glu Lys Ile Asn Tyr Ser Val Ser Val His
530 535 540

Pro Val Leu Val Pro Ala Ala Asn Pro Ser Lys Ala Val Ile Asp Glu
545 550 555 560

Ala Gly Gln Ser Val Asn Gly Lys Thr Val Leu Pro Asn Ala Thr Leu
565 570 575

Asp Tyr Val Ala Lys Gln Asn Phe Ser Gln Tyr Lys Gly Ile Lys Ala
580 585 590

Ser Ala Glu Ala Ile Ala Lys Gly Phe Ala Phe Val Asp Gln Pro Asn
595 600 605

Glu Ala Leu Ala Glu Leu Thr Val Lys Ser Ile Lys Ala Ser Asn Gly
610 615 620

Asp Asp Val Ser Ser Leu Leu Glu Met Arg His Val Leu Ser Lys Asp
625 630 635 640

Thr Leu Asp Gln Lys Leu Gln Ser Leu Ile Lys Glu Ala Gly Ile Ser
645 650 655

Pro Val Gly Glu Phe Tyr Met Trp Thr Ala Lys Asp Pro Gln Ala Phe
660 665 670

Tyr Lys Ala Tyr Val Gln Lys Gly Leu Asp Ile Thr Tyr Asn Leu Ser
675 680 685

Phe Lys Ile Lys Ala Asn Phe Thr Lys Gly Gln Ile Lys Asn Gly Val
    690                 695                 700

Ala Gln Ile Asp Phe Gly Asn Gly Tyr Thr Gly Asn Ile Val Val Asn
705                 710                 715                 720

Asp Val Thr Val Pro Glu Val His Lys Asp Ile Leu Asp Lys Glu Asp
                725                 730                 735

Gly Lys Ser Ile Asn Asn Ser Thr Val Lys Leu Gly Asp Glu Val Thr
            740                 745                 750

Tyr Lys Leu Glu Gly Trp Val Val Pro Ala Asn Arg Gly Tyr Asp Leu
        755                 760                 765

Phe Glu Tyr Lys Phe Val Asp Gln Leu Gln His Thr His Asp Leu Tyr
    770                 775                 780

Leu Arg Asp Lys Val Val Ala Lys Val Asp Val Thr Leu Lys Asp Gly
785                 790                 795                 800

Thr Val Ile Lys Lys Gly Thr Asn Leu Gly Glu Tyr Thr Glu Thr Val
                805                 810                 815

Tyr Asn Lys Thr Thr Gly His Tyr Glu Leu Ala Phe Lys Lys Glu Phe
            820                 825                 830

Leu Ala Lys Val Ser Arg Glu Ser Glu Phe Gly Ala Asp Asp Phe Ile
        835                 840                 845

Val Val Lys Arg Ile Lys Ala Gly Asp Val Tyr Asn Thr Ala Asp Leu
    850                 855                 860

Tyr Val Asn Gly Tyr Lys Val Lys Ser Glu Ala Val Val Thr His Thr
865                 870                 875                 880

Thr Glu Lys Ser Lys Pro Val Glu Pro Gln Lys Ala Thr Pro Lys Ala
                885                 890                 895

Pro Ala Lys Gly Leu Pro Ser Thr Gly Glu Ala Ser Met Thr Pro Leu
            900                 905                 910

Thr Ala Ile Gly Ala Ile Ile Leu Ser Ala Leu Gly Leu Ala Gly Phe
        915                 920                 925

Lys Lys Arg Gln Lys
    930

<210> 278

<211> 753

<212> PRT

<213> Streptococcus agalactiae

<400> 278

Met Lys Gln Ile Lys Ile Ile Thr Gly Leu Thr Val Ala Thr Leu Ser
1 5 10 15

Ala Val Val Gly Asn Val Tyr Ala Glu Asp Ile Thr Pro Thr Ala Pro
20 25 30

Val Asn Glu Pro Gln Val Ser Ser Glu Thr Ala Lys Thr Pro Gln Val
35 40 45

Thr Glu Ser Gln Val Asn Ser Ala Lys Val Thr Ala Asp Gln Ala Ile
50 55 60

Ser Asp Val Asn Asn Gln Gln Ile Val Val Asp Glu Ala Gln Lys Gln
65 70 75 80

Lys Asp Gln Ser Gln Gln Asn Leu Val Lys Ala Thr Ser Thr Val Thr
85 90 95

Glu Ala Glu Lys Val Ala Ala Glu Ala Thr Pro Glu Val Val Lys Glu
100 105 110

Ala Ile Lys Ala Val Thr Glu Ala Lys Glu Ala Val Thr Asp Ala Glu
115 120 125

Ala Asn Val Val Asp Ala Gln Lys Thr Glu Gln Lys Ala Asn Gln Glu
130 135 140

Val Gln Ser Gln Ala Lys Thr Val Asp Glu Asn Val Lys Val Val Ala
145 150 155 160

Asp Lys Glu Ser Glu Val Lys Gln Ala Glu Gly Val Val Thr Thr Ala
165 170 175

Gln Glu Ala Ile Asp Ser Lys Thr Ala Asn Thr Asn Ala Ser Glu Ala
180 185 190

Glu Lys Ala Val Thr Glu Lys Gln Thr Lys Leu Glu Thr Ala Glu Thr
195 200 205

Asn Leu Thr Glu Ala Gln Lys Gln Asp Ala Lys Ile Ala Glu Glu Lys
210 215 220

Arg Leu Ala Glu Gln Glu Val Val Asn Lys Gln Leu Ala Val Thr Asp
225 230 235 240

Thr Gln Thr Leu Leu Lys Lys Leu Val Thr Glu Ile Asn Asn Glu Lys
245 250 255

Val Ser Thr Ser Leu Glu Asn Gln Ala Tyr Phe Asn Gln Arg Asp Gly
260 265 270

Ser Trp Ala Gly Tyr Tyr Gly Asn Tyr Thr Phe Ala Ala Thr Gly Cys
275 280 285

Val Pro Ser Ser Leu Ala Met Val Phe Thr Glu Leu Ala Arg Arg Gln
290 295 300

Ile Thr Pro Thr Glu Ile Ala Asn Tyr Leu Trp Asn Asn Ser Asn Glu
305 310 315 320

Phe Asn Lys Asn Tyr Gly Gly Thr Ser Gly Lys Gly Leu Val Gln Ala
325 330 335

Thr Lys His Phe Gly Phe Val Pro Thr His Leu Ala Ser Gln Ser Ala
340 345 350

Ile Val Glu Ala Leu Gln Ala Gly His His Val Leu Ala Ala Val Gln
355 360 365

Gln Asp Lys Phe Ser Pro Trp Gly Ile Asn Tyr Ser His Glu Ile Val
370 375 380

Leu Arg Gly Tyr Ser Asn Gly Asn Thr Tyr Val Tyr Asp Pro Tyr Asn
385 390 395 400

Arg Ala Asn Ile Gly Trp Tyr Pro Val Ala Asn Leu Trp Asn Glu Gln
405 410 415

Ser Arg Asp Ala Ile Asp Thr Ser Ser Val Gly Val Pro Phe Phe Lys
420 425 430

Ile Thr Thr Gln Lys Met Ala Gln Leu Glu Ala Gln Lys Ala Gln Val
435 440 445

Gln Ser Ser Leu Asn Thr Ala Lys Asn Gln Leu Ala Lys Thr Gln Asp
450 455 460

Val Leu Arg Thr Leu Glu Ala Thr Pro Leu Lys Thr Pro Glu Ala Gln
465 470 475 480

Ala Lys Leu Asn Gln Ala Lys Glu Ala Leu Ala Leu Ala Gln Ala Asp
485 490 495

Tyr Thr Lys Ala Gln Glu Ala Val Lys Leu Ala Ser Gln Asp Leu Ala
500 505 510

Val Lys Glu Glu Thr Leu Lys Asn Ala Gln Ala Asp Leu Leu Thr Lys
515 520 525

Gln Thr Ala Leu Lys Asp Ala Gln Thr Val Leu Val Ala Ser Gln Val
530 535 540

Lys Leu Ala Asp Leu Lys Ala Thr Leu Ala Thr Val Glu Asn Asn Val
545 550 555 560

Lys Lys Ala Gln Ala Thr Leu Thr Asp Ala Lys Ala Ile Val Gly Gln
565 570 575

Lys Gln Ala Lys Leu Leu Ala Leu Gln Asn Ala Pro Lys Ile Leu Ala
580 585 590

Asp Ala Gln Ala Lys Leu Val Thr Ala Lys Asn Asp Leu Ala Asn Lys
595 600 605

Met Ala Ile Leu Asp Glu Ala Val Ala Lys Leu Lys Ser Leu Gln Ala
610 615 620

Val Gln Ala Glu Ala Gln Lys Gln Tyr His Val Val Phe Glu Ala Tyr
625 630 635 640

Lys Ala Val Arg Asp Ala Lys Glu Gln Ala Lys Leu Ala Glu Ser Tyr
645 650 655

Asn His Ile Ile Ala Arg Gly Gly Glu Ala Ile Pro Val Val Asp Glu
660 665 670

Thr Asp Lys Ile Thr Gly Tyr Val Asp Gly Ser Gln Lys Ala Val Ala
675 680 685

Asn Glu Val Thr Leu Ala Leu Thr Ser Asn Gly Ala Pro Leu Glu Ser
690 695 700

Pro Val Asn Lys Glu Asn Gln Asn Val Thr Lys Ser Ser Gln Ala Leu
705 710 715 720

Pro His Thr Gly Glu Ala Gly Leu Ser Ile Leu Ser Val Leu Gly Val
725 730 735

Gly Leu Ile Ser Thr Leu Gly Leu Thr Ser Leu Lys Lys Arg Arg Pro
740 745 750

His

<210> 279

<211> 639

<212> PRT

<213> Streptococcus agalactiae

<400> 279

Val Arg Leu Thr His Val Ser Leu Trp Met Pro Ser Lys Arg Ser Trp
1 5 10 15

Pro Leu Lys Leu Gln Leu Leu Arg Lys Gly Val Ile Glu Leu Glu Asp
20 25 30

Glu Leu Lys Thr Pro Tyr Leu Asp Gln Tyr Thr Asp Asn Leu Thr Ala
35 40 45

Lys Val Thr Lys Lys Ser Asp Asp Tyr Gln Val Tyr Gly Arg Asn Lys
50 55 60

Glu Val Gln Ser Val Ile Ile Ser Leu Leu Arg Arg Thr Lys Asn Asn
65 70 75 80

Pro Ile Leu Val Gly Glu Ala Gly Val Gly Lys Ser Ala Ile Val Glu
85 90 95

Gly Ile Thr Leu Ala Ile Leu Arg Gly Gln Val Pro Glu Pro Leu Lys
100 105 110

Gly Leu Thr Val Arg Ser Leu Glu Leu Ser Ser Leu Met Ser Glu Asp
115 120 125

Asp Glu Gly Phe Ile Ala Lys Phe Lys Lys Ile Ile Glu Glu Met Val
130 135 140

Ala Thr Arg Gly His Asn Leu Leu Phe Val Asp Glu Phe His Thr Ile
145 150 155 160

Ile Gly Ala Gly Ser Gln Asn Gly Gln Ala Leu Asp Ala Gly Asn Val
165 170 175

Ile Lys Pro Val Leu Ala Arg Gly Asp Ile Gln Leu Ile Gly Ala Thr
180 185 190

Thr Leu Asp Glu Phe His Glu Tyr Ile Glu Thr Asp Arg Ala Leu Glu
195 200 205

Arg Arg Met Gln Pro Val Met Val Glu Glu Pro Thr Ile Ser Gln Ala
210 215 220

Ile Thr Ile Ile Glu Gln Ala Lys Val Ile Tyr Glu Lys Phe His Gly
225 230 235 240

Ile Gln Ile Ser Ser Asp Ala Val His Gln Ala Ile Arg Leu Ser Val
245 250 255

Arg Tyr Leu Thr Asp Arg Phe Leu Pro Asp Lys Ala Phe Asp Leu Ile
260 265 270

Asp Glu Ala Ala Thr Ile Ala Ser Val Glu Gly Lys Ser Lys Val Thr
275 280 285

Glu Lys Asp Ile Ala Gln Val Leu Lys Asp Lys Thr Gly Ile Pro Val
290 295 300

Thr Thr Ile Leu Lys Gly Asp Gln Glu Arg Leu Glu Gly Phe Lys Glu
305 310 315 320

Arg Leu Met Asn Arg Val Lys Gly Gln Glu Asp Ala Ile Glu Ala Val
325 330 335

Val Asp Ala Val Thr Ile Ala Gln Ala Gly Leu Gln Asn Glu Lys Arg
340 345 350

Pro Leu Ala Ser Phe Leu Phe Leu Gly Pro Thr Gly Val Gly Lys Thr
355 360 365

Glu Leu Ala Lys Ala Ile Ala Glu Ala Leu Phe Asp Asp Glu Ala Ala
370 375 380

Met Ile Arg Phe Asp Met Ser Glu Tyr Lys Gln Lys Glu Asp Val Thr
385 390 395 400

Lys Leu Ile Gly Asn Arg Ala Thr Arg Ile Lys Gly Gln Leu Thr Glu
405 410 415

Gly Val Lys Gln Lys Pro Tyr Cys Val Leu Leu Leu Asp Glu Ile Glu
420 425 430

Lys Ala His Ser Glu Val Met Asp Leu Phe Leu Gln Val Leu Asp Asp
435 440 445

Gly Arg Leu Thr Asp Ser Ser Gly Arg Leu Ile Ser Phe Lys Asn Thr
450 455 460

Ile Val Ile Met Thr Thr Asn Ile Gly Ala Lys Lys Ile Ile Asn Lys
465 470 475 480

Trp Glu Leu Lys Gly Asn Phe Lys Asp Leu Thr Asp Arg Asp Arg Lys
485 490 495

Gln Phe Glu Lys Ser Met Asp Ser Glu Leu Gln Asn Glu Phe Arg Pro
500 505 510

Glu Phe Leu Asn Arg Ile Glu Asn Lys Leu Ile Phe Asn Leu Leu Glu
515 520 525

Arg Asp Val Ile Glu Lys Ile Ala Glu Lys Asn Leu Ser Glu Ile Ala
530 535 540

Asp Arg Met Lys Arg Gln Asn Leu Thr Leu Ser Tyr Glu Pro Ser Leu
545 550 555 560

Ile Gln Tyr Leu Ser Asp Val Gly Thr Asp Val Lys Asn Gly Ala Arg
565 570 575

Pro Leu Glu Arg Leu Met Lys Arg Lys Val Leu Ala Pro Ile Ser Val
580 585 590

Lys Ser Leu Gln Leu Asp Lys Ser Lys Gln Gly Tyr Asn Val His Leu
595 600 605

Trp Val Glu Gly Arg Ala Pro Asp Gly Asn His Arg Gln Glu Gln Arg
610 615 620

Gln Ile His Met Glu Ile Glu Gly Glu Arg Asp Asn Phe Phe Ser
625 630 635

<210> 280

<211> 1576

<212> PRT

<213> Streptococcus agalactiae

<400> 280

Met Ala Glu Glu Asn Ala Gln Gln Pro Ser Leu Arg Gly Lys Ser Arg
1 5 10 15

Arg Glu Arg Val Glu Phe Ala Arg Ser Arg Asp Ile Leu Asp Val Ala
20 25 30

His Glu Leu Asn Met Glu Leu Phe Arg Asp Gly Lys Asn Tyr Arg Trp
35 40 45

Lys Glu His Asp Ser Met Val Ile Thr Pro Ala Thr Asn Gln Trp Tyr
50 55 60

Trp Phe Ser Gln Arg Gln Gly Gly Asp Val Ile Ala Leu Val Glu Thr
65 70 75 80

Ile Lys Glu Ile Gly Phe Asn Gln Ala Phe Glu Tyr Leu Asn Glu Gly
85 90 95

Thr Phe Lys Glu Phe Thr Val Val Asn Gln Val Lys Glu Pro Phe Ser
100 105 110

Tyr Tyr Leu Glu Pro Tyr Glu Gln Leu Phe Val Glu Ala Arg Arg Tyr
115 120 125

Leu Lys Glu Asn Arg Gly Leu Ser Asp Asp Thr Ile Asp Phe Phe Tyr
130 135 140

Asp Lys Gly Val Leu Ala Gln Ala Asn Ala Lys Val Gly Asp Met Ile
145 150 155 160

Glu Pro Val Leu Val Phe Lys Asn Leu Asp Lys Asn Gly Gln Val Val
165 170 175

Gly Ala Ala Leu Gln Gly Leu Val Ala Ala Pro Asp Lys Tyr Phe Gly
180 185 190

Arg Gly Tyr Leu Lys Gln Ile Met Lys Asn Ser Gln Pro Tyr Asn Gly
195 200 205

Met His Val Asp Ile Gly Thr Pro Asn Arg Leu Val Phe Ala Glu Ser
210 215 220

Ser Ile Asp Leu Met Ser Tyr Tyr Glu Ile His Lys Asp Ser Leu Ser
225 230 235 240

Asp Val Arg Leu Val Ser Leu Glu Gly Leu Lys Thr Gly Thr Ile Gly
245 250 255

Arg His Leu Ile Gln Leu Arg Ala Glu Met Glu Arg Arg Pro Leu Ser
260 265 270

Ser Ser Trp Thr Asp Glu Ile Leu Ala Gln Gly Leu Asp Glu Ala Val
275 280 285

Lys Gln Gly Tyr Phe Lys Asp Gly Lys Asn Ser His Leu Leu Thr Leu
290 295 300

Ala Val Asp Asn Asp Val Lys Gly Lys Gln Leu Ile Glu Glu Leu Lys
305 310 315 320

Asp Lys Ser Ile Pro Val Ile Asp Ala Thr Pro Pro Lys Ala Glu Gly
325 330 335

Gln Ser Lys Met Asp Trp Asn Ala Tyr Leu Gln Glu Thr Lys Ala Thr
340 345 350

Phe Ser Thr Glu Lys Tyr Gln Glu Lys Ile Asp His Leu Ile Ser Asp
355 360 365

Val Ile Leu Gly Asp Glu Thr Tyr Tyr Leu Trp His Asp Asp Glu Leu
370 375 380

Val Asn Leu Gly Ala Gly Asp Ser Ile Ile Gln Ala Phe His His Gln
385 390 395 400

Leu Glu Asp Arg Arg Tyr Val Ile Asn Gln Ala Glu Leu Tyr Val Glu
405 410 415

Glu Ser Ser Asn Asp Gly Ala Thr Gly Tyr Leu Ser Ile Glu Gly His
420 425 430

Val Leu Asp Lys Asp Gly Ile Ser Asp Tyr Leu Ser Asp Gln Ala Leu
435 440 445

Thr Asp Ala Glu Lys Val Ala Phe Leu Glu Thr Leu Gln Thr Glu Leu
450 455 460

Pro Asp Ile Trp Asp Glu Ile Val Asn His Tyr Asp Lys Val Phe Glu
465 470 475 480

Glu Val Val Val Lys Tyr Gly Leu Arg Glu Lys His Ala Asp Ile Ile
485 490 495

Gln Glu Gln Glu Leu Asp Leu Asp Pro Leu Val Val Pro Glu Ala Lys
500 505 510

Glu Lys Ser Leu Glu Met Asn Gln Glu Thr Asn Thr Gly Gly Glu Leu
515 520 525

Phe Asn Arg Asn Ser Ser Phe Leu Gly Glu Asp Ser Pro Gly Thr Ala
530 535 540

Pro Gln Pro Val Glu Pro Thr Ala Gln Pro Asp Phe Pro Thr Asn Val
545 550 555 560

Arg Leu His Phe Thr Thr Asp Asp Gly Asn Met Ser Asn Lys Ala Phe
565 570 575

Arg Lys Asn Met Arg Thr Leu Asn Leu Tyr Ala Asn Thr Met Arg Asp
580 585 590

Ser Ala Gln Trp Tyr Leu Ser Glu Ile Ala Asp Thr Thr Met Ser Tyr
595 600 605

Val Tyr Lys Thr Pro His Glu Glu Gly Val Gln Val Leu Ser Val His
610 615 620

Phe Gly Lys Lys Asn Trp Met His Leu Thr Gly Val Thr Pro Val Tyr
625 630 635 640

Glu Asn Trp Val Asp Ser Leu Ser Glu Gln Phe Ile Asp Asp Ile Ala
645 650 655

Asn Ser Lys Gly His Phe Lys Asn Leu Lys Phe Ala Leu Gly Thr Pro
660 665 670

Asp Lys Leu Lys Val Leu Asn Leu Leu Pro Glu Ile Ile Glu Ser Asp
675 680 685

Thr Phe Val Phe Asn Asp Leu Ser Ser Val Gln Lys Leu Asn Asn Leu
690 695 700

Asp Leu Ser Gln Ala Leu Asn Pro Glu Asp Ser Asp Leu Leu Leu Leu
705 710 715 720

Phe Arg Asp Glu Gly Leu His Gln Val Pro Ala Ser Leu Met Arg Ile
725 730 735

Lys Gly Asp Leu Glu Glu Arg Leu Ser His Ile Asp Ser Gly Thr Val
740 745 750

Leu Gly Val Tyr Arg Glu Arg Asn Gly Gln Leu Glu Gln Val Ser Val
755 760 765

Asn Glu Glu Tyr Val Lys Asp Ser Gly Gln Glu Met Leu Ser Ile Leu
770 775 780

Gln Asn Lys His Tyr Glu Glu Ala Leu Asp Ser Gly Gln Glu Met Val
785 790 795 800

Gln Thr Asp Gly Phe Ser Ala Glu Asp Phe Thr Lys Val Leu Asp Ala
805 810 815

Val Tyr His Val Gly Val Pro Asp Asp Leu Ala Arg Val Pro Glu Gly
820 825 830

Val Leu Pro Val Trp Gln Lys Tyr Leu Glu Val Ser Glu Glu Asn Gln
835 840 845

Trp Asp Leu Glu Gln Met Ile Asp Tyr Ala Asp Lys Asn Ser Leu Leu
850 855 860

Val Lys Asp Ser Ala Phe Tyr Lys Glu Trp Lys Glu Asp Met Ile Tyr
865 870 875 880

Lys Asn Asp Tyr His Val Arg Leu Gln Phe Ala Glu Asn Trp Asp Asn
885 890 895

Gly Val Glu Leu Pro Phe Arg Thr Glu Gln Leu Ile Asp Tyr Lys Thr
900 905 910

Phe Val Thr Gly Leu Tyr Glu Ala Asn Gln Ala His His Gln Arg Arg
915 920 925

Gln Glu Ser Gln Leu Pro Tyr Thr Lys Thr Glu Phe Asp Ile Tyr Ala
930 935 940

Pro Gly Gly Gln Leu Ile Lys Asp Asn Val His Tyr Ala Ile Gly Asp
945 950 955 960

Glu Thr Arg Pro Val Ser Gln Leu Met Gly Leu Gly Tyr Arg Arg Leu
965 970 975

Pro Gly Tyr Gln Glu Leu Ala Val Ile Asp Asn Ser Ile Leu Ser Gln
980 985 990

Leu Glu Asn Lys Glu Leu Asn Gln Glu Ile Ala Ser Glu Ala Asn Glu
995 1000 1005

His Ser Leu Asn Ser Gln Glu Ile Pro Lys Glu Asp Asn Tyr Pro
1010 1015 1020

Arg Glu Ala Phe Thr Ser Pro Lys Gln Asp Ile Lys Lys Gly Leu
1025 1030 1035

Ala Gln Arg Val Glu Glu Ile Val Ala Glu Asp Ala Thr Lys Ile
1040 1045 1050

Leu Val Ser Ser Ile Pro Gln Val Gln Glu Asn Leu Ser Val Glu
1055 1060 1065

Gly Asn Leu Val Gly Thr Pro Gln Ala Asp Asn Arg Met Leu Tyr
1070 1075 1080

Thr Asn Leu Glu Asp Phe Gly Gln Asp Tyr Gln Leu Glu Leu Ala
1085 1090 1095

Val Tyr Ser Pro Lys Arg Val Asp Phe Leu Glu Asp Val Gln Ala
1100 1105 1110

Pro Trp Thr Leu Ala Leu Ile Arg Lys Glu Lys Lys Ile Gly Tyr
1115 1120 1125

Leu Ala Tyr Gly Ser Asp Trp Ala Lys Glu Phe Gln Ile Glu Glu
1130 1135 1140

Glu Leu Glu His Leu Ala Ala Gln Ile Gly Asp Glu Lys Val Pro
1145 1150 1155

Glu Gly Leu Tyr Lys Gln Ala Glu Val Glu Ala Phe Ile Ala Ser
1160 1165 1170

His Gln Gly Asn Glu Ser Leu Gln Glu Pro Ile Pro Thr Ile Val
1175 1180 1185

Ala Glu Pro Phe Asp Tyr Thr Ser Ala Ser Ala Tyr Glu Ile Ser
1190 1195 1200

Glu His Ala Phe Gln Lys Ile Arg Glu Tyr Thr Gln Ser Pro Glu
1205 1210 1215

Asp Leu Leu Glu Tyr Met Asp Phe Met Ser Lys Phe Pro Gln Leu
1220 1225 1230

Ser Pro Arg Asn Val Ala Leu Ile His Glu Gln Trp Arg Gly Ala
1235 1240 1245

Asn Ala Val Ala Thr Tyr Glu Gln Trp Lys Ala Met Gly Glu Ala
1250 1255 1260

Leu Gly Ile Lys Pro Asp Asp Val Val Gln Thr Lys Ala Thr Tyr
1265 1270 1275

Val Asn Lys Arg Thr Gly Glu Thr Lys Glu Val Val His Gln Gly
1280 1285 1290

Leu Ser Val Lys Thr Gly Glu Lys Ser Lys Ile Thr Leu Phe Arg
1295 1300 1305

Pro Leu Met Val Lys Met Ile Pro Val Leu Asp Glu Asn Gly Gln
1310 1315 1320

Gln Leu Lys Asn Asp Lys Gly Asn Pro Lys Tyr Lys Lys Leu Ser
1325 1330 1335

Glu Ala Ser Leu Gln Glu Lys Ala Leu Val Lys Asp Gly Lys Leu
1340 1345 1350

Pro Val Arg Gln Phe Gln Glu Arg Asp Ser Lys Thr Gly Gln Pro
1355 1360 1365

Arg Phe Thr Thr Tyr Lys Val Phe Glu Leu Ser Gln Thr Thr Leu
1370 1375 1380

Lys Pro Gly Ser Tyr Pro Lys Ala Met Pro Asn Arg His Phe Asn
1385 1390 1395

Phe Asn Val Asp Lys Val Lys Thr Lys Glu Val Leu Glu Gly Leu
1400 1405 1410

Cys Asp Tyr Ala Glu Lys Ile Gly Val Ser Leu Met Lys Asp Asp
1415 1420 1425

Ala His Val Leu Asp Asn Ala Lys Gly Ala Phe Tyr Ser Glu Glu
1430 1435 1440

Gln Leu Ile Leu Ile Asn Pro Asn Asn Thr Pro Gly Glu Lys Ile
1445 1450 1455

Ala Thr Thr Ile His Glu Leu Ala His Ala Thr Leu His Asn Pro
1460 1465 1470

Lys Leu Glu Lys Gln Tyr Lys Glu Leu Pro Lys Gly Gln Lys Glu
1475 1480 1485

Phe Glu Ala Glu Met Thr Ser Tyr Leu Leu Ser Lys His Phe Gly
1490 1495 1500

Leu Asp Thr Ser Glu Lys Ala Ile His Tyr Met Ala Ser Trp Thr
1505 1510 1515

Asp Asn Leu Lys Ala Leu Glu Asp Lys Gln Leu Ala Asp Ser Leu
1520 1525 1530

Lys Arg Val His Gln Thr Val Ser Lys Met Leu Lys Gln Val Glu
1535 1540 1545

Lys Tyr Thr Asn Pro His Gln Leu Gly Arg Gly Lys Glu His Gly
1550 1555 1560

Leu Asn Phe Pro Lys Ala Pro Thr Lys Gly Ser Ser Arg
1565 1570 1575

<210> 281

<211> 788

<212> PRT

<213> Streptococcus agalactiae

<400> 281

Met Asp Val Ser Ser Ser Pro Asn Ile Thr Phe Met Leu Gln Tyr Thr
1 5 10 15

Glu Ala Asn Pro Gln Tyr Val Asp Tyr Thr Asn Arg Glu Glu Ala Val
20 25 30

Lys Ile Asp Glu Glu Leu Ser Leu Glu Thr Asn Arg Gln Met Ile Glu
35 40 45

Gly Leu Thr Glu Asp Glu Leu Thr Arg Ile Gln Glu Ala Val Pro Glu
50 55 60

Thr Gln Leu Asn Phe Arg Glu Tyr Ile Asp Tyr Met Asn Arg Ser Tyr
65 70 75 80

Ala Thr Glu Glu Gln Ser Lys Glu Leu Thr Ala Ile Phe Thr Gln Glu
85 90 95

Ala Asp Tyr Leu Gln Lys Leu Arg Leu Ile Asp Leu Lys Asn Lys Leu
100 105 110

Glu Ser Ala Tyr Gln Asn Gly Ser Leu Leu Trp Gln Gly Val Ile Ser
115 120 125

Phe Asp Asn Ala Phe Leu Ala Glu Gln Gly Leu Tyr Asp Val Ala Thr
130 135 140

Gly Gln Val Asp Gln Lys Ala Ile Lys Ala Val Met Arg Asp Met Met
145 150 155 160

Pro Thr Leu Ile Gln Lys Glu Gly Leu Ser Asp Ser Ala Phe Trp Trp
165 170 175

Gly Asn Ile His Leu Asn Thr Asp Asn Ile His Ile His Phe Gly Leu
180 185 190

Ser Glu Val Glu Ser Asn Arg Glu Lys Ile Phe Tyr Gln Pro Arg Gly
195 200 205

Arg Met Glu Tyr Lys Gly Asn Phe Ser Gln Lys Thr Ile Asn Arg Phe
210 215 220

Lys Ser Gly Val Tyr His Gly Leu Leu Lys Glu Glu Thr Arg Ser Asn
225 230 235 240

Leu Leu Arg Lys Glu Gln Ile Leu Ala Asn Leu Lys Ala Asp Phe Ile
245 250 255

Thr Ser Ile Tyr Gln Lys Asp Lys Ile Thr Ser Ser Ala Glu Lys Asn
260 265 270

Phe Leu Glu Gln Ala Tyr Asn His Leu Pro Leu Asn Lys Lys Trp Arg
275 280 285

Tyr Gly Ser Asn Ala Arg Asp Phe Ala Val Ser Lys Phe Phe Leu Asp
290 295 300

Arg Tyr Leu Asp Ser Tyr Leu Asn Asn Glu Gly Ser Ala Ala Tyr Gln
305 310 315 320

Glu Phe Leu Lys Glu Thr Arg Asp Phe Leu Gln Thr Tyr Glu Gly Val
325 330 335

Tyr Ser Ala Glu Lys Asn Lys Ile Tyr Glu Lys Leu Arg Lys Val Asp
340 345 350

Gly Gln Thr Ile Arg Thr Leu Ala Glu Ser Lys Gly Tyr Asp Leu Glu
355 360 365

His His Leu Ala Arg Arg Val Met Asp Leu Arg Glu Arg Leu Ala Asn
370 375 380

Asn Ile Leu Arg Ser Phe Arg Glu Ala Ala Pro Gln Ile Gln Asp Val
385 390 395 400

Gln Leu Glu Lys Asn Leu Glu Ser Phe Ser Val Leu Asn Gln Lys Lys
405 410 415

Ile Leu Glu Gln His Pro Glu Ala Ser Val Val Lys Ser Gln Lys Ala
420 425 430

Trp Gln Lys Leu Gly Tyr Phe Val Lys Ala Gly Glu Gln Pro Leu Glu
435 440 445

Ile Ile Arg Pro Val Tyr Lys Ser Tyr Asp Lys His Gly Lys Gly Ile
450 455 460

Gly Arg Pro Glu Phe Val Ser Asp Thr Val Tyr Asp Ile Ser Gln Leu
465 470 475 480

Thr Glu Asn Ile Gln Leu Lys Ser Leu Thr Leu Lys Asp Leu Ser Leu
485 490 495

Phe Ser Ser Asn Glu Leu Lys Glu Leu Val Asp Ala Ala Lys Leu Lys
500 505 510

Thr Asn Pro Thr Glu Arg Glu Arg Arg Glu Leu Gly Thr Tyr Arg Tyr
515 520 525

Ala Leu Lys Leu Ser Ile Leu Glu Ser Ser Gln Lys Glu Leu Gln Val
530 535 540

Arg Gln Lys Leu Leu Glu Gln Val Gln Pro Leu Ala Ser Asp Gln Pro
545 550 555 560

Phe Leu Asp Phe Lys Lys Gln Leu Ile Ala Gln Glu Leu Gln Ala Ile
565 570 575

Ala Leu Gln Leu Thr Pro Asn Tyr Lys Leu Ser Glu Asp Asp Lys Ala
580 585 590

Leu Lys Asn Arg Leu Lys Arg Gln Phe Glu Asp Ser Val Ala Leu Pro
595 600 605

Val Ser Lys Ala Thr Pro Gly Ala Ile Gln Leu Pro Ile Arg Gln Leu
610 615 620

Trp Thr Glu Leu Gly Leu Val His His Ile Gln Asp Glu Asn Ile Leu
625 630 635 640

Thr Leu Leu Lys Gly Thr Ser Thr Thr Lys Gln Ala Tyr Ile Glu Glu
645 650 655

Leu Gln Thr His Ile Ser Ile Phe Gln Leu Lys Tyr Gln Ile Asn Asn
660 665 670

Arg Asn Lys Gln Ile Ser Gln Leu Ser Asp Glu Ala Thr Ile Lys Glu
675 680 685

Met Arg Ile Ala Asn Ala Lys Gly Phe Ser Glu Leu Lys Arg Leu Tyr
690 695 700

Asp Thr Leu Gln Pro Ser Asp Asp Gly Gln Asn Gln Ile Ser Gln Ala
705 710 715 720

Val Ser Lys Gln Leu Gln Glu Arg Lys Val Ile Lys Lys Ala Gln Leu
725 730 735

Gln Gln Thr Gln Arg Ser Gly Lys Ile Asn Thr Asp Phe Met Arg Gln
740 745 750

Leu Thr Ala Ser Leu Asn Arg Ser Gln Gln Ala Ser Lys Lys Ala Leu
755 760 765

Met Glu Arg Ala Arg Ser Asp Glu Arg Glu Glu Gln Glu Glu Arg Arg
770 775 780

Gln Ala Gln Arg
785

<210> 282

<211> 266

<212> PRT

<213> Streptococcus agalactiae

<400> 282

Met Lys Lys Asn Lys Phe Leu Leu Val Ser Ile Val Phe Ile Ile Ile
1 5 10 15

Phe Val Val Gln Pro Gln Asn Phe Gln Ser Leu Lys Asn Ile Phe Thr
20 25 30

Gln Asn Asp Ile Ala Ser Gln Leu Asn Ile Ser Ser Ser Pro Glu Glu
35 40 45

Lys Asn Asp Gly Leu Gly Thr Ala Tyr Gln Thr Gln Asn Glu Asp Leu
50 55 60

Lys Ser Lys Ser Phe Asp Gly Gln His Gln Val Ile Val Val Asn Glu
65 70 75 80

Lys Ala Gln Phe Thr Ala Glu Glu Leu Ser Met Arg Asn Gly Ser Trp
85 90 95

Glu Lys Tyr Asp Asn Leu Asp Phe Leu Asn Arg Val Gly Val Ala Glu
100 105 110

Ala Met Leu Gly Lys Glu Leu Met Pro Lys Glu Ala Arg Gln Asp Ile
115 120 125

Ser Ser Val Lys Pro Thr Gly Trp Lys Asn Lys Lys Ile Thr Phe Asn
130 135 140

Gly Lys Gln Asp Tyr Leu Tyr Asn Arg Ser His Leu Ile Gly Phe Gln
145 150 155 160

Leu Ser Gly Glu Asn Ala Asn Val Lys Asn Leu Phe Thr Gly Thr Arg
165 170 175

Ala Leu Asn Ala Asn Phe Asn Asp Asp Lys Ser Ser Met Val Tyr Tyr
180 185 190

Glu Asn Glu Val Ala Asn Tyr Ile Lys Lys Thr Asn His His Val Arg
195 200 205

Tyr Arg Val Thr Pro Leu Phe Lys Asn Val Glu Leu Val Ala Arg Gly
210 215 220

Val Arg Ile Glu Ala Gln Ser Ile Glu Asp Glu Thr Ile Ser Phe Asp
225 230 235 240

Val Tyr Ile Phe Asn Gly Gln Pro Gly Tyr Asp Ile Asp Tyr Leu Thr
245 250 255

Gly Ser Ser Glu Lys Ile Met Ile Thr Lys
260 265

<210> 283

<211> 115

<212> PRT

<213> Streptococcus agalactiae

<400> 283

Val Thr Lys Glu Ile Lys Ile Arg Ser Ile Pro Glu Lys Thr Trp Ala
1 5 10 15

Gln Leu His Met Ile Ser Glu Glu Tyr Glu Tyr Pro Ser Phe Asn Glu
20 25 30

Phe Met Leu Ala Gln Leu Gln Arg Ile Val Glu Asn Gly Gly Leu Asp
35 40 45

Leu Tyr Asp Asn Lys Phe Ala Glu Thr Leu Ala Val Ile Lys Glu Gln
50 55 60

Gln Ala Gln Ile Leu Asp Gln Leu Leu Lys Asn Glu Ile Lys Leu Leu
65 70 75 80

Ala Tyr His Ala Lys Gln Asp Ile Val Glu Glu Leu Thr Thr Asp Trp
85 90 95

Leu Arg Phe Met Asp Asp Val Asp Ala Leu Ala Ala Glu Arg Gly Ala
100 105 110

Gly Gly Arg
115

<210> 284

<211> 280

<212> PRT

<213> Streptococcus agalactiae

<400> 284

Leu Leu Tyr Tyr Phe Ile Tyr Leu Ile Lys Val Ile Gly Asn Gly Leu
1 5 10 15

Lys Leu Ser Leu Ile Cys Gly Leu Asn Trp Leu Ile Lys Ile Val Phe
20 25 30

Lys Gly Gln Phe Tyr Leu Phe Ser Ala Val Phe Cys Gly Leu Leu Thr
35 40 45

Tyr Tyr Met Pro Gln Asp Ile Gln Leu Phe Thr Val Arg Val Leu Glu
50 55 60

Leu Ile Ile Met Leu Lys Val Ile Ile Asp Val Thr His Thr Ala Leu
65 70 75 80

Ser Arg Asp Phe Lys Arg Met Lys Thr Pro Leu Phe Leu Gly Val Met
85 90 95

Tyr Val Phe Phe Leu Ala Gly Asn Ser Tyr Ile Lys Ala His Leu Leu
100 105 110

Thr Glu Val Met Val Asn His Leu Ile Ser Phe Trp Leu Ile Ser Leu
115 120 125

Phe Phe Ala Thr Leu Val Ile Val Ile Gln Pro Arg Leu Phe Lys His
130 135 140

Tyr Leu Leu Lys Lys Val Ile Asp Lys Glu Tyr Leu Gly Ile Arg Lys
145 150 155 160

Phe Thr Asp Ser Leu Pro Pro Glu Ile Asn Leu Tyr Lys Asp Ala Asp
165 170 175

Glu Glu Asp Ala Asp Lys Arg Met Arg Leu Ile Asn Gln Asn Val Ile
180 185 190

Lys His Pro Tyr Gln Glu Val Val Glu Leu Ser Phe Leu Asn Arg Glu
195 200 205

Val Ile Thr Ala Ile Gly Tyr Lys Ala Val Pro Phe Glu Lys Glu Thr
210 215 220

Glu Arg Thr Phe Ile Asp Asp Asp Thr Ile Tyr Tyr Pro Ile Phe Thr
225 230 235 240

Val His Pro Phe Arg Asn Leu Glu Gly Lys Ser Asp Phe Tyr His Ile
245 250 255

Leu Met Lys Leu Lys Leu Ser Arg Lys Ala Ala Phe Thr Lys Asn Gly
260 265 270

Glu Arg Leu Leu Ile Arg Asp Phe
275 280

<210> 285

<211> 164

<212> PRT

<213> Streptococcus agalactiae

<400> 285

Met Ile Arg Asn Glu Phe Tyr Asn Gln Leu Ile Asn Ser Glu Pro Ile
1 5 10 15

Gly Phe Ile Asp Pro Phe Thr Asp Leu Gly Glu Phe Asp Ser Ile Gln
20 25 30

Met Lys Phe Lys Gln Pro Val Arg Asn Leu Val Asn Lys Tyr Ser Gly
35 40 45

Lys Pro Tyr Asn Leu Ser Trp Gln Asn Lys Ile Glu Gln Met Arg Val
50 55 60

Leu Tyr Ile Lys Tyr Gln Lys Ser Leu Lys Leu Glu Asp Glu Glu Gln
65 70 75 80

Glu Val His Asn Arg Val Lys Asn Lys Lys Ser Lys Lys Tyr Val His
85 90 95

Glu Ile Val Thr Thr Tyr Leu Lys Leu Gly Phe Arg Phe Lys Glu Ile
100 105 110

Glu Ala Arg Val Ser Leu Phe Asn Thr Arg Leu Arg Arg Asn Trp Lys
115 120 125

Arg Ser Asp Tyr Val Thr Thr Asp Asn Pro Glu Phe Tyr Leu Lys Lys
130 135 140

Asp Leu Gln Asn Gly Tyr Cys Ser Pro Asn Ser Phe Leu Pro Arg Ser
145 150 155 160

Met Lys Ile Asn

<210> 286

<211> 423

<212> PRT

<213> Streptococcus agalactiae

<400> 286

Met Asn Glu Ile Lys Cys Pro His Cys Gly Thr Ala Phe Ala Ile Asn
1 5 10 15

Glu Ser Glu Tyr His Gln Leu Leu Glu Gln Ile Arg Gly Asp Ala Phe
20 25 30

Asp Lys Glu Val Ser Glu Arg Leu Glu Lys Glu Arg Leu Ile Leu Gly
35 40 45

Glu Gln Ala Lys Asn Gln Leu Gln Glu Val Val Val Glu Lys Asp Lys
50 55 60

Glu Ile Ala Lys Leu Gln Tyr Lys Val Lys Gln Phe Leu Ile Glu Lys
65 70 75 80

Asp Asn Leu Leu Lys Asp Asn Glu Tyr Gln Leu Ala Glu Gln Leu Asn
85 90 95

Gln Lys Asp Met Met Leu Arg Asp Leu Glu Asn Gln Ile Asp Arg Leu
100 105 110

Arg Leu Glu His Glu Asn Ser Leu Gln Glu Ala Leu Thr Lys Val Glu
115 120 125

Arg Glu Arg Asp Ala Ile Gln Asn Gln Leu His Ile Gln Glu Lys Glu
130 135 140

Lys Asp Leu Ala Leu Ala Ser Val Lys Ser Asp Tyr Glu Val Gln Leu
145 150 155 160

Lys Ala Ala Asn Glu Gln Val Glu Phe Tyr Lys Asn Phe Lys Ala Gln
165 170 175

Gln Ser Thr Lys Ala Val Gly Glu Ser Leu Glu His Tyr Ala Glu Thr
180 185 190

Glu Phe Asn Lys Val Arg His Leu Ala Phe Pro Asn Ala Tyr Phe Glu
195 200 205

Lys Asp Asn Thr Leu Ser Ser Arg Gly Ser Lys Gly Asp Phe Ile Tyr
210 215 220

Arg Glu Lys Asp Glu Asn Asp Leu Glu Phe Leu Ser Ile Met Phe Glu
225 230 235 240

Met Lys Asn Glu Ser Asp Asp Thr Ile Lys Lys His Lys Asn Glu Asp
245 250 255

Phe Phe Lys Glu Leu Asp Lys Asp Arg Arg Glu Lys Ser Cys Glu Tyr
260 265 270

Ala Val Leu Val Thr Met Leu Glu Ala Asp Asn Asp Tyr Tyr Asn Thr
275 280 285

Gly Ile Val Asp Val Ser His Lys Tyr Pro Lys Met Tyr Val Ile Arg
290 295 300

Pro Gln Phe Phe Ile Gln Leu Ile Gly Ile Leu Arg Asn Ala Ala Leu
305 310 315 320

Asn Thr Leu Lys Tyr Lys Gln Glu Leu Ala Leu Met Lys Glu Gln Asn
325 330 335

Ile Asp Ile Thr His Phe Glu Glu Asp Leu Asp Ile Phe Lys Asn Ala
340 345 350

Phe Ala Lys Asn Tyr Asn Ser Ala Ser Lys Asn Phe Gln Lys Ala Ile
355 360 365

Asp Glu Ile Asp Lys Ser Ile Lys Arg Met Glu Ala Val Lys Ala Ala
370 375 380

Leu Thr Thr Ser Glu Asn Gln Leu Arg Leu Ala Asn Asn Lys Leu Asp
385 390 395 400

Asp Val Ser Val Lys Lys Leu Thr Arg Lys Asn Pro Thr Met Lys Ala
405 410 415

Lys Phe Asp Ala Leu Lys Asp
420

<210> 287

<211> 280

<212> PRT

<213> Streptococcus agalactiae

<400> 287

Met Asn His Phe Glu Leu Phe Lys Leu Lys Lys Ala Gly Leu Thr Asn
1 5 10 15

Leu Asn Ile Asn Asn Ile Ile Asn Tyr Leu Lys Lys Asn Ser Leu Thr
20 25 30

Ser Leu Ser Val Arg Asn Met Ala Val Val Ser Lys Cys Lys Asn Pro
35 40 45

Thr Phe Phe Ile Glu Asn Tyr Lys Gln Leu Asp Leu Lys Lys Leu Arg
50 55 60

Gln Glu Phe Lys Lys Phe Pro Val Leu Ser Ile Leu Asp Ser Asn Tyr
65 70 75 80

Pro Leu Glu Leu Lys Glu Ile Tyr Asn Pro Pro Val Leu Leu Phe Tyr
85 90 95

Gln Gly Asn Ile Glu Leu Leu Ser Lys Pro Lys Leu Ala Val Val Gly
100 105 110

Ala Arg Gln Ala Ser Gln Ile Gly Cys Gln Ser Val Lys Lys Ile Ile
115 120 125

Lys Glu Thr Asn Asn Gln Phe Val Ile Val Ser Gly Leu Ala Arg Gly
130 135 140

Ile Asp Thr Ala Ala His Val Ser Ala Leu Lys Asn Gly Gly Ser Ser
145 150 155 160

Ile Ala Val Ile Gly Ser Gly Leu Asp Val Tyr Tyr Pro Thr Glu Asn
165 170 175

Lys Lys Leu Gln Glu Tyr Met Ser Tyr Asn His Leu Val Leu Ser Glu
180 185 190

Tyr Phe Thr Gly Glu Gln Pro Leu Lys Phe His Phe Pro Glu Arg Asn
195 200 205

Arg Ile Ile Ala Gly Leu Cys Gln Gly Ile Val Val Ala Glu Ala Lys
210 215 220

Met Arg Ser Gly Ser Leu Ile Thr Cys Glu Arg Ala Leu Glu Glu Gly
225 230 235 240

Arg Glu Val Phe Ala Ile Pro Gly Asn Ile Ile Asp Gly Lys Ser Asp
245 250 255

Gly Cys His His Leu Ile Gln Glu Gly Ala Lys Cys Ile Ile Ser Gly
260 265 270

Lys Asp Ile Leu Ser Glu Tyr Gln
275 280

<210> 288

<211> 118

<212> PRT

<213> Streptococcus agalactiae

<400> 288

Met Thr Glu Arg Thr Phe Glu Asp Ile Glu Leu Asp Leu Lys Leu Phe
1 5 10 15

Gln Ile Lys Leu Asp Asn Ala Glu Asn Ser Lys Arg Leu Leu Gln Lys
20 25 30

Leu Lys Asn Asp Val Met Glu Leu Gln Ile Glu Leu Leu Glu Ser Leu
35 40 45

Lys Leu Gly Asp Ala Tyr Leu Thr Glu Ser Glu Glu Leu Glu Glu Asn
50 55 60

Asn Asp Phe Ile Leu Thr Val Asn Ser Glu Thr Leu Ser Leu Ser Tyr
65 70 75 80

Asp Asn Arg Ile Asn Leu Val Ser Lys Glu Ile Met Asp Tyr Glu Asn
85 90 95

Ala Leu Asp Lys Leu Tyr Tyr Glu Lys Gln Ser Leu Met Gln Lys Ser
100 105 110

Asn Glu Arg Lys Gly Gly
115

<210> 289

<211> 410

<212> PRT

<213> Streptococcus agalactiae

<400> 289

Leu Phe Asn Lys Ile Gly Phe Arg Thr Trp Lys Ser Gly Lys Leu Trp
1 5 10 15

Leu Tyr Met Gly Val Leu Gly Ser Thr Ile Ile Leu Gly Ser Ser Pro
20 25 30

Val Ser Ala Met Asp Ser Val Gly Asn Gln Ser Gln Gly Asn Val Leu
35 40 45

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
50 55 60

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
65 70 75 80

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
85 90 95

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
100 105 110

Glu Arg Arg Gln Arg Asp Val Glu Asn Lys Ser Gln Gly Asn Val Leu
115 120 125

Glu Arg Arg Gln Arg Asp Ala Glu Asn Lys Ser Gln Gly Asn Val Leu
130 135 140

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
145 150 155 160

Glu Arg Arg Gln Arg Asp Val Glu Asn Lys Ser Gln Gly Asn Val Leu
165 170 175

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
180 185 190

Glu Arg Arg Gln Arg Asp Val Glu Asn Lys Ser Gln Gly Asn Val Leu
195 200 205

Glu Arg Arg Gln Arg Asp Val Glu Asn Lys Ser Gln Gly Asn Val Leu
210 215 220

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
225 230 235 240

Glu Arg Arg Gln Arg Asp Val Glu Asn Lys Ser Gln Gly Asn Val Leu
245 250 255

Glu Arg Arg Gln Arg Asp Val Glu Asn Lys Ser Gln Gly Asn Val Leu
260 265 270

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
275 280 285

Glu Arg Arg Gln Arg Asp Ala Glu Asn Arg Ser Gln Gly Asn Val Leu
290 295 300

Glu Arg Arg Gln Arg Asp Ala Glu Asn Lys Ser Gln Val Gly Gln Leu
305 310 315 320

Ile Gly Lys Asn Pro Leu Leu Ser Lys Ser Ile Ile Ser Arg Glu Asn
325 330 335

Asn His Ser Ser Gln Gly Asp Ser Asn Lys Gln Ser Phe Ser Lys Lys
340 345 350

Val Ser Gln Val Thr Asn Val Ala Asn Arg Pro Met Leu Thr Asn Asn
355 360 365

Ser Arg Thr Ile Ser Val Ile Asn Lys Leu Pro Lys Thr Gly Asp Asp
370 375 380

Gln Asn Val Ile Phe Lys Leu Val Gly Phe Gly Leu Ile Leu Leu Thr
385 390 395 400

Ser Arg Cys Gly Leu Arg Arg Asn Glu Asn
405 410

<210> 290

<211> 573

<212> PRT

<213> Streptococcus agalactiae

<400> 290

Met Lys Arg Leu Thr Tyr Tyr Phe Lys Gly Tyr Ile Lys Glu Thr Ile
1 5 10 15

Phe Gly Pro Leu Phe Lys Leu Leu Glu Ala Ser Phe Glu Leu Leu Val
20 25 30

Pro Ile Val Ile Ala Lys Met Ile Asp Glu Thr Ile Pro Arg Gly Asp
35 40 45

Arg Ser Ser Leu Leu Leu Gln Ile Gly Leu Ile Phe Phe Leu Ala Ala
50 55 60

Val Gly Val Val Val Ala Ile Thr Ala Gln Tyr Tyr Ser Ser Lys Ala
65 70 75 80

Ala Val Gly Tyr Thr Arg Gln Leu Thr Glu Asp Leu Tyr Gln Lys Val
85 90 95

Met Ser Leu Gly Lys Lys Asp Arg Asp Glu Leu Gly Thr Ala Ser Leu
100 105 110

Ile Thr Arg Leu Thr Ala Asp Thr Phe Gln Ile Gln Thr Gly Leu Asn
115 120 125

Gln Phe Leu Arg Leu Phe Leu Arg Ala Pro Ile Ile Val Phe Gly Ala
130 135 140

Ile Ile Met Ala Phe Ser Ile Ser Pro Ser Leu Thr Ile Trp Phe Leu
145 150 155 160

Val Met Val Val Thr Leu Phe Ile Ile Val Phe Val Met Ser Arg Leu
165 170 175

Leu Asn Pro Ile Tyr Leu Lys Ile Arg Thr Ser Thr Asp Tyr Leu Val
180 185 190

Lys Leu Thr Arg Gln Gln Leu Gln Gly Val Arg Val Ile Arg Ala Phe
195 200 205

Asn Gln Val Asp Arg Glu Ser Glu Ala Phe Asn Asp Ile Asn Tyr His
210 215 220

Tyr Thr Asn Leu Gln Leu Lys Ala Gly Arg Leu Ser Ser Leu Val Thr
225 230 235 240

Pro Leu Thr Phe Leu Val Val Asn Ile Thr Leu Val Val Ile Ile Trp
245 250 255

Arg Gly Asn Leu Asn Ile Ala Asn His Leu Leu Ser Gln Gly Met Leu
260 265 270

Val Ala Leu Ile Asn Tyr Leu Leu Gln Ile Leu Val Glu Leu Leu Lys
275 280 285

Met Thr Met Leu Val Thr Ser Leu Asn Gln Ser Tyr Ile Ser Ala Lys
290 295 300

Arg Ile Ile Ala Val Phe Glu Arg Pro Ser Glu Ile Ile Asp Asp Lys
305 310 315 320

Leu Glu Pro Lys Tyr Ser Asn Lys Ala Leu Glu Val Gln Glu Met Ala
325 330 335

Phe Ser Tyr Pro Asn Ser Ser Glu Lys Ala Leu Ser Asp Ile Thr Phe
340 345 350

Ser Met Asn Val Gly Glu Thr Leu Gly Ile Ile Gly Gly Thr Gly Ser
355 360 365

Gly Lys Ser Thr Leu Val Asn Leu Leu Leu His Ile Tyr Lys Val Gln
370 375 380

Glu Gly Asp Ile Asp Ile Tyr His Gln Gly Lys Ser Pro Asp Thr Ile
385 390 395 400

Ser Asn Trp Arg Thr Leu Val Arg Val Val Pro Gln Asn Ala Gln Leu
405 410 415

Phe Lys Gly Thr Ile Arg Ser Asn Leu Ser Leu Gly Leu Gly Lys Val
420 425 430

Ser Glu Glu Lys Leu Trp Thr Ala Leu Glu Ile Ala Gln Ala Ser Asp
435 440 445

Phe Val Lys Glu Lys Asp Gly Gln Leu Asp Ala Pro Val Glu Ser Phe
450 455 460

Gly Arg Asn Phe Ser Gly Gly Gln Arg Gln Arg Leu Thr Ile Ala Arg
465 470 475 480

Ala Leu Val Gln Asp Lys Ile Pro Phe Leu Ile Leu Asp Asp Ala Thr
485 490 495

Ser Ala Leu Asp Tyr Leu Thr Glu Ala Arg Leu Phe Lys Ala Ile Thr
500 505 510

Lys His Phe Asn Gln Thr Asn Leu Ile Ile Val Ser Gln Arg Ile Asn
515 520 525

Ser Ile Gln Asn Ala Asp Arg Ile Leu Leu Leu Asp Lys Gly Lys Gln
530 535 540

Val Gly Phe Asp Asn His Gln Ser Leu Leu Ala His Asn Lys Val Tyr
545 550 555 560

Lys Ser Ile Tyr His Ser Gln Asn Phe Lys Glu Glu Glu
565 570

<210> 291

<211> 424

<212> PRT

<213> Streptococcus agalactiae

<400> 291

Met Lys Phe Asn Glu Gln Ser Asn Ser Gln Ala Ala Leu Leu Gly Leu
1 5 10 15

Gln His Leu Leu Ala Met Tyr Ala Gly Ser Ile Leu Val Pro Ile Met
20 25 30

Ile Ala Ser Ala Leu Gly Tyr Asn Ala Glu Gln Leu Thr Tyr Leu Ile
35 40 45

Ala Thr Asp Ile Phe Met Cys Gly Ile Ala Thr Leu Leu Gln Leu Gln
50 55 60

Leu Ser Lys His Phe Gly Val Gly Leu Pro Val Val Leu Gly Cys Ala
65 70 75 80

Phe Gln Ser Val Ala Pro Leu Ser Ile Ile Gly Ala Gln Gln Gly Ser
85 90 95

Gly Tyr Met Phe Gly Ala Leu Ile Ala Ser Gly Ile Tyr Val Val Leu
100 105 110

Val Ala Gly Ile Phe Ser Lys Val Ala Asn Phe Phe Pro Pro Ile Val
115 120 125

Thr Gly Ser Val Ile Thr Thr Ile Gly Leu Thr Leu Ile Pro Val Ala
130 135 140

Met Gly Asn Met Gly Asp Asn Ala Lys Glu Pro Ser Leu Gln Ser Leu
145 150 155 160

Thr Leu Ser Leu Val Thr Ile Gly Val Val Leu Leu Ile Asn Ile Phe
165 170 175

Ala Lys Gly Phe Leu Lys Ser Ile Ser Ile Leu Ile Gly Leu Ile Ser
180 185 190

Gly Thr Ile Leu Ala Ala Phe Met Gly Leu Val Asp Ala Ser Val Val
195 200 205

Ala Glu Ala Pro Leu Val His Ile Pro Lys Pro Phe Tyr Phe Gly Ala
210 215 220

Pro Arg Phe Glu Phe Thr Ser Ile Leu Met Met Cys Ile Ile Ala Thr
225 230 235 240

Val Ser Met Val Glu Ser Thr Gly Val Tyr Leu Ala Leu Ser Asp Ile
245 250 255

Thr Asn Asp Lys Leu Asp Ser Lys Arg Leu Arg Asn Gly Tyr Arg Ser
260 265 270

Glu Gly Leu Ala Val Leu Leu Gly Gly Leu Phe Asn Thr Phe Pro Tyr
275 280 285

Thr Gly Phe Ser Gln Asn Val Gly Leu Val Gln Ile Ser Gly Ile Arg
290 295 300

Thr Arg Lys Pro Ile Tyr Phe Thr Ala Leu Phe Leu Val Ile Leu Gly
305 310 315 320

Leu Leu Pro Lys Phe Gly Ala Met Ala Gln Met Ile Pro Ser Pro Val
325 330 335

Leu Gly Gly Ala Met Leu Val Leu Phe Gly Met Val Ala Leu Gln Gly
340 345 350

Met Lys Met Leu Asn Gln Val Asp Phe Glu His Asn Glu His Asn Phe
355 360 365

Ile Ile Ala Ala Val Ser Ile Ala Ala Gly Val Gly Phe Asn Gly Thr
370 375 380

Asn Leu Phe Ile Ser Leu Pro Asn Thr Leu Gln Met Phe Leu Thr Asn
385 390 395 400

Gly Ile Val Ile Ser Thr Leu Thr Ala Val Val Leu Asn Ile Ile Leu
405 410 415

Asn Gly Leu Pro Lys Lys Leu Ile
420

<210> 292

<211> 1078

<212> PRT

<213> Streptococcus agalactiae

<400> 292

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Met Ala Asn Thr Tyr Asp Leu Ile Ser Gln Arg Ile Glu Ala Gln Arg
1               5                   10                  15

Gln Lys Leu Ile Ala Ile Asp Ile Val Ala Val Ala Ser Ser Leu Gly
            20                  25                  30

Leu Asn Leu Lys Gln Gly Ser Gly Gly His Leu Tyr Trp Asp Glu His
        35                  40                  45

Asp Ser Phe His Ile Tyr Pro Gln Thr Asn Thr Phe Arg Trp Trp Ser
    50                  55                  60

Arg Ser Met Gly Thr Asn Thr Ile Asp Leu Val Gln Val Ile Gln Glu
65                  70                  75                  80

Glu Leu Thr Gly Lys Lys Pro Ser Phe Arg Glu Thr Val Asn Phe Leu
                85                  90                  95

Glu Thr Gly Gln Phe Glu Ser Val Thr Val Thr Pro Val Val Arg Glu
            100                 105                 110

Pro Phe Lys His Tyr Leu Ala Pro Tyr Glu His His Asn Phe Asp Leu
        115                 120                 125

Gly Arg Gln Tyr Leu Lys Glu Glu Arg Gly Leu Ser Asp Glu Thr Ile
    130                 135                 140

Asp Phe Ala Leu Ala Ser Gly Ser Met Ser Ser Ala Thr Leu Lys Lys
145                 150                 155                 160

Gly Asp Tyr Phe Glu Pro Val Ile Ile Phe Lys Ser Phe Ala Glu Asp
                165                 170                 175

Gly Arg Met Ile Gly Gly Ser Leu Gln Gly Ile Val Glu Asn Lys Val
            180                 185                 190

Gln His Pro Glu Arg Gly Arg Leu Lys Gln Ile Met Lys His Ser Asp
        195                 200                 205

Gly Leu Ala Gly Phe His Leu Asp Val Gly Thr Pro Lys Arg Leu Val
    210                 215                 220
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Phe Ser Glu Ala Pro Ile Asp Leu Leu Ser Tyr Tyr Glu Leu His Lys
225 230 235 240

Glu Ser Leu Gln Asn Val Arg Leu Val Ala Met Asp Gly Val Lys Lys
245 250 255

Gly Val Ile Ser Arg Tyr Thr Ala Asp Leu Leu Thr Asp Gly Gln Tyr
260 265 270

Ser Gln Thr Met Pro Arg Glu Ser Ile Arg Gly Ala Ile Asp Ala Ile
275 280 285

Asn Gln Thr Thr Arg Ile Leu Lys Asn Asn Pro Asn Met Ile Thr Ile
290 295 300

Ala Val Asp Asn Asp Glu Ala Gly Arg Asn Phe Ile Lys Glu Leu Gln
305 310 315 320

Glu Asp Gly Ile Pro Ile Asn Val Asp Leu Pro Pro Arg Lys Glu His
325 330 335

Gln Ser Lys Met Asp Trp Asn Asn Tyr Leu Lys Gln Lys Lys Gly Leu
340 345 350

Leu Lys Met Pro Gln Thr Glu Gly Thr Gln Lys Ala Pro Glu Gln Val
355 360 365

Leu Glu His Glu Lys Met Asp Arg Ser Gln Ile Ser Ser Gly Ser Leu
370 375 380

Glu Asp Asp Pro Gln Gly Ser Ala Lys Pro Val Ser Lys Arg Asp Thr
385 390 395 400

Phe Glu Gln Ala Val Thr Ser His Pro Thr Phe Ser Tyr Pro Leu Leu
405 410 415

Gln Phe Ser Thr Glu Glu Ala Phe Val Ser Asn Val Arg Asp Gly Tyr
420 425 430

His Ile Ala Ser Glu Glu Asp Ile Arg Asn Leu Asn Tyr Tyr Ala Pro
435 440 445

Ser Leu Gln Gln Thr Ala Asn Trp Tyr Arg Asp Asn Leu Ala Asp Arg
450 455 460

Gln Val Thr Tyr Met Leu Lys Gly Asp Lys Glu Ile Lys Ala Leu Gln
465 470 475 480

Val Ser Phe Ala Lys Asp Lys Phe Ala His Leu Thr Gly Ile Arg Pro
485 490 495

Ile Gly Lys Gly Leu Ser Ala Glu Lys Leu Leu Asp Asp Phe Ala Lys
500 505 510

Gly Arg Gly Ser Tyr Pro Asn Leu Thr Leu Ser Asn Gly Phe Asn Asp
515 520 525

Lys Ile Gln Val Leu Pro Met Ile Gln Glu Leu Ser Gln Ser Lys Ser
530 535 540

Phe Val Phe Thr Asp Leu Glu Glu Val Gln Lys Met Arg Asn Leu Lys
545 550 555 560

Ala Ser His Ala Ile Gln Ser Asn Asn Arg Ser Leu Val Val Ala Leu
565 570 575

Lys Thr Ile Asp Asp Val Thr Phe Pro Ser Ser Leu Leu Arg Gly Lys
580 585 590

Lys Asn Leu Asn Asp Asp Leu Ile Gln Lys Ala Lys Glu Asn Glu Val
595 600 605

Leu Gly Val Leu Ser Glu Lys Asp Gly Asn Ile Thr Val Leu Ser Val
610 615 620

Asn Asp Lys Tyr Ile Gln Asp Gly Gly Gln Ala Leu Lys Asp Met Ile
625 630 635 640

Lys Asn Gly Glu Leu Glu Pro Leu Gln Met Glu Thr Ile Gln Arg His
645 650 655

Val Pro His Glu Asn Ala Tyr Pro Lys Asp Ser Asp Gly Asp Gly Leu
660 665 670

Thr Asp Asp Glu Glu Ile Ala Leu Gly Thr Asn Pro Phe Ser Ser Asp
675 680 685

Ser Asp Gly Asp Gly Thr Pro Asp Asn Val Glu Lys Ala Asn Gly Thr
690 695 700

Asp Pro Thr Asn Ala Ser Asp Asn Glu Val Thr Arg Gln Gln Glu Ala
705 710 715 720

Asn Lys Arg Asp Phe Thr Leu Ser Glu Met Ile Lys Ala Lys Asn Thr
725 730 735

Ala Ala Leu Asn Gln His Leu Gln Asp Gly Ile Lys Gln Tyr Phe Asp
740 745 750

Ser Asp Thr Tyr Lys Gln Tyr Leu Glu Gly Met Ala His Phe Asn Asn
755 760 765

Tyr Ser Pro Arg Asn Ile Gln Leu Ile Met Ser Gln Phe Pro Glu Ala
770 775 780

Ser Met Val Ala Ser Phe Gln Glu Trp Arg Lys Arg Asn Gly Ser Val
785 790 795 800

Lys Lys Gly Glu Lys Ala Ile Tyr Ile Gln Ala Pro Val Ser Val Met
805 810 815

Lys Lys Asp Glu Asn Gly Lys Pro Ile Leu Asn Pro Glu Thr Gly Glu
820 825 830

Lys Glu Thr Ile Thr Tyr Phe Lys Pro Val Pro Val Phe Asp Ile Lys
835 840 845

Gln Val Ser Pro Gln Glu Gly Lys Glu Leu Asn Leu Pro Lys Ala Met
850 855 860

Gly Thr Ile Pro Glu Gln Leu Asp Lys Glu Tyr Tyr Gln Asn Val Tyr
865 870 875 880

Arg Ser Leu Arg Asp Ile Ser Gln Asn Asn Asn Lys Val Pro Ile Arg
885 890 895

Phe Arg Glu Leu Gly Gln Glu Asp Gly Phe Tyr Ser Pro Gln Thr Asn
900 905 910

Glu Ile Val Ile Lys Lys Gly Met Ser Tyr Glu Arg Thr Leu Ser Thr
915 920 925

Leu Ile His Glu Met Ala His Ser Glu Leu His Asn Lys Gln Ser Leu
930 935 940

Thr Glu Arg Phe Asp Gly Lys Leu Thr Arg Ser Thr Lys Glu Leu Gln
945 950 955 960

Ala Glu Ser Ile Ala Tyr Val Val Ser Ser His Leu Gly Phe Asp Thr
965 970 975

Ser Gln Glu Ser Phe Pro Tyr Leu Ala Ser Trp Ser Lys Glu Lys Asp
980 985 990

Gly Leu Ala Asn Leu Thr Ala Gln Leu Glu Ile Val Gln Glu Glu Ala
995 1000 1005

Lys Asn Leu Met Glu Arg Ile Asp Gln Gln Leu Ser Gln Tyr Gln
1010 1015 1020

Thr Val Thr Leu Asn Lys Glu Thr Gln Gln Leu Thr Lys Gln Glu
1025 1030 1035

Met Lys Lys Gln Thr His Pro Phe Tyr Gln Ser Leu Ala Ala Ala
1040 1045 1050

Lys Thr Ser Arg Ala Gln Val Thr Thr Gln Glu Lys Glu Ala Ser
1055 1060 1065

Val Lys Lys Asp Asn Arg Pro Thr Met Pro
1070 1075

<210> 293

<211> 932

<212> PRT

<213> Streptococcus agalactiae

<400> 293

Met Asn Ser Gln Glu Thr Lys Gly His Gly Phe Phe Arg Lys Ser Lys
1 5 10 15

Ala Tyr Gly Leu Val Cys Gly Ile Ala Leu Ala Gly Ala Phe Thr Leu
20 25 30

Ala Thr Ser Gln Val Ser Ala Asp Gln Val Thr Thr Gln Ala Thr Thr
35 40 45

Gln Thr Val Thr Gln Asn Gln Ala Glu Thr Val Thr Ser Thr Gln Leu
50 55 60

Asp Lys Ala Val Asp Thr Ala Lys Lys Ala Ala Val Ala Val Thr Thr
65 70 75 80

Thr Thr Ala Val Asn His Ala Thr Thr Thr Asp Ala Gln Ala Asp Leu
85 90 95

Ala Asn Gln Thr Gln Ala Val Lys Asp Val Thr Ala Lys Ala Gln Ala
100 105 110

Asn Thr Gln Ala Ile Lys Asp Ala Thr Ala Glu Asn Ala Lys Ile Asp
115 120 125

Ala Glu Asn Lys Ala Glu Ala Glu Arg Val Ala Lys Ala Asn Lys Ala
130 135 140

Gly Gln Ala Glu Val Asp Ala Arg Asn Lys Ala Gly Gln Ala Ala Val
145 150 155 160

Asp Ala Arg Asn Lys Ala Lys Gln Gln Ala Gln Asp Asp Gln Lys Ala
165 170 175

Lys Ile Asp Ala Glu Asn Lys Ala Glu Ser Gln Arg Val Ser Gln Leu
180 185 190

Asn Ala Gln Asn Lys Ala Lys Ile Asp Ala Glu Asn Lys Asp Ala Gln
195 200 205

Ala Lys Ala Asp Ala Thr Asn Ala Gln Leu Gln Lys Asp Tyr Gln Thr
210 215 220

Lys Leu Ala Asn Ile Lys Ser Val Glu Ala Tyr Asn Ala Gly Val Arg
225 230 235 240

Gln Arg Asn Lys Asp Ala Gln Ala Lys Ala Asp Ala Thr Asn Ala Gln
245 250 255

Leu Gln Lys Asp Tyr Gln Ala Lys Leu Ala Leu Tyr Asn Gln Ala Leu
260 265 270

Lys Ala Lys Ala Glu Ala Asp Lys Gln Ser Ile Asn Asn Val Ala Phe
275 280 285

Asp Ile Lys Ala Gln Ala Lys Gly Val Asp Asn Ala Glu Tyr Gly Asn
290 295 300

Ser Ile Met Thr Ala Lys Thr Lys Pro Asp Gly Ser Phe Glu Phe Asn
305 310 315 320

His Asp Met Ile Asp Gly Val Lys Thr Ile Gly Tyr Gly Lys Leu Thr
325 330 335

Gly Lys Val Asn His His Tyr Val Ala Asn Lys Asp Gly Ser Val Thr
340 345 350

Ala Phe Val Asp Ser Val Thr Leu Tyr Lys Tyr Glu Tyr Arg Asn Val
355 360 365

Ala Gln Asn Ala Ala Val Asn Gln Asn Ile Val Phe Arg Val Leu Thr
370 375 380

Lys Asp Gly Arg Pro Ile Phe Glu Lys Ala His Asn Gly Asn Lys Thr
385 390 395 400

Phe Ala Glu Thr Leu Asn Lys Thr Leu Gln Leu Asn Leu Lys Tyr Glu
405 410 415

Leu Lys Pro His Ala Ser Ser Gly Asn Val Glu Val Phe Lys Ile His
420 425 430

Asp Asp Trp Val His Asp Thr His Gly Ser Ala Leu Val Ser Tyr Val
435 440 445

Asn Asn Asn Asp Ala Val Pro Asn Val Val Ile Pro Glu Gln Pro Thr
450 455 460

Pro Pro Lys Pro Glu Lys Val Thr Pro Glu Ala Glu Lys Pro Val Pro
465 470 475 480

Glu Lys Pro Val Glu Pro Lys Leu Val Thr Pro Val Leu Lys Thr Tyr
485 490 495

Thr Pro Val Lys Phe Ile Pro Arg Glu Tyr Lys Pro Val Pro Ser Thr
500 505 510

Pro Glu Thr Phe Thr Pro Glu Lys Phe Thr Pro Ala Gln Pro Lys Val
515 520 525

Lys Pro His Val Ser Val Pro Glu Lys Ile Asn Tyr Lys Val Ala Val
530 535 540

His Pro Val Gln Ile Pro Lys Ala Thr Pro Thr Lys Lys Val Leu Asp
545 550 555 560

Glu Asn Gly Gln Ser Ile Asn Gly Lys Ser Val Leu Pro Asn Ala Thr
565 570 575

Leu Asp Tyr Val Ala Lys Gln Asn Phe Ser Gln Tyr Lys Gly Ile Lys
580 585 590

Ala Ser Ala Glu Ala Ile Ala Lys Gly Phe Ala Phe Val Asp Gln Pro
595 600 605

Asn Glu Ala Leu Ala Glu Leu Thr Val Lys Ser Ile Lys Ala Ser Asn
610 615 620

Gly Asp Asp Val Ser Ser Leu Leu Glu Met Arg His Val Leu Ser Lys
625 630 635 640

Asp Thr Leu Asp Gln Lys Leu Gln Ser Leu Ile Lys Glu Ala Gly Ile
645 650 655

Ser Pro Val Gly Glu Phe Tyr Met Trp Thr Ala Lys Asp Pro Gln Ala
660 665 670

Phe Tyr Lys Ala Tyr Val Gln Lys Gly Leu Asp Ile Thr Tyr Asn Leu
675 680 685

Ser Phe Lys Val Lys Lys Glu Phe Thr Lys Gly Gln Ile Lys Asn Gly
690 695 700

Val Ala Gln Ile Asp Phe Gly Asn Gly Tyr Thr Gly Asn Ile Val Val
705 710 715 720

Asn Asp Leu Thr Thr Pro Glu Val His Lys Asp Val Leu Asp Lys Glu
725 730 735

Asp Gly Lys Ser Ile Asn Asn Gly Thr Val Lys Leu Gly Asp Glu Val
740 745 750

Thr Tyr Lys Leu Glu Gly Trp Val Val Pro Ala Asn Arg Gly Tyr Asp
755 760 765

Leu Phe Glu Tyr Lys Phe Val Asp His Leu Gln His Thr His Asp Leu
770 775 780

Tyr Leu Lys Asp Lys Val Val Ala Lys Val Ala Ile Thr Leu Lys Asp
785 790 795 800

Gly Thr Val Ile Pro Lys Gly Thr Asn Leu Val Gln Tyr Thr Glu Thr
805 810 815

Val Tyr Asn Lys Glu Thr Gly Arg Tyr Glu Leu Ala Phe Lys Ala Asp
820 825 830

Phe Leu Ala Gln Val Ser Arg Ser Ser Ala Phe Gly Ala Asp Asp Phe
835 840 845

Ile Val Val Lys Arg Ile Lys Ala Gly Asp Val Tyr Asn Thr Ala Asp
850 855 860

Phe Phe Val Asn Gly Asn Lys Val Lys Thr Glu Thr Val Val Thr His
865 870 875 880

Thr Pro Glu Lys Pro Lys Pro Val Met Pro Gln Lys Val Thr Pro Lys
885 890 895

Ala Pro Ala Leu Pro Ser Thr Gly Glu Gln Gly Val Ser Val Leu Thr
900 905 910

Val Leu Gly Ala Ala Leu Leu Ser Leu Leu Gly Leu Val Gly Phe Lys
915 920 925

Lys Arg Gln Gln
930

<210> 294

<211> 743

<212> PRT

<213> Streptococcus agalactiae

<400> 294

Met Asn Gln Ile Lys Ile Ile Thr Gly Leu Thr Val Ala Thr Leu Ser
1               5                   10                  15

Ala Val Val Gly Asn Val Tyr Ala Glu Asp Ile Thr Pro Thr Ala Pro
            20                  25                  30

Val Asn Glu Pro Gln Val Ser Ser Glu Thr Ala Lys Thr Pro Gln Val
        35                  40                  45

Thr Glu Ser Gln Val Asn Ser Ala Lys Val Thr Ala Asp Gln Ala Thr
    50                  55                  60

Ser Asp Val Asn Ala Gln Lys Asn Val Val Asn Asn Ala Gln Asn Gln
65                  70                  75                  80

Lys Asn Gln Ala Gln Gln Lys Leu Val Asn Ala Thr Thr Thr Leu Asn
                85                  90                  95

Glu Thr Gln Lys Leu Val Gln Glu Ser Thr Asn Gln Asn Gln Val Gln
            100                 105                 110

Gln Thr Val Asp Ser Ala Lys Gln Arg Leu Ser Gln Thr Glu Ala Asn
        115                 120                 125

Gln Lys Ile Thr Gln Thr Glu Gln Val Lys Ala Gln Asn Gln Val Asn
    130                 135                 140

Ala Gln Gln Thr Val Val Val Asn Asn Glu His Asp Val Ala Thr Lys
145                 150                 155                 160

Thr Ala Asp Val Lys Gln Ala Gln Ala Ser Val Asp Thr Ala Lys Asp
                165                 170                 175

Ala Leu Thr Asn Thr Ile Val Asn Ser Asp Leu Asn Lys Ala Gln Ser
            180                 185                 190

Asn Val Thr Thr Lys Thr Ala Asp Val Lys Thr Ala Thr Asp Ala Leu
        195                 200                 205

Thr Lys Ala Gln Ala Thr Asp Lys Thr Leu Thr Asn Gln Lys Ala Lys
    210                 215                 220

Ala Gln Gln Ile Val Asp Ser Ala Lys Gln Asn Leu Ser Ala Lys Asp
225                 230                 235                 240

Thr Gln Leu Ser Gln Ala Asn Ala Glu Val Asn His His Lys Phe Lys
                245                 250                 255

Thr Ala Leu Gly Gln Ser His Tyr Tyr Asn Gln Arg Asp Asn Ala Trp
            260                 265                 270

Ala Gly Val Tyr Gly Gly His Thr Phe Ala Ser Thr Gly Cys Val Pro
275 280 285

Ser Ala Leu Ala Met Val Tyr Ser Asp Leu Ser Asn Arg Thr Ile Thr
290 295 300

Pro Arg Glu Ile Ala Asp Tyr Leu Tyr Asn Asn Thr Asp Glu Phe Asn
305 310 315 320

Lys Arg Phe Gly Gly Thr Ser Gly Lys Gly Ile Ile Ser Ala Thr Lys
325 330 335

Ala Phe Gly Tyr Val Val Thr His Leu Ala Ser Lys Asn Ala Ile Thr
340 345 350

Glu Ala Leu Lys Ala Gly His His Val Val Ala Ala Val Gln Asn Asn
355 360 365

Lys Phe Ser Pro Trp Gly Pro Gln Tyr Ser His Glu Ile Val Leu Arg
370 375 380

Gly Ser Ser Asn Gly Asn Thr Tyr Val Tyr Asp Pro Tyr Asn Arg Asp
385 390 395 400

Asn Asn Gly Phe Tyr Ser Val Asp Arg Ile Trp Asn Glu Gln Ser Arg
405 410 415

Asp Ser Ile Asp Thr Ala Gly Val Gly Val Pro Phe Phe Ala Ile Met
420 425 430

Thr Lys Asn Met Ala Asn Ala Leu Thr Lys Gln Ser Gln Ala Leu Ala
435 440 445

Ser Gln Gln Val Ala Gln Lys Gln Leu Asn Asp Ala Gln Ala Lys Ala
450 455 460

Thr Gly Leu Asn Ala Val Thr Met Gln Thr Pro Ile Ala Gln Ala Asn
465 470 475 480

Leu Ile Lys Ala Gln Ser Asn Leu Lys Asp Ala Gln Lys Arg Leu Ala
485 490 495

Glu Ala Gln Ala Ser Val Lys Leu Ala Asn Gln Asp Asn Val Lys Lys
500 505 510

Gln Ala Asp Leu Thr Lys Ala Glu Ser Lys Leu Lys Asp Ala Gln Lys
515 520 525

Gln Leu Ala Ala Ala Gln Ala Lys Leu Thr Thr Ser Lys Thr Lys Leu
530 535 540

Asn Gln Leu Lys Gln Val Leu Ala Glu Ala Ser Gln Gln Val Ala Gln
545 550 555 560

Ala Asn Gln Asp Tyr Lys Gln Ala Lys Asp Asn Leu Thr Gln Lys Thr
565 570 575

Ala Tyr Leu Thr Asn Leu Arg Asn Ala Gln Ala Asn Leu Ile Lys Ala
580 585 590

Gln Ser Asp Val Ala Gln Ala Lys Asp Asn Leu Ala Asn Lys Ile Ala
595 600 605

Lys Leu Gln Arg Glu Val Ala Tyr Leu Gln Glu Leu Lys Thr Lys Ala
610 615 620

Val Asp Ala Gln Ser Gln Tyr Gln Lys Val Leu Ser Ala Tyr Lys Ser
625 630 635 640

Val Leu Ser Ala Lys Ala Ser Leu Lys Leu Ala Glu Glu Lys Ala Arg
645 650 655

Leu Asp Lys Lys Gly His Glu Ala Val Ala Val Val Asp Glu Thr Gly
660 665 670

Lys Ile Thr Ser Tyr Ile Thr Ser Lys His Lys Ile Glu Met Lys Ser
675 680 685

Leu Val Ala Thr Lys Thr Thr Asp Val Lys Gln Val Ser Val Ala Lys
690 695 700

Ala Ser Val Leu Pro Ser Thr Gly Asp Val Lys Gln Val Ser Val Ala
705 710 715 720

Leu Leu Gly Met Leu Leu Thr Phe Ser Gly Phe Leu Gly Ile Arg Lys
725 730 735

Gln Ser Lys Lys Val Ile Asn
740

<210> 295

<211> 253

<212> PRT

<213> Streptococcus agalactiae

<400> 295

Met Ile Ser Arg Lys Val Ala Leu Val Thr Gly Ala Ser Ala Gly Phe
1 5 10 15

Gly Ala Ala Ile Val Thr Lys Leu Val Ser Asp Gly Tyr Ser Val Ile
20 25 30

Gly Cys Ala Arg Arg Met Asp Lys Leu Lys Cys Phe Gly Glu Lys Phe
35 40 45

Ser Glu Gly Tyr Phe Tyr Pro Leu Gln Met Asp Ile Thr Ser Arg Glu
50 55 60

Ser Val Asp Lys Ala Leu Glu Ser Leu Pro Lys Asn Leu Gln Ser Ile
65 70 75 80

Asp Leu Leu Val Asn Asn Ala Gly Leu Ala Leu Gly Leu Asp Lys Ser
85 90 95

Tyr Glu Ala Asp Phe Glu Asp Trp Met Thr Met Ile Asn Thr Asn Val
100 105 110

Val Gly Leu Ile Tyr Leu Thr Arg Cys Ile Leu Pro Lys Met Val Glu
115 120 125

Val Asn Arg Gly Leu Ile Ile Asn Leu Gly Ser Thr Ala Gly Thr Ile
130 135 140

Pro Tyr Pro Gly Ala Asn Val Tyr Gly Ala Ser Lys Ala Phe Val Lys
145 150 155 160

Gln Phe Ser Leu Asn Leu Arg Ala Asp Leu Ala Gly Thr Lys Ile Arg
165 170 175

Val Thr Asn Leu Glu Pro Gly Leu Cys Glu Gly Thr Glu Phe Ser Thr
180 185 190

Val Arg Phe Lys Gly Asp His Lys Arg Val Glu Lys Leu Tyr Glu Gly
195 200 205

Ala His Ala Ile Gln Ala Glu Asp Ile Ala Asn Thr Val Ser Trp Val
210 215 220

Ala Ser Gln Pro Glu His Ile Asn Ile Asn Arg Ile Glu Ile Met Pro
225 230 235 240

Val Ser Gln Thr Tyr Gly Pro Gln Pro Val Tyr Arg Asp
245 250

<210> 296

<211> 371

<212> PRT

<213> Streptococcus agalactiae

<400> 296

Met Ile Tyr Leu Asp Asn Ala Ala Thr Thr Ala Leu Thr Pro Ser Val
1 5 10 15

Ile Glu Lys Met Thr Asn Val Met Thr Ser Asn Tyr Gly Asn Pro Ser
20 25 30

Ser Ile His Thr Phe Gly Arg Gln Ala Asn Gln Leu Leu Arg Glu Cys
35 40 45

Arg Gln Ile Ile Ala Glu Tyr Leu Asn Val Asn Ser Arg Glu Ile Ile
50 55 60

Phe Thr Ser Gly Gly Thr Glu Ser Asn Asn Thr Ala Ile Lys Gly Tyr
65 70 75 80

Ala Leu Ala Asn Gln Leu Lys Gly Lys His Ile Ile Thr Ser Glu Ile
85 90 95

Glu His His Ser Val Leu His Thr Met Thr Tyr Leu Ser Glu Arg Phe
100 105 110

Gly Phe Asp Ile Thr Tyr Leu Lys Pro Asn His Gly Gln Ile Thr Ala
115 120 125

Lys Asp Val Gln Glu Ala Leu Arg Asp Asp Thr Ile Met Val Ser Leu
130 135 140

Met Phe Ala Asn Asn Glu Thr Gly Asp Phe Leu Pro Ile Gln Glu Ile
145 150 155 160

Gly Gln Leu Leu Arg Asn His Gln Ala Val Phe His Val Asp Ala Val
165 170 175

Gln Val Phe Ser Lys Met Glu Leu Asp Pro His Ser Leu Gly Ile Asp
180 185 190

Phe Leu Ala Ala Ser Ala His Lys Phe His Gly Pro Lys Gly Val Gly
195 200 205

Ile Leu Tyr Cys Ala Pro His His Phe Asp Ser Leu Leu His Gly Gly
210 215 220

Asp Gln Glu Glu Lys Arg Arg Ala Ser Thr Glu Asn Ile Ile Gly Ile
225 230 235 240

Ala Gly Met Ser Gln Ala Leu Thr Asp Ala Thr Thr Asn Thr Leu Lys
245 250 255

Asn Trp Thr His Ile Ser Gln Leu Arg Thr Thr Phe Leu Asp Ala Ile
260 265 270

Ser Asp Leu Asp Phe Tyr Leu Asn Asn Gly Gln Asp Cys Leu Pro His
275 280 285

Val Leu Asn Ile Gly Phe Pro Arg Gln Asn Asn Gly Leu Leu Leu Thr
290 295 300

Gln Leu Asp Leu Ala Gly Phe Ala Val Ser Thr Gly Ser Ala Cys Thr
305 310 315 320

Ala Gly Thr Val Glu Pro Ser His Val Leu Thr Ser Leu Tyr Gly Ala
325 330 335

Asn Ser Pro Arg Leu Asn Glu Ser Ile Arg Ile Ser Phe Ser Glu Leu
340 345 350

Asn Thr Gln Glu Glu Ile Leu Glu Leu Ala Lys Thr Leu Arg Lys Ile
355 360 365

Ile Gly Asp
370

<210> 297

<211> 447

<212> PRT

<213> Streptococcus agalactiae

<400> 297

Met Ser Arg Lys Thr Phe Lys His Ile Leu Ser Ile Gly Val Cys Thr
1 5 10 15

Leu Val Leu Ser Met Ser Leu Tyr Tyr Thr Glu Lys Ala His Ala Ile
20 25 30

Ala Gly Pro Ser Asp Arg Gln Tyr Val Glu Asn Pro Asn Pro His Ile
35 40 45

Ile Val Asn Val Thr Gly Thr Asp Gln Asn Gly Asn Ser Ile Leu Pro
50 55 60

His Tyr Ile Glu Val Asn Val Lys Met Gly Gln Thr Leu Ser Lys Glu
65 70 75 80

Glu Ile Leu Asp Tyr Ile Ala Arg Asn Leu Asn Ser Ser Val Gly Gly
85 90 95

Glu Ser Lys Asn Val Gln Tyr Ser Asn Ile Glu Phe Lys Glu Ser Ala
100 105 110

Tyr Leu Lys Arg Gln Leu Asp Asp Gly Lys Thr Glu Glu Ile Ala Ile
115 120 125

Asp Asn Asp Gly Val Thr Val Pro Lys Asp Gly Pro Asn Lys Phe Trp
130 135 140

Ile Asp Val Pro Val Thr Cys Thr Val Thr Pro Ile Val Thr Glu Thr
145 150 155 160

His Glu Val Arg Trp Gly Thr Pro Val Ala Ile Ser His Arg Ile Tyr
165 170 175

Phe Val Glu Glu Ser Ser Gly Lys Val Leu Asp Glu Tyr Thr Asn Leu
180 185 190

His Thr Ala Asp Ser Glu Leu Asn Gly Tyr Arg Val Gly Asp Tyr Ile
195 200 205

Thr Asp Tyr Ala Leu Ser Lys Ser Ala Tyr Glu Ala Phe Leu Asn Ser
210 215 220

Arg Leu Asp Lys Glu Gly Tyr Lys Leu Gln His Arg Ile Ser Thr Asn
225 230 235 240

Val Arg Gln Asn Leu Gln Ile Asp Lys Leu Ile Phe Asn Tyr Asp Phe
245 250 255

Asn Glu Glu Asn Ile Tyr Tyr Gln Ile Gly Asn Ile Arg Pro Leu Leu
260 265 270

Ser Arg Ser Ser Ala Glu Val Glu Ser Asp Ile Ile Thr Glu Arg Tyr
275 280 285

Tyr Val Ser Lys Asn Ala Lys Ser Leu Ala Arg Thr Glu Ser Thr Ile
290 295 300

Ser Ile Lys Met Val Asp Ala Lys Thr Glu Gln Pro Leu Phe Asn His
305 310 315 320

Thr Leu Thr Gly Tyr Gln Leu Ala Thr Val Ser His Val Tyr Asn Arg
325 330 335

Leu Phe Glu Glu Asn Leu Ile Pro Thr Thr Lys Ser Gly Glu Arg Tyr
340 345 350

Phe Ile Gln Asn Met Lys Lys Thr Ala Glu Gln Glu Tyr Thr Val Tyr
355 360 365

Leu Ser Glu Thr Pro Tyr Ser Lys Glu Asn Ala Pro Val Ile Ser Tyr
370 375 380

Asp Ala Arg Pro Val Asp Trp Asp Tyr His Ser Gly Ala Ser Gly Ser
385 390 395 400

Leu Glu Asn Gln Pro Asn Ile Tyr Thr Glu Glu Asp Ser Thr Glu Phe
405 410 415

Leu Gly Asn Lys Pro Gln Ala Ala Cys Tyr Pro Asn Lys Gln Phe Ala
420 425 430

Cys Glu Asn Thr Asp Ser Lys Tyr Asn Tyr Ser Tyr Leu Glu Lys
435 440 445

<210> 298

<211> 759

<212> PRT

<213> Streptococcus agalactiae

<400> 298

Met Asn Pro Leu Ile Ile Gly Met Asn Asp Lys Gln Ala Glu Ala Val
1 5 10 15

Gln Thr Thr Asp Gly Pro Leu Leu Ile Met Ala Gly Ala Gly Ser Gly
20 25 30

Lys Thr Arg Val Leu Thr His Arg Ile Ala Tyr Leu Ile Asp Glu Lys
35 40 45

Tyr Val Asn Pro Trp Asn Ile Leu Ala Ile Thr Phe Thr Asn Lys Ala
50 55 60

Ala Arg Glu Met Arg Glu Arg Ala Ile Ala Leu Asn Pro Ala Thr Gln
65 70 75 80

Asp Thr Leu Ile Ala Thr Phe His Ser Met Cys Val Arg Ile Leu Arg
85 90 95

Arg Glu Ala Asp Tyr Ile Gly Tyr Asn Arg Asn Phe Thr Ile Val Asp
100 105 110

Pro Gly Glu Gln Arg Thr Leu Met Lys Arg Ile Ile Lys Gln Leu Asn
115 120 125

Leu Asp Thr Lys Lys Trp Asn Glu Arg Ser Ile Leu Gly Thr Ile Ser
130 135 140

Asn Ala Lys Asn Asp Leu Leu Asp Glu Ile Ala Tyr Glu Lys Gln Ala
145 150 155 160

Gly Asp Met Tyr Thr Gln Val Ile Ala Lys Cys Tyr Lys Ala Tyr Gln
165 170 175

Glu Glu Leu Arg Arg Ser Glu Ala Met Asp Phe Asp Asp Leu Ile Met
180 185 190

Met Thr Leu Arg Leu Phe Asp Gln Asn Lys Asp Val Leu Ala Tyr Tyr
195 200 205

Gln Gln Arg Tyr Gln Tyr Ile His Val Asp Glu Tyr Gln Asp Thr Asn
210 215 220

His Ala Gln Tyr Gln Leu Val Lys Leu Leu Ala Ser Arg Phe Lys Asn
225 230 235 240

Ile Cys Val Val Gly Asp Ala Asp Gln Ser Ile Tyr Gly Trp Arg Gly
245 250 255

Ala Asp Met Gln Asn Ile Leu Asp Phe Glu Lys Asp Tyr Pro Gln Ala
260 265 270

Lys Val Val Leu Leu Glu Glu Asn Tyr Arg Ser Thr Lys Lys Ile Leu
275 280 285

Gln Ala Ala Asn Asn Val Ile Asn His Asn Lys Asn Arg Arg Pro Lys
290 295 300

Lys Leu Trp Thr Gln Asn Asp Glu Gly Glu Gln Ile Val Tyr His Arg
305 310 315 320

Ala Asn Asn Glu Gln Glu Glu Ala Val Phe Val Ala Ser Thr Ile Asp
325 330 335

Asn Ile Val Arg Glu Gln Gly Lys Asn Phe Lys Asp Phe Ala Val Leu
340 345 350

Tyr Arg Thr Asn Ala Gln Ser Arg Thr Ile Glu Glu Ala Leu Leu Lys
355 360 365

Ser Asn Ile Pro Tyr Thr Met Val Gly Gly Thr Lys Phe Tyr Ser Arg
370 375 380

Lys Glu Ile Arg Asp Val Ile Ala Tyr Leu Asn Ile Leu Ala Asn Thr
385 390 395 400

Ser Asp Asn Ile Ser Phe Glu Arg Ile Val Asn Glu Pro Lys Arg Gly
405 410 415

Val Gly Pro Gly Thr Leu Glu Lys Ile Arg Ser Phe Ala Tyr Glu Gln
420 425 430

Asn Met Ser Leu Leu Asp Ala Ser Ser Asn Val Met Met Ser Pro Leu
435 440 445

Lys Gly Lys Ala Ala Gln Ala Val Trp Asp Leu Ala Asn Leu Ile Leu
450 455 460

Thr Leu Arg Ser Lys Leu Asp Ser Leu Thr Val Thr Glu Ile Thr Glu
465 470 475 480

Asn Leu Leu Asp Lys Thr Gly Tyr Leu Glu Ala Leu Gln Val Gln Asn
485 490 495

Thr Leu Glu Ser Gln Ala Arg Ile Glu Asn Ile Glu Glu Phe Leu Ser
500 505 510

Val Thr Lys Asn Phe Asp Asp Asn Pro Glu Ile Thr Val Glu Gly Glu
515 520 525

Thr Gly Leu Asp Arg Leu Ser Arg Phe Leu Asn Asp Leu Ala Leu Ile
530 535 540

Ala Asp Thr Asp Asp Ser Ala Thr Glu Thr Ala Glu Val Thr Leu Met
545 550 555 560

Thr Leu His Ala Ala Lys Gly Leu Glu Phe Pro Val Val Phe Leu Ile
565 570 575

Gly Met Glu Glu Gly Val Phe Pro Leu Ser Arg Ala Ile Glu Asp Ala
580 585 590

Asp Glu Leu Glu Glu Glu Arg Arg Leu Ala Tyr Val Gly Ile Thr Arg
595 600 605

Ala Glu Gln Ile Leu Phe Leu Thr Asn Ala Asn Thr Arg Thr Leu Phe
610 615 620

Gly Lys Thr Ser Tyr Asn Arg Pro Thr Arg Phe Ile Arg Glu Ile Asp
625 630 635 640

Asp Glu Leu Ile Gln His Gln Gly Leu Ala Arg Pro Val Asn Ser Ser
645 650 655

Phe Gly Val Lys Tyr Ser Lys Glu Gln Pro Thr Gln Phe Gly Gln Gly
660 665 670

Met Ser Leu Gln Gln Ala Leu Gln Ala Arg Lys Ser Asn Ser Gln Pro
675 680 685

Gln Val Thr Ala Gln Leu Gln Ala Leu Asn Ala Asn Asn Ser His Glu
690 695 700

Thr Ser Trp Glu Ile Gly Asp Val Ala Thr His Lys Lys Trp Gly Asp
705 710 715 720

Gly Thr Val Leu Glu Val Ser Gly Ser Gly Lys Thr Gln Glu Leu Lys
725 730 735

Ile Asn Phe Pro Gly Ile Gly Leu Lys Lys Leu Leu Ala Ser Val Ala
740 745 750

Pro Ile Ser Lys Lys Glu Asn
755

<210> 299

<211> 130

<212> PRT

<213> Streptococcus agalactiae

<400> 299

Met Lys Leu Tyr Val Gln Leu Met Val Ile Leu Thr Phe Ser Phe Ala
1 5 10 15

Gly Glu Val Leu Ser Thr Ile Phe Asn Leu Pro Val Pro Gly Ser Ile
20 25 30

Ile Gly Leu Ile Leu Leu Phe Leu Ala Leu Lys Tyr Lys Ile Ile Arg
35 40 45

Leu Arg His Ile Asp Ala Val Gly Asn Phe Leu Leu Ala Asn Met Thr
50 55 60

Ile Leu Phe Leu Pro Pro Ala Val Gly Leu Met Glu His Phe Gln Asp
65 70 75 80

Ile Lys Pro Tyr Leu Phe Gly Ile Ala Ile Ile Ile Leu Gly Ala Leu
85 90 95

Phe Leu Asn Ile Leu Thr Ile Gly Leu Val Ser Gln Trp Ile Lys Lys
100 105 110

Arg Tyr Glu Gly Asp Tyr Pro Glu Ile Gly Gly Lys Asn Gly Asn Phe
115 120 125

Asn Glu
130

<210> 300

<211> 157

<212> PRT

<213> Streptococcus agalactiae

<400> 300

Met Ile Phe Val Thr Val Gly Thr His Glu Gln Gln Phe Asn Arg Leu
1               5                   10                  15

Ile Lys Glu Val Asp Arg Leu Lys Gly Thr Gly Ala Ile Asp Gln Glu
            20                  25                  30

Val Phe Ile Gln Thr Gly Tyr Ser Asp Phe Glu Pro Gln Asn Cys Gln
        35                  40                  45

Trp Ser Lys Phe Leu Ser Tyr Asp Asp Met Asn Ser Tyr Met Lys Glu
    50                  55                  60

Ala Glu Ile Val Ile Thr His Gly Gly Pro Ala Thr Phe Met Ser Val
65                  70                  75                  80

Ile Ser Leu Gly Lys Leu Pro Val Val Val Pro Arg Arg Lys Gln Phe
                85                  90                  95

Gly Glu His Ile Asn Asp His Gln Ile Gln Phe Phe Lys Lys Ile Ala
            100                 105                 110

His Leu Tyr Pro Leu Ala Trp Ile Glu Asp Val Asp Gly Leu Ala Glu
        115                 120                 125

Val Leu Lys Arg Asn Ile Ala Thr Glu Lys Tyr Gln Gly Asn Asn Asp
    130                 135                 140

Met Phe Cys His Lys Leu Glu Lys Ile Ile Gly Glu Ile
145                 150                 155

<210> 301

<211> 253

<212> PRT

<213> Streptococcus agalactiae

<400> 301

Met Val Met Lys Ile Ile Glu Leu Lys Glu Ala Thr Val Gln Val Ser
1               5                   10                  15

Asn Gly Leu Ala Glu Met Lys Thr Ile Leu Asp His Val Asn Leu Ser
20 25 30

Ile Tyr Glu His Asp Phe Ile Thr Ile Leu Gly Gly Asn Gly Ala Gly
35 40 45

Lys Ser Thr Leu Phe Asn Val Ile Ala Gly Thr Leu Met Leu Ser Gly
50 55 60

Gly Asn Ile Tyr Ile Met Gly Gln Asp Val Thr Asn Leu Pro Ala Glu
65 70 75 80

Lys Arg Ala Lys Tyr Leu Ser Arg Val Phe Gln Asp Pro Lys Met Gly
85 90 95

Thr Ala Pro Arg Met Thr Val Ala Glu Asn Leu Leu Val Ala Lys Phe
100 105 110

Arg Gly Glu Lys Arg Pro Leu Val Pro Arg Lys Ile Thr Asn Tyr Thr
115 120 125

Glu Glu Phe Gln Lys Leu Ile Ala Arg Thr Gly Asn Gly Leu Asp Arg
130 135 140

His Leu Glu Thr Pro Thr Gly Leu Leu Ser Gly Gly Gln Arg Gln Ala
145 150 155 160

Leu Ser Leu Leu Met Ala Thr Leu Lys Lys Pro Asn Leu Leu Leu Leu
165 170 175

Asp Glu His Thr Ala Ala Leu Asp Pro Arg Thr Ser Val Ser Leu Met
180 185 190

Gly Leu Thr Asp Glu Phe Ile Lys Gln Asp Ser Leu Thr Ala Leu Met
195 200 205

Ile Thr His His Met Glu Asp Ala Leu Lys Tyr Gly Asn Arg Ile Leu
210 215 220

Val Met Lys Asp Gly Lys Ile Val Arg Asp Leu Asn Gln Ala Gln Lys
225 230 235 240

Asn Lys Met Ala Ile Ala Asp Tyr Tyr Gln Leu Phe Asp
245 250

<210> 302

<211> 1072

<212> PRT

<213> Streptococcus agalactiae

<400> 302

Met Glu Ile Lys Lys Lys His Arg Ile Met Leu Tyr Ser Ala Leu Ile
1 5 10 15

Leu Gly Thr Ile Leu Val Asn Asn Ser Tyr Gln Ala Lys Ala Glu Glu
20 25 30

Leu Thr Lys Thr Thr Ser Thr Ser Gln Ile Arg Asp Thr Gln Thr Asn
35 40 45

Asn Ile Glu Val Leu Gln Thr Glu Ser Thr Thr Val Lys Glu Thr Ser
50 55 60

Thr Thr Thr Thr Gln Gln Asp Leu Ser Asn Pro Thr Ala Ser Thr Ala
65 70 75 80

Thr Ala Thr Ala Thr His Ser Thr Met Lys Gln Val Val Asp Asn Gln
85 90 95

Thr Gln Asn Lys Glu Leu Val Lys Asn Gly Asp Phe Asn Gln Thr Asn
100 105 110

Pro Val Ser Gly Ser Trp Ser His Thr Ser Ala Arg Glu Trp Ser Ala
115 120 125

Trp Ile Asp Lys Glu Asn Thr Ala Asp Lys Ser Pro Ile Ile Gln Arg
130 135 140

Thr Glu Gln Gly Gln Val Ser Leu Ser Ser Asp Lys Gly Phe Arg Gly
145 150 155 160

Ala Val Thr Gln Lys Val Asn Ile Asp Pro Thr Lys Lys Tyr Glu Val
165 170 175

Lys Phe Asp Ile Glu Thr Ser Asn Lys Ala Gly Gln Ala Phe Leu Arg
180 185 190

Ile Met Glu Lys Lys Asp Asn Asn Thr Arg Leu Trp Leu Ser Glu Met
195 200 205

Thr Ser Gly Thr Thr Asn Lys His Thr Leu Thr Lys Ile Tyr Asn Pro
210 215 220

Lys Leu Asn Val Ser Glu Val Thr Leu Glu Leu Tyr Tyr Glu Lys Gly
225 230 235 240

Thr Gly Ser Ala Thr Phe Asp Asn Ile Ser Met Lys Ala Lys Gly Pro
245 250 255

Lys Asp Ser Glu His Pro Gln Pro Val Thr Thr Gln Ile Glu Glu Ser
260 265 270

Val Asn Thr Ala Leu Asn Lys Asn Tyr Val Phe Asn Lys Ala Asp Tyr
275 280 285

Gln Tyr Thr Leu Thr Asn Pro Ser Leu Gly Lys Ile Val Gly Gly Ile
290 295 300

Leu Tyr Pro Asn Ala Thr Gly Ser Thr Thr Val Lys Ile Ser Asp Lys
305 310 315 320

Ser Gly Lys Ile Ile Lys Glu Val Pro Leu Ser Val Thr Ala Ser Thr
325 330 335

Glu Asp Lys Phe Thr Lys Leu Leu Asp Lys Trp Asn Asp Val Thr Ile
340 345 350

Gly Asn His Val Tyr Asp Thr Asn Asp Ser Asn Met Gln Lys Ile Asn
355 360 365

Gln Lys Leu Asp Glu Thr Asn Ala Lys Asn Ile Lys Thr Ile Lys Leu
370 375 380

Asp Ser Asn His Thr Phe Leu Trp Lys Asp Leu Asp Asn Leu Asn Asn
385 390 395 400

Ser Ala Gln Leu Thr Ala Thr Tyr Arg Arg Leu Glu Asp Leu Ala Lys
405 410 415

Gln Ile Thr Asn Pro His Ser Thr Ile Tyr Lys Asn Glu Lys Ala Ile
420 425 430

Arg Thr Val Lys Glu Ser Leu Ala Trp Leu His Gln Asn Phe Tyr Asn
435 440 445

Val Asn Lys Asp Ile Glu Gly Ser Ala Asn Trp Trp Asp Phe Glu Ile
450 455 460

Gly Val Pro Arg Ser Ile Thr Ala Thr Leu Ala Leu Met Asn Asn Tyr
465 470 475 480

Phe Thr Asp Ala Glu Ile Lys Thr Tyr Thr Asp Pro Ile Glu His Phe
485 490 495

Val Pro Asp Ala Gly Tyr Phe Arg Lys Thr Leu Asp Asn Pro Phe Lys
500 505 510

Ala Leu Gly Gly Asn Leu Val Asp Met Gly Arg Val Lys Ile Ile Glu
515 520 525

Gly Leu Leu Arg Lys Asp Asn Thr Ile Ile Glu Lys Thr Ser His Ser
530 535 540

Leu Lys Asn Leu Phe Thr Thr Ala Thr Lys Ala Glu Gly Phe Tyr Ala
545 550 555 560

Asp Gly Ser Tyr Ile Asp His Thr Asn Val Ala Tyr Thr Gly Ala Tyr
565 570 575

Gly Asn Val Leu Ile Asp Gly Leu Thr Gln Leu Leu Pro Ile Ile Gln
580 585 590

Glu Thr Asp Tyr Lys Ile Ser Asn Gln Glu Leu Asp Met Val Tyr Lys
595 600 605

Trp Ile Asn Gln Ser Phe Leu Pro Leu Ile Val Lys Gly Glu Leu Met
610 615 620

Asp Met Ser Arg Gly Arg Ser Ile Ser Arg Glu Ala Ala Ser Ser His
625 630 635 640

Ala Ala Ala Val Glu Val Leu Arg Gly Phe Leu Arg Leu Ala Asn Met
645 650 655

Ser Asn Glu Glu Arg Asn Leu Asp Leu Lys Ser Thr Ile Lys Thr Ile
660 665 670

Ile Thr Ser Asn Lys Phe Tyr Asn Val Phe Asn Asn Leu Lys Ser Tyr
675 680 685

Ser Asp Ile Ala Asn Met Asn Lys Met Leu Asn Asp Ser Thr Val Ala
690 695 700

Thr Lys Pro Leu Lys Ser Asn Leu Ser Thr Phe Asn Ser Met Asp Arg
705 710 715 720

Leu Ala Tyr Tyr Asn Ala Glu Lys Asp Phe Gly Phe Ala Leu Ser Leu
725 730 735

His Ser Lys Arg Thr Leu Asn Tyr Glu Gly Met Asn Asp Glu Asn Thr
740 745 750

Arg Asp Trp Tyr Thr Gly Asp Gly Met Phe Tyr Leu Tyr Asn Ser Asp
755 760 765

Gln Ser His Tyr Ser Asn His Phe Trp Pro Thr Val Asn Pro Tyr Lys
770 775 780

Met Ala Gly Thr Thr Glu Lys Asp Ala Lys Arg Glu Asp Thr Thr Lys
785 790 795 800

Glu Phe Met Ser Lys His Ser Lys Asp Ala Lys Glu Lys Thr Gly Gln
805 810 815

Val Thr Gly Thr Ser Asp Phe Val Gly Ser Val Lys Leu Asn Asp His
820 825 830

Phe Ala Leu Ala Ala Met Asp Phe Thr Asn Trp Asp Arg Thr Leu Thr
835 840 845

Ala Gln Lys Gly Trp Val Ile Leu Asn Asp Lys Ile Val Phe Leu Gly
850 855 860

Ser Asn Ile Lys Asn Thr Asn Gly Ile Gly Asn Val Ser Thr Thr Ile
865 870 875 880

Asp Gln Arg Lys Asp Asp Ser Lys Thr Pro Tyr Thr Thr Tyr Val Asn
885 890 895

Gly Lys Thr Ile Asp Leu Lys Gln Ala Ser Ser Gln Gln Phe Thr Asp
900 905 910

Thr Lys Ser Val Phe Leu Glu Ser Lys Glu Pro Gly Arg Asn Ile Gly
915 920 925

Tyr Ile Phe Phe Lys Asn Ser Thr Ile Asp Ile Glu Arg Lys Glu Gln
930 935 940

Thr Gly Thr Trp Asn Ser Ile Asn Arg Thr Ser Lys Asn Thr Ser Ile
945 950 955 960

Val Ser Asn Pro Phe Ile Thr Ile Ser Gln Lys His Asp Asn Lys Gly
965 970 975

Asp Ser Tyr Gly Tyr Met Met Val Pro Asn Ile Asp Arg Thr Ser Phe
980 985 990

Asp Lys Leu Ala Asn Ser Lys Glu Val Glu Leu Leu Glu Asn Ser Ser
995 1000 1005

Lys Gln Gln Val Ile Tyr Asp Lys Asn Ser Gln Thr Trp Ala Val
1010 1015 1020

Ile Lys His Asp Asn Gln Glu Ser Leu Ile Asn Asn Gln Phe Lys
1025 1030 1035

Met Asn Lys Ala Gly Leu Tyr Leu Val Gln Lys Val Gly Asn Asp
1040 1045 1050

Tyr Gln Asn Val Tyr Tyr Gln Pro Gln Thr Met Thr Lys Thr Asp
1055 1060 1065

Gln Leu Ala Ile
1070

<210> 303

<211> 77

<212> PRT

<213> Streptococcus agalactiae

<400> 303

Met His Ser Phe Ser Asn Pro Gly Tyr Pro Tyr Asp Asn Ala Val Thr
1 5 10 15

Glu Ala Phe Phe Lys Tyr Leu Lys His Arg Gln Ile Asn Arg Lys His
20 25 30

Tyr Gln Asn Ile Lys Gln Val Gln Leu Asp Cys Phe Glu Tyr Ile Glu
35 40 45

Asn Phe Tyr Asn Asn Tyr Asn Pro His Thr Ala Asn Leu Gly Leu Thr
50 55 60

Pro Asn Gln Lys Glu Glu Asn Tyr Phe Asn Ala Ile Lys
65 70 75

<210> 304

<211> 822

<212> PRT

<213> Streptococcus agalactiae

<400> 304

Val Lys Lys Thr Tyr Gly Tyr Ile Gly Ser Val Ala Ala Ile Leu Leu
1 5 10 15

Ala Thr His Ile Gly Ser Tyr Gln Leu Gly Lys His His Met Gly Leu
20 25 30

Ala Thr Lys Asp Asn Gln Ile Ala Tyr Ile Asp Asp Ser Lys Gly Lys
35 40 45

Ala Lys Ala Pro Lys Thr Asn Lys Thr Met Asp Gln Ile Ser Ala Glu
50 55 60

Glu Gly Ile Ser Ala Glu Gln Ile Val Val Lys Ile Thr Asp Gln Gly
65 70 75 80

Tyr Val Thr Ser His Gly Asp His Tyr His Phe Tyr Asn Gly Lys Val
85 90 95

Pro Tyr Asp Ala Ile Ile Ser Glu Glu Leu Leu Met Thr Asp Pro Asn
100 105 110

Tyr Arg Phe Lys Gln Ser Asp Val Ile Asn Glu Ile Leu Asp Gly Tyr
115 120 125

Val Ile Lys Val Asn Gly Asn Tyr Tyr Val Tyr Leu Lys Pro Gly Ser
130 135 140

Lys Arg Lys Asn Ile Arg Thr Lys Gln Gln Ile Ala Glu Gln Val Ala
145 150 155 160

Lys Gly Thr Lys Glu Ala Lys Glu Lys Gly Leu Ala Gln Val Ala His
165 170 175

Leu Ser Lys Glu Glu Val Ala Ala Val Asn Glu Ala Lys Arg Gln Gly
180 185 190

Arg Tyr Thr Thr Asp Asp Gly Tyr Ile Phe Ser Pro Thr Asp Ile Ile
195 200 205

Asp Asp Leu Gly Asp Ala Tyr Leu Val Pro His Gly Asn His Tyr His
210 215 220

Tyr Ile Pro Lys Lys Asp Leu Ser Pro Ser Glu Leu Ala Ala Ala Gln
225 230 235 240

Ala Tyr Trp Ser Gln Lys Gln Gly Arg Gly Ala Arg Pro Ser Asp Tyr
245 250 255

Arg Pro Thr Pro Ala Pro Gly Arg Arg Lys Ala Pro Ile Pro Asp Val
260 265 270

Thr Pro Asn Pro Gly Gln Gly His Gln Pro Asp Asn Gly Gly Tyr His
275 280 285

Pro Ala Pro Pro Arg Pro Asn Asp Ala Ser Gln Asn Lys His Gln Arg
290 295 300

Asp Glu Phe Lys Gly Lys Thr Phe Lys Glu Leu Leu Asp Gln Leu His
305 310 315 320

Arg Leu Asp Leu Lys Tyr Arg His Val Glu Glu Asp Gly Leu Ile Phe
325 330 335

Glu Pro Thr Gln Val Ile Lys Ser Asn Ala Phe Gly Tyr Val Val Pro
340 345 350

His Gly Asp His Tyr His Ile Ile Pro Arg Ser Gln Leu Ser Pro Leu
355 360 365

Glu Met Glu Leu Ala Asp Arg Tyr Leu Ala Gly Gln Thr Glu Asp Asn
370 375 380

Asp Ser Gly Ser Glu His Ser Lys Pro Ser Asp Lys Glu Val Thr His
385 390 395 400

Thr Phe Leu Gly His Arg Ile Lys Ala Tyr Gly Lys Gly Leu Asp Gly
405 410 415

Lys Pro Tyr Asp Thr Ser Asp Ala Tyr Val Phe Ser Lys Glu Ser Ile
420 425 430

His Ser Val Asp Lys Ser Gly Val Thr Ala Lys His Gly Asp His Phe
435 440 445

His Tyr Ile Gly Phe Gly Glu Leu Glu Gln Tyr Glu Leu Asp Glu Val
450 455 460

Ala Asn Trp Val Lys Ala Lys Gly Gln Ala Asp Glu Leu Ala Ala Ala
465 470 475 480

Leu Asp Gln Glu Gln Gly Lys Glu Lys Pro Leu Phe Asp Thr Lys Lys
485 490 495

Val Ser Arg Lys Val Thr Lys Asp Gly Lys Val Gly Tyr Met Met Pro
500 505 510

Lys Asp Gly Lys Asp Tyr Phe Tyr Ala Arg Asp Gln Leu Asp Leu Thr
515 520 525

Gln Ile Ala Phe Ala Glu Gln Glu Leu Met Leu Lys Asp Lys Lys His
530 535 540

Tyr Arg Tyr Asp Ile Val Asp Thr Gly Ile Glu Pro Arg Leu Ala Val
545 550 555 560

Asp Val Ser Ser Leu Pro Met His Ala Gly Asn Ala Thr Tyr Asp Thr
565 570 575

Gly Ser Ser Phe Val Ile Pro His Ile Asp His Ile His Val Val Pro
580 585 590

Tyr Ser Trp Leu Thr Arg Asp Gln Ile Ala Thr Val Lys Tyr Val Met
595 600 605

Gln His Pro Glu Val Arg Pro Asp Val Trp Ser Lys Pro Gly His Glu
610 615 620

Glu Ser Gly Ser Val Ile Pro Asn Val Thr Pro Leu Asp Lys Arg Ala
625 630 635 640

Gly Met Pro Asn Trp Gln Ile Ile His Ser Ala Glu Glu Val Gln Lys
645 650 655

Ala Leu Ala Glu Gly Arg Phe Ala Thr Pro Asp Gly Tyr Ile Phe Asp
660 665 670

Pro Arg Asp Val Leu Ala Lys Glu Thr Phe Val Trp Lys Asp Gly Ser
675 680 685

Phe Ser Ile Pro Arg Ala Asp Gly Ser Ser Leu Arg Thr Ile Asn Lys
690 695 700

Ser Asp Leu Ser Gln Ala Glu Trp Gln Gln Ala Gln Glu Leu Leu Ala
705 710 715 720

Lys Lys Asn Thr Gly Asp Ala Thr Asp Thr Asp Lys Pro Lys Glu Lys
725 730 735

Gln Gln Ala Asp Lys Ser Asn Glu Asn Gln Gln Pro Ser Glu Ala Ser
740 745 750

Lys Glu Glu Lys Glu Ser Asp Asp Phe Ile Asp Ser Leu Pro Asp Tyr
755 760 765

Gly Leu Asp Arg Ala Thr Leu Glu Asp His Ile Asn Gln Leu Ala Gln
770 775 780

Lys Ala Asn Ile Asp Pro Lys Tyr Leu Ile Phe Gln Pro Glu Gly Val
785 790 795 800

Gln Phe Tyr Asn Lys Asn Gly Glu Leu Val Thr Tyr Asp Ile Lys Thr
805 810 815

Leu Gln Gln Ile Asn Pro
820

<210> 305

<211> 306

<212> PRT

<213> Streptococcus agalactiae

<400> 305

Met Lys Lys Gly Phe Phe Leu Met Ala Met Val Val Ser Leu Val Met
1 5 10 15

Ile Ala Gly Cys Asp Lys Ser Ala Asn Pro Lys Gln Pro Thr Gln Gly
20 25 30

Met Ser Val Val Thr Ser Phe Tyr Pro Met Tyr Ala Met Thr Lys Glu
35 40 45

Val Ser Gly Asp Leu Asn Asp Val Arg Met Ile Gln Ser Gly Ala Gly
50 55 60

Ile His Ser Phe Glu Pro Ser Val Asn Asp Val Ala Ala Ile Tyr Asp
65 70 75 80

Ala Asp Leu Phe Val Tyr His Ser His Thr Leu Glu Ala Trp Ala Arg
85 90 95

Asp Leu Asp Pro Asn Leu Lys Lys Ser Lys Val Asp Val Phe Glu Ala
100 105 110

Ser Lys Pro Leu Thr Leu Asp Arg Val Lys Gly Leu Glu Asp Met Glu
115 120 125

Val Thr Gln Gly Ile Asp Pro Ala Thr Leu Tyr Asp Pro His Thr Trp
130 135 140

Thr Asp Pro Val Leu Ala Gly Glu Glu Ala Val Asn Ile Ala Lys Glu
145 150 155 160

Leu Gly Arg Leu Asp Pro Lys His Lys Asp Ser Tyr Thr Lys Lys Ala
165 170 175

Lys Ala Phe Lys Lys Glu Ala Glu Gln Leu Thr Glu Glu Tyr Thr Gln
180 185 190

Lys Phe Lys Lys Val Arg Ser Lys Thr Phe Val Thr Gln His Thr Ala
195 200 205

Phe Ser Tyr Leu Ala Lys Arg Phe Gly Leu Lys Gln Leu Gly Ile Ser
210 215 220

Gly Ile Ser Pro Glu Gln Glu Pro Ser Pro Arg Gln Leu Lys Glu Ile
225 230 235 240

Gln Asp Phe Val Lys Glu Tyr Asn Val Lys Thr Ile Phe Ala Glu Asp
245 250 255

Asn Val Asn Pro Lys Ile Ala His Ala Ile Ala Lys Ser Thr Gly Ala
260 265 270

Lys Val Lys Thr Leu Ser Pro Leu Glu Ala Ala Pro Ser Gly Asn Lys
275 280 285

Thr Tyr Leu Glu Asn Leu Arg Ala Asn Leu Glu Val Leu Tyr Gln Gln
    290                 295                 300

Leu Lys
305

<210> 306

<211> 1150

<212> PRT

<213> Streptococcus agalactiae

<400> 306

Leu Arg Lys Lys Gln Lys Leu Pro Phe Asp Lys Leu Ala Ile Ala Leu
1               5                   10                  15

Met Ser Thr Ser Ile Leu Leu Asn Ala Gln Ser Asp Ile Lys Ala Asn
            20                  25                  30

Thr Val Thr Glu Asp Thr Pro Ala Thr Glu Gln Thr Val Glu Thr Pro
        35                  40                  45

Gln Pro Thr Ala Val Ser Glu Glu Ala Pro Ser Ser Lys Glu Thr Lys
    50                  55                  60

Thr Pro Gln Thr Pro Ser Asp Ala Gly Glu Thr Val Ala Asp Asp Ala
65                  70                  75                  80

Asn Asp Leu Ala Pro Gln Ala Pro Ala Lys Thr Ala Asp Thr Pro Ala
                85                  90                  95

Thr Ser Lys Ala Thr Ile Arg Asp Leu Asn Asp Pro Ser Gln Val Lys
            100                 105                 110

Thr Leu Gln Glu Lys Ala Gly Lys Gly Ala Gly Thr Val Val Ala Val
        115                 120                 125

Ile Asp Ala Gly Phe Asp Lys Asn His Glu Ala Trp Arg Leu Thr Asp
    130                 135                 140

Lys Ala Lys Ala Arg Tyr Gln Ser Lys Glu Asp Leu Glu Lys Ala Lys
145                 150                 155                 160

Lys Glu His Gly Ile Thr Tyr Gly Glu Trp Val Asn Asp Lys Val Ala
                165                 170                 175

Tyr Tyr His Asp Tyr Ser Lys Asp Gly Lys Thr Ala Val Asp Gln Glu
            180                 185                 190

His Gly Thr His Val Ser Gly Ile Leu Ser Gly Asn Ala Pro Ser Glu
195 200 205

Thr Lys Glu Pro Tyr Arg Leu Glu Gly Ala Met Pro Glu Ala Gln Leu
210 215 220

Leu Leu Met Arg Val Glu Ile Val Asn Gly Leu Ala Asp Tyr Ala Arg
225 230 235 240

Asn Tyr Ala Gln Ala Ile Arg Asp Ala Ile Asn Leu Gly Ala Lys Val
245 250 255

Ile Asn Met Ser Phe Gly Asn Ala Ala Leu Ala Tyr Ala Asn Leu Pro
260 265 270

Asp Glu Thr Lys Lys Ala Phe Asp Tyr Ala Lys Ser Lys Gly Val Ser
275 280 285

Ile Val Thr Ser Ala Gly Asn Asp Ser Ser Phe Gly Gly Lys Thr Arg
290 295 300

Leu Pro Leu Ala Asp His Pro Asp Tyr Gly Val Val Gly Thr Pro Ala
305 310 315 320

Ala Ala Asp Ser Thr Leu Thr Val Ala Ser Tyr Ser Pro Asp Lys Gln
325 330 335

Leu Thr Glu Thr Ala Thr Val Lys Thr Ala Asp Gln Gln Asp Lys Glu
340 345 350

Met Pro Val Leu Ser Thr Asn Arg Phe Glu Pro Asn Lys Ala Tyr Asp
355 360 365

Tyr Ala Tyr Ala Asn Arg Gly Thr Lys Glu Asp Asp Phe Lys Asp Val
370 375 380

Lys Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile Asp Phe Lys Asp
385 390 395 400

Lys Ile Ala Lys Ala Lys Lys Ala Gly Ala Val Gly Val Leu Ile Tyr
405 410 415

Asp Asn Gln Asp Lys Gly Phe Pro Ile Glu Leu Pro Asn Val Asp Gln
420 425 430

Met Pro Ala Ala Phe Ile Ser Arg Lys Asp Gly Leu Leu Leu Lys Asp
435 440 445

Asn Pro Gln Lys Thr Ile Thr Phe Asn Ala Thr Pro Lys Val Leu Pro
450 455 460

Thr Ala Ser Gly Thr Lys Leu Ser Arg Phe Ser Ser Trp Gly Leu Thr
465 470 475 480

Ala Asp Gly Asn Ile Lys Pro Asp Ile Ala Ala Pro Gly Gln Asp Ile
485 490 495

Leu Ser Ser Val Ala Asn Asn Lys Tyr Ala Lys Leu Ser Gly Thr Ser
500 505 510

Met Ser Ala Pro Leu Val Ala Gly Ile Met Gly Leu Leu Gln Lys Gln
515 520 525

Tyr Glu Thr Gln Tyr Pro Asp Met Thr Pro Ser Glu Arg Leu Asp Leu
530 535 540

Ala Lys Lys Val Leu Met Ser Ser Ala Thr Ala Leu Tyr Asp Glu Asp
545 550 555 560

Glu Lys Ala Tyr Phe Ser Pro Arg Gln Gln Gly Ala Gly Ala Val Asp
565 570 575

Ala Lys Lys Ala Ser Ala Ala Thr Met Tyr Val Thr Asp Lys Asp Asn
580 585 590

Thr Ser Ser Lys Val His Leu Asn Asn Val Ser Asp Lys Phe Glu Val
595 600 605

Thr Val Thr Val His Asn Lys Ser Asp Lys Pro Gln Glu Leu Tyr Tyr
610 615 620

Gln Ala Thr Val Gln Thr Asp Lys Val Asp Gly Lys His Phe Ala Leu
625 630 635 640

Ala Pro Lys Ala Leu Tyr Glu Thr Ser Trp Gln Lys Ile Thr Ile Pro
645 650 655

Ala Asn Ser Ser Lys Gln Val Thr Val Pro Ile Asp Ala Ser Arg Phe
660 665 670

Ser Lys Asp Leu Leu Ala Gln Met Lys Asn Gly Tyr Phe Leu Glu Gly
675 680 685

Phe Val Arg Phe Lys Gln Asp Pro Lys Lys Glu Glu Leu Met Ser Ile
690 695 700

Pro Tyr Ile Gly Phe Arg Gly Asp Phe Gly Asn Leu Ser Ala Leu Glu
705 710 715 720

Lys Pro Ile Tyr Asp Ser Lys Asp Gly Ser Ser Tyr Tyr His Glu Ala
725 730 735

Asn Ser Asp Ala Lys Asp Gln Leu Asp Gly Asp Gly Leu Gln Phe Tyr
740 745 750

Ala Leu Lys Asn Asn Phe Thr Ala Leu Thr Thr Glu Ser Asn Pro Trp
755 760 765

Thr Ile Ile Lys Ala Val Lys Glu Gly Val Glu Asn Ile Glu Asp Ile
770 775 780

Glu Ser Ser Glu Ile Thr Glu Thr Ile Phe Ala Gly Thr Phe Ala Lys
785 790 795 800

Gln Asp Asp Asp Ser His Tyr Tyr Ile His Arg His Ala Asn Gly Lys
805 810 815

Pro Tyr Ala Ala Ile Ser Pro Asn Gly Asp Gly Asn Arg Asp Tyr Val
820 825 830

Gln Phe Gln Gly Thr Phe Leu Arg Asn Ala Lys Asn Leu Val Ala Glu
835 840 845

Val Leu Asp Lys Glu Gly Asn Val Val Trp Thr Ser Glu Val Thr Glu
850 855 860

Gln Val Val Lys Asn Tyr Asn Asn Asp Leu Ala Ser Thr Leu Gly Ser
865 870 875 880

Thr Arg Phe Glu Lys Thr Arg Trp Asp Gly Lys Asp Lys Asp Gly Lys
885 890 895

Val Val Ala Asn Gly Thr Tyr Thr Tyr Arg Val Arg Tyr Thr Pro Ile
900 905 910

Ser Ser Gly Ala Lys Glu Gln His Thr Asp Phe Asp Val Ile Val Asp
915 920 925

Asn Thr Thr Pro Glu Val Ala Thr Ser Ala Thr Phe Ser Thr Glu Asp
930 935 940

Arg Arg Leu Thr Leu Ala Ser Lys Pro Lys Thr Ser Gln Pro Val Tyr
945 950 955 960

Arg Glu Arg Ile Ala Tyr Thr Tyr Met Asp Glu Asp Leu Pro Thr Thr
965 970 975

Glu Tyr Ile Ser Pro Asn Glu Asp Gly Thr Phe Thr Leu Pro Glu Glu
980 985 990

Ala Glu Thr Met Glu Gly Ala Thr Val Pro Leu Lys Met Ser Asp Phe
995 1000 1005

Thr Tyr Val Val Glu Asp Met Ala Gly Asn Ile Thr Tyr Thr Pro
1010 1015 1020

Val Thr Lys Leu Leu Glu Gly His Ser Asn Lys Pro Glu Gln Asp
1025 1030 1035

Gly Ser Asp Gln Ala Pro Asp Lys Lys Pro Glu Ala Lys Pro Glu
1040 1045 1050

Gln Asp Gly Ser Gly Gln Thr Pro Asp Lys Lys Thr Glu Thr Lys
1055 1060 1065

Pro Glu Lys Asp Ser Ser Gly Gln Thr Pro Gly Lys Thr Pro Gln
1070 1075 1080

Lys Gly Gln Pro Ser Arg Thr Leu Glu Lys Arg Ser Ser Lys Arg
1085 1090 1095

Ala Leu Ala Thr Lys Ala Ser Thr Arg Asp Gln Leu Pro Thr Thr
1100 1105 1110

Asn Asp Lys Asp Thr Asn Arg Leu His Leu Leu Lys Leu Val Met
1115 1120 1125

Thr Thr Phe Phe Leu Gly Leu Val Ala His Ile Phe Lys Thr Lys
1130 1135 1140

Arg Gln Lys Glu Thr Lys Lys
1145 1150

<210> 307

<211> 403

<212> PRT

<213> Streptococcus agalactiae

<400> 307

Phe Ser Val Thr Tyr Ser Gln Ser Glu Arg Thr Val Val Phe Ser Phe
1 5 10 15

Gly Glu Ile Thr Phe Ser Arg Ser Arg Trp Thr Asn Gly Phe Glu Thr
20 25 30

Arg Ile Pro Val Asp Glu Trp Leu Gly Leu Glu Lys Tyr Lys Arg Tyr
35 40 45

Ser Ile Glu Phe Leu Tyr His Val Ala Lys Leu Ala Thr Met Met Pro
50 55 60

Tyr Arg Gln Val Cys Lys Val Ile Asp Ser Thr Leu Gln Thr Ile Ile
65 70 75 80

Thr Lys Asp Cys Val Leu Lys Ala Val Lys Phe Val Glu Lys Leu Leu
85 90 95

Lys Glu Lys Glu Arg Tyr Arg Phe Tyr Leu Glu Glu Pro Pro Glu Arg
100 105 110

Lys Lys Val Lys Lys Leu Tyr Val Glu Gly Asp Gly Val Met Ile Lys
115 120 125

Ser Thr Asp Ser Arg Glu Glu Arg Arg Tyr Leu Asp Leu Thr His Phe
130 135 140

Val Ile His Thr Gly Ser Lys Lys Val Ser Thr Lys Arg Tyr Glu Leu
145 150 155 160

Gln Asp Lys His Glu Ile Leu Gln Leu Asn Tyr Asp Lys Ala Lys Tyr
165 170 175

Asn Leu Leu Asp Tyr Ile Tyr Asn Asn Tyr Glu Val Asp Asp Asp Thr
180 185 190

Ile Leu Ile Thr Asn Ser Asp Met Gly Lys Gly Tyr Thr Ser Arg Val
195 200 205

Phe Lys Glu Leu Gly Lys Ala Leu Lys Val Lys Lys His Glu His Phe
210 215 220

Trp Asp Ile Tyr His Val Lys Glu Lys Leu Ser Ser Tyr Leu Arg Lys
225 230 235 240

Tyr Pro Ile Glu Leu Thr Asp Phe Ala Leu Asp Ala Val Lys Lys Tyr
245 250 255

Asn Ser Asp Lys Leu Glu Leu Val Phe Asp Thr Val Glu Ser Leu Ile
260 265 270

Cys Asp Glu Leu Glu Asp Gln Glu Phe Gln Lys Phe Lys Lys Lys Val
275 280 285

Leu Asn Asn Phe Lys Tyr Ile Lys Pro Ala His Leu Arg Asn Leu Ser
290 295 300

Asn Arg Gly Ile Gly Ile Met Glu Ser Gln His Arg Lys Ile Thr Tyr
305 310 315 320

Arg Met Lys Arg Arg Gly Met Tyr Trp Ser Lys Trp Gly Ile Ser Thr
325 330 335

Met Ala Asn Met Ile Ile Leu Glu Arg Ala Asn Gly Leu Arg Glu Leu
340 345 350

Phe Phe Gly Ser Trp Arg Lys Val Tyr Ser Glu Tyr Lys Glu Gly Ser
355 360 365

Phe Ser Ala Gly Arg Leu Phe Lys Lys Thr Asp Glu Leu Asp Lys Phe
370 375 380

Ser Lys Pro Leu Leu Lys Asn Gly Arg Lys Trp Ser Ile Thr Gly Ile
385 390 395 400

Lys Thr Lys

<210> 308

<211> 278

<212> PRT

<213> Streptococcus agalactiae

<400> 308

Lys Ala Ser Ser Gly Asp Tyr Gly Thr Lys Arg Glu Ile Ile Thr Ala
1 5 10 15

Asn Lys Asp Lys Tyr Ser Ile Ser Lys Met Cys Arg Trp Leu Asn Met
20 25 30

Pro Arg Ser Ser Tyr Tyr Tyr Gln Ala Val Glu Ser Val Ser Lys Thr
35 40 45

Glu Phe Glu Glu Thr Ile Lys Arg Ile Phe Leu Asp Ser Glu Ser Arg
50 55 60

Tyr Gly Ser Arg Lys Ile Lys Ile Cys Leu Asn Asn Glu Gly Ile Thr
65 70 75 80

Leu Ser Arg Arg Arg Ile Arg Arg Ile Met Lys Arg Leu Asn Leu Val
85 90 95

Ser Val Tyr Gln Lys Ala Thr Phe Lys Pro His Ser Arg Gly Lys Asn
100 105 110

Glu Ala Pro Ile Pro Asn His Leu Asp Arg Gln Phe Lys Gln Glu Arg
115 120 125

Pro Leu Gln Ala Leu Val Thr Asp Leu Thr Tyr Val Arg Val Gly Asn
130 135 140

Arg Trp Ala Tyr Val Cys Leu Ile Ile Asp Leu Tyr Asn Arg Glu Ile
145 150 155 160

Ile Gly Leu Ser Leu Gly Trp His Lys Thr Ala Glu Leu Val Lys Gln
165 170 175

Ala Ile Gln Ser Ile Pro Tyr Ala Leu Thr Lys Val Lys Met Phe His
180 185 190

Ser Asp Arg Gly Lys Glu Phe Asp Asn Gln Leu Ile Asp Glu Ile Leu
195 200 205

Glu Ala Phe Gly Ile Thr Arg Ser Leu Ser Gln Ala Gly Cys Pro Tyr
210 215 220

Asp Asn Ala Val Ala Glu Ser Thr Tyr Arg Ala Phe Lys Ile Glu Phe
225 230 235 240

Val Tyr Gln Glu Thr Phe Gln Ser Leu Glu Glu Leu Ala Leu Lys Thr
245 250 255

Glu Lys Ala Thr Leu Phe Cys Thr Thr Phe Ile Lys Cys Cys Leu Phe
260 265 270

Arg Phe Leu Pro Met Leu
275

<210> 309

<211> 104

<212> PRT

<213> Streptococcus agalactiae

<400> 309

Met Lys Thr Arg Asn Arg Lys Gly Gly Tyr Leu Ala Asn Thr Ala Asn
1 5 10 15

Glu Tyr Ile Asp Ser Lys Gln Ala Ile His Cys Leu Ser Val Glu Leu
20 25 30

Glu Pro Gln Ile Arg Phe Glu Glu Gly Gln Pro Thr Gly Glu Ile Ile
35 40 45

Ala Tyr Lys Ala Trp Phe Ser Gln Lys Gly Leu Pro Pro Phe Met Val
50 55 60

Lys Phe Glu Asn Glu Val Thr Leu Pro Ala Tyr Met Val Met Val Gln
65 70 75 80

Phe Glu Asn Leu Gln Ala Cys Glu Val Gly Phe Asn Val Tyr Phe Lys
85 90 95

Ala Asp Asn Leu Lys Glu Val Lys
100

<210> 310

<211> 2066

<212> PRT

<213> Streptococcus agalactiae

<400> 310

Leu Ser Thr Phe Asp Ser Val Thr Gly Arg Thr Asn His Leu Glu Ala
1 5 10 15

Tyr Glu Gly Leu Asn Leu Ser Glu Lys Phe Ala Ile Leu Ser His Phe
20 25 30

Asp Lys Leu Arg Asn Glu Leu Gln Thr Pro Ser Ile Gln Leu Gly Glu
35 40 45

Phe Asp Arg Glu Met Glu Ala Phe Ser Ile Thr Leu Gly Asn Glu Leu
50 55 60

Leu Gly Tyr Leu Glu Ala Asn Gly Ser Pro Tyr Glu Leu Lys Arg Glu
65 70 75 80

Leu Asn Gln Ala Glu Met Met Ala Val Leu Glu Leu Ser Arg Gln Leu
85 90 95

Val Ala Lys Phe Ser Thr Lys Leu Glu Glu Leu Gly Ile Asp Leu Gly
100 105 110

Ser Phe Gln Pro Asp Gln Val Asn Ile Leu Leu Asp Ala Val Gly Arg
115 120 125

Phe Arg Leu Lys Asn Ala Asp Ile Ala Leu Leu Gly Gly Tyr Pro Lys
130 135 140

Ala Ser Val Ser Gln Leu Ala Leu Ala Thr Glu Leu Leu Gln Met Gly
145 150 155 160

Leu Ser His Asp Lys Val Glu Phe Phe Leu Thr Ser Gln Leu Gln Leu
165 170 175

Glu Asp Met Arg Gln Val Ala Phe Ala Phe Leu His Glu Ser Leu Thr
180 185 190

Arg Glu Glu Ala Glu Gln Phe Glu Thr Asp Arg Phe Arg His Thr Ser
195 200 205

Leu Asn Phe Arg Glu Trp Arg Glu Leu Leu Glu Lys Gln Glu Pro Glu
210 215 220

Met Val Glu Met Ser Asp Val Ser Pro Leu Val Arg Glu Val Leu His
225 230 235 240

His Tyr Pro Leu Gly Ser Arg Val Thr Tyr Lys Gly Gln Glu Phe Glu
245 250 255

Ile Leu Ser Ile Glu Ala Ala Asp Met Asp Asn Leu Ile Arg Ile Glu
260 265 270

Leu Gln Asn Asp Phe Ser Tyr Leu Ile Glu Gln Asn Pro Val Leu Tyr
275 280 285

Phe Gln Asn Leu Ala Glu Ile Arg Gln Val Leu His Leu Ser Arg Ser
290 295 300

Glu Ile Val Glu Arg Glu Glu Gln Pro Glu Glu Glu Trp Thr Leu Phe
305 310 315 320

Ser Phe Met Asp Glu Gly Thr Glu Asp Asn Glu Lys Glu Pro Glu Ile
325 330 335

Val Phe Glu Ser Thr Asp Lys Val Val Thr Leu Asp Ser Gln Pro Ala
340 345 350

Gln Val Ser Glu Thr Ile Ser Glu Ser Val Pro Glu Thr Lys Glu Val
355 360 365

Ile Glu Ala Glu Gln Ala Ile Ala Val Asp Phe Ser Phe Pro Glu Asp
370 375 380

Leu Thr Asn Phe Tyr Pro Lys Thr Ala Arg Asp Lys Val Val Ala Asn
385 390 395 400

Leu Val Ala Ile Arg Leu Val Lys Glu Leu Glu Ser Ala Asn Gln Ser
405 410 415

Ala Thr Pro Asn Glu Gln Glu Ile Leu Ala Lys Tyr Val Gly Trp Gly
420 425 430

Gly Leu Ala Asn Glu Phe Phe Asp Glu Tyr Asn Pro Lys Phe Ser Lys
435 440 445

Glu Arg Glu Glu Leu Lys Thr Leu Val Ser Asp Lys Glu Tyr Ser Asp
450 455 460

Met Lys Gln Ser Ser Leu Thr Ala Tyr Tyr Thr Asp Pro Leu Leu Ile
465 470 475 480

Arg Gln Met Trp Ser Lys Leu Glu Gln Asp Gly Phe Ser Gly Gly Lys
485 490 495

Ile Leu Asp Pro Ser Met Gly Thr Gly Asn Phe Phe Ala Ala Met Pro
500 505 510

Ala His Leu Arg Glu Lys Ser Glu Leu Cys Gly Val Glu Leu Asp Thr
515 520 525

Ile Thr Gly Ala Ile Ala Lys Gln Leu His Ser Asn Val His Ile Glu
530 535 540

Val Lys Gly Phe Glu Thr Val Ala Phe Asn Asp Asn Ser Phe Asp Leu
545 550 555 560

Val Ile Ser Asn Val Pro Phe Ala Asn Ile Arg Ile Ala Asp Asn Gln
565 570 575

Tyr Asp Lys Pro Tyr Met Ile His Asp Tyr Phe Val Lys Lys Ser Leu
580 585 590

Asp Leu Val His Asp Gly Gly Gln Val Ala Ile Ile Ser Ser Thr Gly
595 600 605

Thr Met Asp Lys Arg Thr Glu Asn Ile Leu Gln Asp Ile Arg Glu Thr
610 615 620

Thr Asp Phe Leu Gly Gly Val Arg Leu Pro Asp Thr Ala Phe Lys Ala
625 630 635 640

Ile Ala Gly Thr Ser Val Thr Thr Asp Met Leu Phe Phe Gln Lys His
645 650 655

Leu Asn Lys Gly Tyr Gln Ala Asp Asp Ile Ala Phe Ser Gly Ser Val
660 665 670

Arg Tyr Asp Lys Asp Glu Arg Ile Trp Leu Asn Pro Tyr Phe Asp Gly
675 680 685

Glu Tyr Asn Ala Gln Val Leu Gly Arg Tyr Glu Ile Lys Asn Phe Asn
690 695 700

Gly Gly Thr Leu Ser Val Lys Glu Thr Thr Asp Asn Leu Ile Ala Ser
705 710 715 720

Val Arg Glu Ala Leu Gln His Val Lys Ala Pro Arg Val Ile Asp Lys
725 730 735

Thr Glu Val Met Ile Asn Ser Asp Val Ile Ala Arg Gln Val Ile Asp
740 745 750

Thr Thr Ile Pro Pro Glu Ile Arg Glu Asn Leu Glu Gln Tyr Ser Tyr
755 760 765

Gly Tyr Lys Gly Ser Thr Ile Tyr Tyr Arg Asp Asn Lys Gly Ile Arg
770 775 780

Val Gly Thr Lys Thr Glu Glu Ile Ser Tyr Tyr Val Asp Asp Glu Gly
785 790 795 800

Asn Phe Gln Ala Trp Glu Ser Lys His Ser Gln Lys Gln Ile Asp Arg
805 810 815

Phe Asn Asn Leu Glu Val Thr Asp Ser Thr Ala Leu Asp Val Tyr Val
820 825 830

Thr Glu Glu Pro Ala Lys Arg Gly Gln Phe Lys Gly Tyr Phe Lys Lys
835 840 845

Ala Val Phe Tyr Glu Ala Pro Leu Ser Glu Lys Glu Val Ala Arg Ile
850 855 860

Lys Gly Met Val Asp Ile Arg Asn Ala Tyr Gln Glu Val Ile Ala Ile
865 870 875 880

Gln Arg Asn Tyr Asp Tyr Asp Lys Asn Glu Phe Asn Arg Leu Leu Gly
885 890 895

Asn Leu Asn Arg Thr Tyr Asp Ser Phe Val Lys Arg Tyr Gly Phe Leu
900 905 910

Asn Ser Pro Val Asn Arg Asn Leu Phe Asp Ser Asp Asp Lys Tyr Ser
915 920 925

Leu Leu Ala Ser Leu Glu Asp Glu Ser Leu Asp Pro Ser Gly Lys Thr
930 935 940

Val Ile Tyr Thr Lys Ser Leu Ala Phe Glu Lys Ala Leu Val Arg Pro
945 950 955 960

Glu Lys Met Val Lys Glu Val Ser Thr Ala Leu Asp Ala Leu Asn Ser
965 970 975

Ser Leu Ala Asp Gly Arg Gly Val Asp Phe Asp Tyr Met Ala Ser Ile
980 985 990

Tyr Gln Thr Ala Ser Lys Ala Ala Leu Ile Glu Glu Leu Gly Asp Gln
995 1000 1005

Ile Ile Pro Asp Pro Glu Ser Tyr Leu Lys Gly Gln Leu Thr Tyr
1010 1015 1020

Val Ser Arg Gln Glu Phe Leu Ser Gly Asp Ile Val Thr Lys Leu
1025 1030 1035

Glu Val Met Asp Leu Leu Leu Lys Gln Asp Asn His Asp Phe Asn
1040 1045 1050

Trp Ala His Tyr Gly Asn Leu Leu Glu Ser Val Arg Pro Ala Arg
1055 1060 1065

Val Met Leu Ala Asp Ile Asp Tyr Arg Ile Gly Ser Arg Trp Ile
1070 1075 1080

Pro Leu Ala Val Tyr Gly Lys Phe Val Gln Glu Ala Phe Met Gly
1085 1090 1095

Lys Asn Tyr Asp Leu Thr Ala Thr Glu Val Glu Glu Val Leu Ser
1100 1105 1110

Val Ser Pro Ile Asp Gly Thr Met Glu Phe Arg Thr Arg Phe Ala
1115 1120 1125

Tyr Thr Tyr Ser Thr Ala Thr Asp Arg Ser Leu Gly Val Ala Gly
1130 1135 1140

Ser Arg Tyr Asp Ser Gly Arg Lys Ile Phe Glu Asn Leu Leu Asn
1145 1150 1155

Ser Asn Gln Pro Thr Ile Thr Lys Gln Ile Gln Glu Gly Asp Lys
1160 1165 1170

Lys Lys Asn Val Thr Asp Val Glu Lys Thr Thr Val Leu Arg Ala
1175 1180 1185

Lys Glu Ala Gln Ile Gln Asp Leu Phe Gln Asp Phe Val Ala Ser
1190 1195 1200

Tyr Pro Glu Ala Gln Gln Met Ile Glu Asp Thr Tyr Asn Ser Leu
1205 1210 1215

Tyr Asn Arg Thr Val Ser Lys Val Tyr Asp Gly Ser Arg Leu Glu
1220 1225 1230

Ile Asp Gly Leu Ala Gln Asn Ile Ser Leu Arg Pro His Gln Lys
1235 1240 1245

Asn Ala Ile Gln Arg Ile Val Glu Glu Lys Arg Ala Leu Leu Ala
1250 1255 1260

His Glu Val Gly Ser Gly Lys Thr Leu Thr Ile Leu Gly Ala Gly
1265 1270 1275

Phe Lys Leu Lys Glu Leu Gly Met Val His Lys Pro Leu Tyr Val
1280 1285 1290

Val Pro Ser Ser Leu Thr Ala Gln Phe Gly Gln Glu Ile Met Lys
1295 1300 1305

Phe Phe Pro Thr Lys Lys Val Tyr Val Thr Thr Lys Lys Asp Phe
1310 1315 1320

Ala Lys Ala Arg Arg Lys Gln Phe Val Ser Arg Ile Ile Thr Gly
1325 1330 1335

Asp Tyr Asp Ala Ile Val Ile Gly Asp Ser Gln Phe Glu Lys Ile
1340 1345 1350

Pro Met Ser Gln Glu Lys Gln Val Thr Tyr Ile Gln Asp Lys Leu
1355 1360 1365

Glu Gln Leu Arg Glu Ile Lys Gln Gly Ser Asp Ser Asp Tyr Thr
1370 1375 1380

Val Lys Glu Ala Glu Arg Ser Ile Lys Gly Leu Glu Asn Gln Leu
1385 1390 1395

Glu Glu Leu Gln Lys Leu Asp Arg Asp Thr Phe Ile Glu Phe Glu
1400 1405 1410

Asn Leu Gly Ile Asp Phe Leu Phe Val Asp Glu Ala His His Phe
1415 1420 1425

Lys Asn Ile Arg Pro Ile Thr Gly Leu Gly Asn Val Ala Gly Ile
1430 1435 1440

Thr Asn Thr Thr Ser Lys Lys Asn Val Asp Met Glu Met Lys Val
1445 1450 1455

Arg Gln Ile Gln Ala Glu Tyr Gly Asp Arg Asn Val Val Phe Ala
1460 1465 1470

Thr Gly Thr Pro Val Ser Asn Ser Ile Ser Glu Leu Tyr Thr Met
1475 1480 1485

Met Asn Tyr Ile Gln Pro Asp Val Leu Glu Arg Tyr Gln Val Ser
1490 1495 1500

Asn Phe Asp Ser Trp Val Gly Ala Phe Gly Asn Ile Glu Asn Ser
1505 1510 1515

Met Glu Leu Ala Pro Thr Gly Asp Lys Tyr Gln Pro Lys Lys Arg
1520 1525 1530

Phe Lys Lys Phe Val Asn Leu Pro Glu Leu Met Arg Ile Tyr Lys
1535 1540 1545

Glu Thr Ala Asp Ile Gln Thr Ser Asp Met Leu Asp Leu Pro Val
1550 1555 1560

Pro Glu Ala Thr Val Ile Ala Val Glu Ser Glu Leu Thr Glu Ala
1565 1570 1575

Gln Lys Asn Tyr Leu Glu Glu Leu Val Asp Arg Ser Asp Ala Ile
1580 1585 1590

Lys Ser Gly Ser Val Asp Pro Ser Val Asp Asn Met Leu Lys Val
1595 1600 1605

Ile Gly Glu Ala Arg Lys Leu Ala Ile Asp Met Arg Leu Ile Asp
1610 1615 1620

Pro Ala Tyr Thr Leu Ser Asp Asn Gln Lys Ile Met Gln Val Val
1625 1630 1635

Asp Asn Val Glu Arg Ile Tyr Arg Glu Gly Lys Gly Asp Lys Ala
1640 1645 1650

Thr Gln Met Ile Phe Ser Asp Ile Gly Thr Pro Lys Ser Lys Glu
1655 1660 1665

Glu Gly Phe Asp Val Tyr Asn Glu Leu Lys Ala Leu Leu Val Asp
1670 1675 1680

Arg Gly Ile Pro Lys Glu Glu Ile Ala Phe Val His Asp Ala Asn
1685 1690 1695

Thr Asp Glu Lys Lys Asn Ser Leu Ser Arg Lys Val Asn Ser Gly
1700 1705 1710

Glu Val Arg Ile Leu Met Ala Ser Thr Glu Lys Gly Gly Thr Gly
1715 1720 1725

Leu Asn Val Gln Ala Arg Met Lys Ala Val His His Leu Asp Val
1730 1735 1740

Pro Trp Arg Pro Ser Asp Ile Gln Gln Arg Asn Gly Arg Leu Ile
1745 1750 1755

Arg Gln Gly Asn Gln His Gln Asn Val Glu Ile Tyr His Tyr Ile
1760 1765 1770

Thr Lys Gly Ser Phe Asp Asn Tyr Leu Trp Ala Thr Gln Glu Asn
1775 1780 1785

Lys Leu Arg Tyr Ile Lys Gln Ile Met Thr Ser Lys Asp Pro Val
1790 1795 1800

Arg Ser Ala Glu Asp Ile Asp Glu Gln Thr Met Thr Ala Ser Asp
1805 1810 1815

Phe Lys Ala Leu Ala Thr Gly Asn Pro Tyr Leu Lys Leu Lys Met
1820 1825 1830

Glu Leu Glu Asn Glu Leu Thr Val Leu Glu Asn Gln Lys Arg Ala
1835 1840 1845

Phe Asn Arg Ser Lys Asp Glu Tyr Arg His Thr Ile Ser Tyr Cys
1850 1855 1860

Glu Lys Asn Leu Pro Val Met Glu Lys Arg Leu Arg Gln Tyr Asp
1865 1870 1875

Arg Asp Ile Glu Lys Ser Gln Ala Thr Lys Asn Gln Glu Phe Ile
1880 1885 1890

Met Arg Phe Asp Asn Gln Thr Ile Asp Asn Arg Ser Glu Ala Gly
1895 1900 1905

Asp Tyr Leu Arg Lys Leu Ile Thr Tyr Asn Arg Ser Glu Thr Lys
1910 1915 1920

Glu Val Arg Thr Leu Ala Thr Phe Arg Gly Phe Glu Leu Lys Met
1925 1930 1935

Ala Thr Arg Ser Pro Gly Glu Pro Leu Ser Asp Met Val Ser Leu
1940 1945 1950

Thr Ile Ser Gly Asp Asn Gln Tyr Ser Val Ser Leu Asp Leu Lys
1955 1960 1965

Ser Asp Val Gly Thr Ile Gln Arg Ile Asn Asn Ala Ile Asp His
1970 1975 1980

Ile Leu Glu Asp Lys Glu Lys Thr Glu Glu Met Thr Asn Asn Leu
1985 1990 1995

Lys Asp Lys Leu Ala Val Ala Arg Val Glu Val Glu Lys Val Phe
2000 2005 2010

Ala Lys Glu Glu Glu Tyr Gln Leu Val Lys Ala Lys Tyr Asp Val
2015 2020 2025

Leu Ala Pro Leu Val Glu Arg Glu Ala Asp Leu Glu Glu Ile Asp
2030 2035 2040

Val Ala Leu Ser Gln Phe Ser Ser Ser Asp Pro Cys Leu Lys Lys
2045 2050 2055

Asp Gln Gln Leu Val Leu Asp Ile
2060 2065

<210> 311

<211> 1634

<212> PRT

<213> Streptococcus agalactiae

<400> 311

Met Thr Thr Lys Cys Asn His His Phe Leu Ile Asn Gln Glu Lys Gly
1 5 10 15

Glu Lys Tyr Val Phe Arg Lys Ser Lys Gln Tyr Arg Thr Leu Cys Ser
20 25 30

Val Ala Leu Gly Thr Val Val Met Ala Phe Val Ala Leu Ala Gly Pro
35 40 45

Met Val Gln Ala Asp Glu Val Gly Arg Thr Val Ala Thr Ser Val Gln
50 55 60

Thr Glu Thr Asn Pro Ala Thr Asn Leu Lys Glu Asn Gln Pro Ser Pro
65 70 75 80

Ile Ala Glu Gln Lys Asp Ser Leu Ala Ala Thr Gly Gln Ser Thr Gly
85 90 95

Thr Val Thr Val Thr Val Pro His Asp Lys Val Thr Gln Ala Val Asp
100 105 110

Lys Ala Lys Thr Glu Gly Ile Lys Ala Val Gln Asp Lys Pro Met Asp
115 120 125

Leu Gly Asn Thr Val Ser Ala Ala Glu Thr Ser Gln Gln Leu Lys Lys
130 135 140

Ala Glu Glu Asp Ala Thr Asn Gln Thr Thr Thr Ile Ser Lys Thr Val
145 150 155 160

Glu Ile Tyr Lys Ser Asp Lys Ala Thr Tyr Glu Ala Glu Lys Lys Trp
165 170 175

Val Glu Lys Arg Asn Glu Glu Leu Thr Ala Ala Tyr Asp Lys Ala Glu
180 185 190

Gln Thr Gly Thr Gly Leu Asn His Ser Val Asp Thr Thr Val Ser Glu
195 200 205

Leu Lys Ser Gln Asp Gln Asn Ala His Val Thr Val Asn Thr Gln Thr
210 215 220

Val Lys Ser Gly Asp Gly Thr Ser Val Ser Gly Tyr Gln Glu Tyr Val
225 230 235 240

Lys Ser Val Ala Ala Ile Asp Lys Lys Asn Lys Ala Asn Leu Ala Asp
245 250 255

Tyr Arg Thr Lys Lys Gln Ala Ala Asp Ala Val Val Ala Lys Asn Gln
260 265 270

Leu Ile Gln Lys Glu Asn Glu Ala Gly Leu Ala Lys Ala Lys Ala Glu
275 280 285

Asn Glu Ala Ile Asp Arg Arg Asn Lys Glu Gly Gln Lys Ala Val Asp
290 295 300

Glu Ala Asn Lys Ala Gly Gln Ala Ala Val Glu Gln Ala Asn Gln Glu
305 310 315 320

Lys Gln Lys Gln Ala Ala Asn Arg Ala Phe Glu Ile Ala Thr Ile Thr
325 330 335

Lys Arg Asn Lys Glu Arg Glu Glu Val Ala Lys Lys Glu Asn Ala Ala
340 345 350

Ile Asp Ala Tyr Asn Ala Lys Glu Trp Ile Arg Tyr Lys Arg Asp Leu
355 360 365

Ala Asn Ile Ser Lys Gly Glu Glu Gly Tyr Ile Ser Glu Ala Leu Ala
370 375 380

Gln Ala Leu Asp Leu Asn His Gly Glu Pro Gln Val Lys His Gly Ala
385 390 395 400

Gly Thr Arg Asn Pro Asp Arg Ile Ile Ser Lys Gly Asp Ala Met Leu
405 410 415

Gly Gly Tyr Ser Asn Ile Leu Asp Ser Thr Gly Phe Phe Val Tyr Asn
420 425 430

His Phe Lys Thr Gly Glu Thr Leu Asn Phe Thr Tyr Gln Asn Leu Lys
435 440 445

His Ala Arg Phe Asp Gly Lys Lys Ile Thr Ala Ile Thr Tyr Asp Ile
450 455 460

Thr Asn Leu Val Ser Pro Thr Gly Thr Asn Ala Val Gln Leu Val Val
465 470 475 480

Pro Asn Asp Pro Thr Glu Gly Phe Ile Ala Tyr Arg Asn Asp Gly Ala
485 490 495

Gly Asn Trp Arg Thr Asp Lys Met Glu Phe Arg Val Lys Ala Arg Tyr
500 505 510

Phe Leu Glu Asp Gly Ser Gln Val Thr Phe Thr Lys Glu Lys Pro Gly
515 520 525

Val Phe Thr His Ser Ser Leu Asn His Asn Asp Ile Gly Leu Glu Tyr
530 535 540

Val Lys Asp Ser Ser Gly Lys Phe Val Pro Ile His Gly Ser Ser Val
545 550 555 560

Gln Val Thr Asn Glu Gly Leu Ala Arg Ser Leu Gly Ser Asn Arg Ala
565 570 575

Ser Asp Leu Lys Leu Pro Glu Glu Trp Asp Thr Thr Ser Ser Arg Tyr
580 585 590

Ala Tyr Lys Gly Ala Ile Val Ser Thr Val Thr Ser Gly Asn Ile Tyr
595 600 605

Thr Val Thr Phe Gly Gln Gly Asp Met Pro Thr Gln Val Gly Gly Lys
610 615 620

Thr Tyr Trp Phe Ala Leu Asn Thr Leu Pro Val Ala Lys Thr Val Thr
625 630 635 640

Pro Tyr Asn Pro Lys Thr His Val Arg Pro Gln Leu Asp Pro Val Pro
645 650 655

Glu Pro Ile Lys Val Thr Pro Glu Thr Tyr Thr Pro Lys Ile Phe Thr
660 665 670

Pro Glu Lys Pro Val Thr Phe Thr Pro Lys Ser Val Glu Lys Val Pro
675 680 685

Gln Pro Ser Leu Thr Leu Thr Lys Val Thr Leu Pro Thr Asn Leu Lys
690 695 700

Leu Glu Pro Leu Pro Lys Ala Pro Gln Lys Pro Thr Val His Tyr His
705 710 715 720

Asp Tyr Leu Leu Thr Thr Thr Pro Ala Ile Ala Lys Glu Val Met Asn
725 730 735

Val Asp Lys Val Asn Leu His Gly Lys Gln Val Ala Lys Asp Ser Thr
740 745 750

Val Ile Tyr Pro Leu Thr Val Asp Val Leu Ser Pro Asn Arg Ser Lys
755 760 765

Ile Thr Ser Leu Ile Phe Glu Asp Tyr Leu Pro Ala Gly Tyr Ala Phe
770 775 780

Asp Met Thr Lys Thr Gln Ala Glu Asn Ser Asp Tyr Asp Leu Thr Phe
785 790 795 800

Asp Lys Asn Lys Asn Phe Val Thr Leu Lys Ala Lys Asp Ser Leu Leu
805 810 815

Gln Thr Leu Asn Lys Glu Leu Asn Lys Ser Tyr Gln Leu Ser Ala Pro
820 825 830

Lys Leu Tyr Gly Ser Val Gln Asn Asp Gly Ala Thr Tyr Ser Asn Ser
835 840 845

Tyr Lys Leu Leu Ile Asn Lys Asp Thr Pro Asn Thr Tyr Thr Val Ile
850 855 860

Ser Asn Val Val Arg Ile Arg Thr Pro Gly Asp Gly Glu Thr Thr Ser
865 870 875 880

Arg Ile Arg Pro Lys Lys Asp Asn Glu Asn Ala Asp Gly Val Leu Ile
885 890 895

Asn Asp Thr Val Val Ala Leu Ser Thr Thr Asn His Tyr Arg Leu Thr
900 905 910

Trp Asp Leu Asp Gln Tyr Lys Gly Asp Thr Ser Ser Lys Asp Thr Ile
915 920 925

Ala Arg Gly Phe Leu Phe Val Asp Asp Tyr Pro Glu Glu Ala Leu Asp
930 935 940

Leu Val Asp Lys Gly Thr Val Ile Thr Thr Leu Asp Gly Lys Ala Val
945 950 955 960

Ser Gly Ile Ser Val Tyr Ser Tyr Thr Ser Leu Asp Lys Ala Pro Lys
965 970 975

Glu Leu Gln Asp Lys Leu Ala Arg Ala Asn Ile Ser Pro Lys Gly Ala
980 985 990

Phe Gln Val Phe Glu Pro Asp Asn His Gln Ala Phe Tyr Asp Thr Tyr
995 1000 1005

Val Lys Thr Gly Gln Ser Leu Ala Leu Leu Thr Lys Met Lys Val
1010 1015 1020

Lys Asp Ser Leu Tyr Gly Gln Thr Val Arg Tyr Lys Asn Lys Ala
1025 1030 1035

Tyr Gln Val Asp Phe Gly Asn Gly Tyr Glu Thr Lys Glu Val Val
1040 1045 1050

Asn Thr Val Val His Pro Glu Pro Lys Lys Gln Asn Leu Asn Lys
1055 1060 1065

Asp Lys Val Asp Ile Asn Gly Lys Ala Met Leu Val Gly Ser Gln
1070 1075 1080

Asn Phe Tyr Thr Leu Ser Trp Asp Leu Asp Gln Tyr Arg Gly Leu
1085 1090 1095

Gln Ala Asp Lys Ser Gln Ile Ala Gln Gly Phe Tyr Phe Val Asp
1100 1105 1110

Asp Tyr Pro Glu Asp Val Leu Leu Pro Asp Thr Lys Ala Ile Gln
1115 1120 1125

Ile Met Thr Lys Asp Gly Lys Ala Val Lys Gly Met Glu Ile Lys
1130 1135 1140

Thr Tyr His Gln Leu Ser Asp Ala Pro Lys Glu Leu Gln Ala Ala
1145 1150 1155

Leu Ala Lys Arg Asn Ile Thr Pro Lys Gly Ala Phe Gln Val Phe
1160 1165 1170

Met Pro Lys Asp Pro Gln Ala Phe Tyr Lys Ala Tyr Val Thr Thr
1175 1180 1185

Gly Gln Asn Leu Thr Ile Val Asn Pro Met Thr Val Arg Glu Ala
1190 1195 1200

Val Tyr Asn Ser Gly Lys Ser Tyr Asp Asn Val Ala Tyr Gln Val
1205 1210 1215

Asp Phe Gly Gln Ala Tyr Glu Thr Asn Ile Val Thr Asn His Val
1220 1225 1230

Pro Thr Val Asn Pro His Lys Ser Asn Thr Asn Lys Glu Gly Val
1235 1240 1245

Ser Ile Glu Gly Lys Thr Val Leu Pro Asn Thr Val Asn Tyr Tyr
1250 1255 1260

Lys Ile Val Leu Asp Tyr Ser Gln Tyr Lys Asn Met Ile Val Thr
1265 1270 1275

Asp Asp Val Leu Val Lys Gly Phe Tyr Met Val Asp Asp Tyr Pro
1280 1285 1290

Glu Glu Ala Leu Thr Pro His Pro Asp Gly Thr Gln Val Met Asp
1295 1300 1305

Gln Asn Gly Lys Phe Val Arg Gly Leu Ser Val Arg Thr Tyr Ala
1310 1315 1320

Ser Leu Ala Asp Ala Pro Lys Ala Val Gln Glu Ala Met Lys Ser
1325 1330 1335

Arg Asn Phe Ile Pro Lys Gly Ala Ile Gln Val Phe Gln Ala Asp
1340 1345 1350

Asp Pro Lys Thr Phe Phe Glu Thr Tyr Val Lys Thr Gly Gln Lys
1355 1360 1365

Leu Val Val Thr Thr Pro Met Thr Val Lys Asn Glu Arg Ile Gln
1370 1375 1380

Thr Gly Gly Gln Tyr Glu Asn Thr Ala Tyr Gln Ile Asp Phe Gly
1385 1390 1395

Ile Ala Tyr Val Thr Glu Thr Val Val Asn Asn Val Pro Lys Leu
1400 1405 1410

Glu Pro Gln Lys Asp Val Val Ile Asp Leu Ser Gln Lys Asp Lys
1415 1420 1425

Ser Leu Asn Gly Lys Ala Ile Ala Leu Asp Gln Val Phe Asn Tyr
1430 1435 1440

Arg Leu Val Gly Ser Leu Ile Pro Arg Asn Arg Ala Thr Ala Leu
1445 1450 1455

Val Glu Tyr Ser Phe Lys Asp Asp Tyr Asp Glu Lys His Asp Glu
1460 1465 1470

Tyr Lys Gly Val Tyr Lys Ala Tyr Thr Leu Arg Asp Val Thr Leu
1475 1480 1485

Lys Asp Gly Thr Val Leu Lys Gln Gly Thr Glu Val Thr Lys Tyr
1490 1495 1500

Thr Leu Gln Ser Val Asp Lys Ala Lys Gly Thr Ile Ala Ile Arg
1505 1510 1515

Phe Asp Thr Ala Phe Leu Glu Asn Ile Ala Asp Glu Ser Glu Phe
1520 1525 1530

Gln Ala Glu Leu Tyr Leu Gln Met Lys Arg Ile Ala Ser Gly Asp
1535 1540 1545

Val Glu Asn Thr Val Ile His Ser Val Asn Gly Tyr Asn Ile Arg
1550 1555 1560

Ser Asn Thr Val Lys Thr Thr Thr Pro Gln Pro Glu Ser Pro Thr
1565 1570 1575

Pro Asp Asn Pro Pro Ser Pro Gln Pro Pro Val Pro Thr Thr Glu
1580 1585 1590

Ser Pro Val Gln Ala Ser Val Leu Pro Ser Thr Gly Glu Ser Gln
1595 1600 1605

Ser Leu Leu Ala Leu Ile Gly Gly Gly Leu Leu Leu Gly Leu Ala
1610 1615 1620

Tyr Gly Leu Ser Lys Arg Lys Lys Glu Lys Asn
1625 1630

<210> 312

<211> 702

<212> PRT

<213> Streptococcus agalactiae

<400> 312

Met Ala Asn Asn Asn Phe Tyr Asn Arg Asp Pro Phe Gly Asn Met Asp
1 5 10 15

Asp Ile Phe Asn Ser Leu Met Gly Asn Met Gly Gly Tyr Asn Ser Glu
20 25 30

Asn Lys Arg Tyr Leu Ile Asn Gly Arg Glu Val Thr Pro Glu Glu Phe
35 40 45

Ser Gln Tyr Arg Gln Thr Gly Lys Leu Pro Gly Gln Glu Leu Asn Asn
50 55 60

Gln Asn Thr Pro Thr Asn Gln Val Ser Ala Asp Ser Val Leu Thr Lys
65 70 75 80

Leu Gly Thr Asn Leu Thr Asp Gln Ala Arg Gln His Leu Leu Asp Pro
85 90 95

Val Ile Gly Arg Asn Lys Glu Ile Gln Glu Thr Ala Glu Ile Leu Ala
100 105 110

Arg Arg Thr Lys Asn Asn Pro Val Leu Val Gly Asp Ala Gly Val Gly
115 120 125

Lys Thr Ala Val Ile Glu Gly Leu Ala Gln Ala Ile Ile Asn Gly Asp
130 135 140

Val Pro Ala Ala Ile Lys Asn Lys Glu Ile Ile Ser Ile Asp Ile Ser
145 150 155 160

Ser Leu Glu Ala Gly Thr Gln Tyr Arg Gly Ser Phe Glu Glu Asn Ile
165 170 175

Gln Asn Ile Ile Lys Glu Val Lys Glu Thr Gly Asn Ile Ile Leu Phe
180 185 190

Phe Asp Glu Ile His Gln Ile Leu Gly Ala Gly Ser Thr Gly Gly Asp
195 200 205

Ser Gly Ser Lys Gly Leu Ala Asp Ile Leu Lys Pro Ala Leu Ser Arg
210 215 220

Gly Glu Leu Thr Val Ile Gly Ala Thr Thr Gln Asp Glu Tyr Arg Asn
225 230 235 240

Thr Ile Leu Lys Asn Ala Ala Leu Ala Arg Arg Phe Asn Glu Val Lys
245 250 255

Val Asn Ala Pro Ser Ala Gln Asp Thr Phe Asn Ile Leu Met Gly Ile
260 265 270

Arg Asn Leu Tyr Glu Gln His His Asn Val Val Leu Pro Asp Ser Val
275 280 285

Leu Lys Ala Ala Val Asp Leu Ser Ile Gln Tyr Ile Pro Gln Arg Ser
290 295 300

Leu Pro Asp Lys Ala Ile Asp Leu Ile Asp Met Thr Ala Ala His Leu
305 310 315 320

Ala Ala Gln His Pro Val Thr Asp Leu Lys Ser Leu Glu Lys Glu Ile
325 330 335

Ala Ala Gln Arg Asp Lys Gln Glu Lys Ala Val Asn Thr Glu Asp Phe
340 345 350

Glu Glu Ala Leu Lys Val Lys Thr Arg Ile Glu Glu Leu Gln Asn Gln
355 360 365

Ile Asp Asn His Thr Glu Gly Gln Lys Val Thr Ala Thr Ile Asn Asp
370 375 380

Ile Ala Met Ser Ile Glu Arg Leu Thr Gly Val Pro Val Ser Asn Met
385 390 395 400

Gly Ala Ser Asp Ile Glu Arg Leu Lys Glu Leu Gly Asn Arg Leu Lys
405 410 415

Gly Lys Val Ile Gly Gln Asn Asp Ala Val Glu Ala Val Ala Arg Ala
420 425 430

Ile Arg Arg Asn Arg Ala Gly Phe Asp Asp Gly Asn Arg Pro Ile Gly
435 440 445

Ser Phe Leu Phe Val Gly Pro Thr Gly Val Gly Lys Thr Glu Leu Ala
450 455 460

Lys Gln Leu Ala Phe Asp Met Phe Gly Ser Lys Asp Ala Ile Val Arg
465 470 475 480

Leu Asp Met Ser Glu Tyr Asn Asp Arg Thr Ala Val Ser Lys Leu Ile
485 490 495

Gly Ala Thr Ala Gly Tyr Val Gly Tyr Asp Asp Asn Ser Asn Thr Leu
500 505 510

Thr Glu Arg Ile Arg Arg Asn Pro Tyr Ser Ile Val Leu Leu Asp Glu
515 520 525

Ile Glu Lys Ala Asp Pro Gln Val Ile Thr Leu Leu Leu Gln Val Leu
530 535 540

Asp Asp Gly Arg Leu Thr Asp Gly Gln Gly Asn Thr Ile Asn Phe Lys
545 550 555 560

Asn Thr Val Ile Ile Ala Thr Ser Asn Ala Gly Phe Gly Asn Glu Ala
565 570 575

Phe Thr Gly Asp Ser Asp Lys Asp Leu Lys Ile Met Glu Arg Ile Ser
580 585 590

Pro Tyr Phe Arg Pro Glu Phe Leu Asn Arg Phe Asn Gly Val Ile Glu
595 600 605

Phe Ser His Leu Ser Lys Asp Asp Leu Asn Glu Ile Val Asp Leu Met
610 615 620

Leu Asp Glu Val Asn Gln Thr Ile Gly Lys Lys Gly Ile Asp Leu Val
625 630 635 640

Val Asp Glu Asn Val Lys Ser His Leu Ile Asp Leu Gly Tyr Asp Glu
645 650 655

Ala Met Gly Val Arg Pro Leu Arg Arg Val Ile Glu Gln Glu Ile Arg
660 665 670

Asp Arg Ile Thr Asp Tyr Tyr Leu Asp His Thr Asp Val Lys His Leu
675 680 685

Lys Ala Asn Leu Gln Asp Gly Gln Ile Val Ile Ser Glu Arg
690 695 700

<210> 313

<211> 314

<212> PRT

<213> Streptococcus agalactiae

<400> 313

Met Gly Arg Phe Lys Glu Leu Leu Glu Ser Lys Lys Ala Leu Ile Leu
1 5 10 15

His Gly Ala Leu Gly Thr Glu Leu Glu Ser Arg Gly Cys Asp Val Ser
20 25 30

Gly Lys Leu Trp Ser Asp Lys Tyr Leu Ile Glu Asp Pro Ala Ala Ile
35 40 45

Gln Thr Ile His Glu Asp Tyr Ile Arg Ala Gly Ala Asp Ile Val Thr
50 55 60

Thr Ser Thr Tyr Gln Ala Thr Leu Gln Gly Leu Ala Gln Val Gly Val
65 70 75 80

Ser Glu Ser Gln Ala Glu Asp Leu Ile Arg Leu Thr Val Gln Leu Ala
85 90 95

Lys Ala Val Arg Glu Gln Val Trp Lys Ser Leu Thr Lys Glu Glu Lys
100 105 110

Ser Glu Arg Ile Tyr Pro Leu Ile Ser Gly Asp Val Gly Pro Tyr Ala
115 120 125

Ala Phe Leu Ala Asp Gly Ser Glu Tyr Thr Gly Leu Tyr Asp Ile Tyr
130 135 140

Lys Glu Gly Leu Lys Asn Phe His Arg His Arg Ile Glu Leu Leu Leu
145                 150                 155                 160

Asp Glu Gly Val Asp Leu Leu Ala Leu Glu Thr Ile Pro Asn Ala Gln
                165                 170                 175

Glu Ala Glu Ala Leu Ile Glu Leu Leu Val Glu Asp Phe Pro Gln Val
            180                 185                 190

Glu Ala Tyr Met Ser Phe Thr Ser Gln Asp Gly Lys Thr Ile Ser Asp
        195                 200                 205

Gly Ser Ala Val Ala Gly Leu Ala Lys Ala Ile Asp Val Ser Pro Gln
    210                 215                 220

Val Val Ala Leu Gly Ile Asn Cys Ser Ser Pro Ser Leu Val Ala Asp
225                 230                 235                 240

Phe Leu Gln Ala Ile Ala Glu Gln Thr Asp Lys Pro Leu Val Thr Tyr
                245                 250                 255

Pro Asn Ser Gly Glu Ile Tyr Asp Gly Ala Ser Gln Ser Trp Gln Ser
            260                 265                 270

Ser Arg Asp His Ser His Thr Leu Leu Glu Asn Thr Ser Asp Trp Gln
        275                 280                 285

Lys Leu Gly Ala Gln Val Val Gly Gly Cys Cys Arg Thr Arg Pro Ala
    290                 295                 300

Asp Ile Ala Asp Leu Ser Glu His Leu Thr
305                 310

<210> 314

<211> 390

<212> PRT

<213> Streptococcus agalactiae

<400> 314

Met Lys Ile Gly Ile Asp Lys Ile Gly Phe Ala Thr Ser Gln Tyr Val
1               5                   10                  15

Leu Glu Met Thr Asp Leu Ala Ile Ala Arg Gln Val Asp Pro Glu Lys
            20                  25                  30

Phe Ser Lys Gly Leu Leu Leu Asp Ser Leu Ser Ile Thr Pro Val Thr
        35                  40                  45

Glu Asp Ile Val Thr Leu Ala Ala Ser Ala Ala Asn Asp Ile Leu Ser
50 55 60

Asp Glu Asp Lys Glu Thr Ile Asp Met Val Ile Val Ala Thr Glu Ser
65 70 75 80

Ser Ile Asp Gln Ser Lys Ala Ala Ser Val Tyr Val His Gln Leu Leu
85 90 95

Glu Ile Gln Pro Phe Ala Arg Ser Phe Glu Met Lys Glu Ala Cys Tyr
100 105 110

Ser Ala Thr Ala Ala Leu Asp Tyr Ala Lys Leu His Val Glu Lys His
115 120 125

Pro Asp Ser Lys Val Leu Val Ile Ala Ser Asp Ile Ala Lys Tyr Gly
130 135 140

Ile Lys Ser Thr Gly Glu Ser Thr Gln Gly Ala Gly Ser Ile Ala Met
145 150 155 160

Leu Ile Ser Gln Asn Pro Ser Ile Leu Glu Leu Lys Glu Asp Arg Leu
165 170 175

Ala Gln Thr Arg Asp Ile Met Asp Phe Trp Arg Pro Asn Tyr Ser Asp
180 185 190

Val Pro Tyr Val Asn Gly Met Phe Ser Thr Lys Gln Tyr Leu Asp Met
195 200 205

Leu Lys Thr Thr Trp Lys Glu Tyr Gln Lys Arg Phe Asn Thr Ser Leu
210 215 220

Ser Asp Tyr Ala Ala Phe Cys Phe His Ile Pro Phe Pro Lys Leu Ala
225 230 235 240

Leu Lys Gly Phe Asn Lys Ile Leu Asp Asn Asn Leu Asp Glu Gln Lys
245 250 255

Lys Ala Glu Leu Gln Glu Asn Phe Glu His Ser Ile Thr Tyr Ser Lys
260 265 270

Lys Ile Gly Asn Cys Tyr Thr Gly Ser Leu Tyr Leu Gly Leu Leu Ser
275 280 285

Leu Leu Glu Asn Ser Gln Asn Leu Lys Ala Gly Asp Gln Ile Ala Phe
290 295 300

Phe Ser Tyr Gly Ser Gly Ala Val Ala Glu Ile Phe Thr Gly Gln Leu
305 310 315 320

Val Asp Gly Tyr Gln Asn Lys Leu Gln Ser Asp Arg Met Asp Gln Leu
325 330 335

Asn Lys Arg Gln Lys Ile Thr Val Thr Glu Tyr Glu Lys Leu Phe Phe
340 345 350

Glu Lys Thr Ile Leu Asp Glu Asn Gly Asn Ala Asn Phe Asn Thr Tyr
355 360 365

Arg Thr Gly Thr Phe Ser Leu Asp Ser Ile Cys Glu His Gln Arg Ile
370 375 380

Tyr Lys Lys Ile Asn Asn
385 390

<210> 315

<211> 304

<212> PRT

<213> Streptococcus agalactiae

<400> 315

Met Lys Ser Ala Tyr Ile Phe Phe Asn Pro Lys Ser Gly Lys Asp Glu
1 5 10 15

Gln Ala Leu Ala Gln Glu Val Lys Ser Tyr Leu Ile Glu His Asp Phe
20 25 30

Gln Asp Asp Tyr Val Arg Ile Ile Thr Pro Ser Ser Val Glu Glu Ala
35 40 45

Val Ala Leu Ala Lys Lys Ala Ser Glu Asp His Ile Asp Leu Val Ile
50 55 60

Pro Leu Gly Gly Asp Gly Thr Ile Asn Lys Ile Cys Gly Gly Val Tyr
65 70 75 80

Ala Gly Gly Ala Tyr Pro Thr Ile Gly Leu Val Pro Ala Gly Thr Val
85 90 95

Asn Asn Phe Ser Lys Ala Leu Asn Ile Pro Gln Glu Arg Asn Leu Ala
100 105 110

Leu Glu Asn Leu Leu Asn Gly His Val Lys Ser Val Asp Ile Cys Lys
115 120 125

Val Asn Asp Asp Tyr Met Ile Ser Ser Leu Thr Leu Gly Leu Leu Ala
130 135 140

Asp Ile Ala Ala Asn Val Thr Ser Glu Met Lys Arg Lys Leu Gly Pro
145 150 155 160

Phe Ala Phe Val Gly Asp Ala Tyr Arg Ile Leu Lys Arg Asn Arg Ser
165 170 175

Tyr Ser Ile Thr Leu Ala Tyr Asp Asn Asn Val Arg Ser Leu Arg Thr
180 185 190

Arg Leu Leu Leu Ile Thr Met Thr Asn Ser Ile Ala Gly Met Pro Ala
195 200 205

Phe Ser Pro Glu Ala Thr Ile Asp Asp Gly Leu Phe Arg Val Tyr Thr
210 215 220

Met Glu His Ile His Phe Phe Lys Leu Leu Leu His Leu Arg Gln Phe
225 230 235 240

Arg Lys Gly Asp Phe Ser Gln Ala Lys Glu Ile Lys His Phe His Thr
245 250 255

Asn Asn Leu Thr Ile Ser Thr Phe Lys Arg Lys Lys Ser Ala Ile Pro
260 265 270

Lys Val Arg Ile Asp Gly Asp Pro Gly Asp Gln Leu Pro Val Lys Val
275 280 285

Glu Val Ile Pro Lys Ala Leu Lys Phe Ile Ile Pro Asn Ser Leu Pro
290 295 300

<210> 316

<211> 284

<212> PRT

<213> Streptococcus agalactiae

<400> 316

Met Thr Thr Phe Thr Ala Lys Phe Ile Asp Gln Glu Trp Glu Val Pro
1 5 10 15

Val Glu Ser Gly Arg Tyr His Met Ile Val Gly Glu Phe Cys Pro Tyr
20 25 30

Ala Gln Arg Pro Gln Ile Ala Arg Gln Leu Leu Gly Leu Asp Lys His
35 40 45

Ile Ser Ile Ser Phe Val Asp Asp Val Pro Ser Asp Ile Gly Leu Ile
50 55 60

Phe Ser Gln Pro Glu Gln Val Thr Gly Ala Lys Ser Leu Arg Asp Ile
65 70 75 80

Tyr His Leu Thr Asp Pro Thr Tyr Lys Gly Pro Tyr Thr Ile Pro Ile
85 90 95

Leu Ile Asp Lys Thr Asp Asn Arg Ile Val Cys Lys Glu Ser Ala Asp
100 105 110

Met Leu Arg Leu Phe Thr Thr Asp Phe Ser Asp Leu His Gln Glu Asp
115 120 125

Ala Pro Val Leu Phe Ser Gln Glu Thr Ala Ser Leu Ile Asp Asn Asp
130 135 140

Ile Lys Asp Ile Asn Asn Asn Phe Gln Ser Leu Met Tyr Lys Leu Ala
145 150 155 160

Phe Leu Asp Lys Gln Ala Asp Tyr Asp Thr Tyr Ser Lys Glu Phe Phe
165 170 175

Thr Phe Leu Asp Gln Lys Glu His Leu Leu Gly Gln Arg Pro Phe Leu
180 185 190

Leu Gly Asp Asn Leu Ser Glu Val Asp Ile His Phe Phe Thr Pro Leu
195 200 205

Val Arg Trp Asp Ile Ala Gly Arg Asp Leu Leu Leu Leu Asn Gln Lys
210 215 220

Ala Leu Glu Asp Tyr Pro Asn Ile Phe Ser Trp Ala Lys Thr Leu Tyr
225 230 235 240

Asn Asp Phe Asn Leu Lys Thr Leu Thr Asn Pro Gln Ser Ile Lys Asn
245 250 255

Asn Tyr Tyr Leu Gly Lys Phe Gly Arg Ala Val Arg His His Thr Ile
260 265 270

Val Pro Thr Gly Pro Asn Met Val Lys Trp Glu Lys
275 280

<210> 317

<211> 690

<212> PRT

<213> Streptococcus agalactiae

<400> 317

Met Lys Lys Lys Ile Ile Leu Lys Ser Ser Val Leu Gly Leu Val Ala
1               5                   10                  15

Gly Thr Ser Ile Met Phe Ser Ser Ala Phe Ala Asp Gln Val Gly Val
            20                  25                  30

Gln Val Ile Gly Val Asn Asp Phe His Gly Ala Leu Asp Asn Thr Gly
        35                  40                  45

Thr Ala Asn Met Pro Asp Gly Lys Val Thr Asn Ala Gly Thr Ala Ala
    50                  55                  60

Gln Leu Asp Ala Tyr Ile Asp Asp Ala Gln Lys Asp Phe Lys Gln Thr
65                  70                  75                  80

Asn Pro Asn Gly Glu Ser Ile Arg Val Gln Ala Gly Asp Met Val Gly
                85                  90                  95

Ala Ser Pro Ala Asn Ser Gly Leu Leu Gln Asp Glu Pro Thr Val Lys
            100                 105                 110

Thr Phe Asn Ala Met Asn Val Glu Tyr Gly Thr Leu Gly Asn His Glu
        115                 120                 125

Phe Asp Glu Gly Leu Ala Glu Tyr Asn Arg Ile Val Thr Gly Lys Ala
    130                 135                 140

Pro Ala Pro Asp Ser Asn Ile Asn Asn Ile Thr Lys Ser Tyr Pro His
145                 150                 155                 160

Glu Ala Ala Lys Gln Glu Ile Val Val Ala Asn Val Ile Asp Lys Val
                165                 170                 175

Asn Lys Gln Ile Pro Tyr Asn Trp Lys Pro Tyr Ala Ile Lys Asn Ile
            180                 185                 190

Pro Val Asn Asn Lys Ser Val Asn Val Gly Phe Ile Gly Ile Val Thr
        195                 200                 205

Lys Asp Ile Pro Asn Leu Val Leu Arg Lys Asn Tyr Glu Gln Tyr Glu
    210                 215                 220

Phe Leu Asp Glu Ala Glu Thr Ile Val Lys Tyr Ala Lys Glu Leu Gln
225                 230                 235                 240

Ala Lys Asn Val Lys Ala Ile Val Val Leu Ala His Val Pro Ala Thr
                245                 250                 255

Ser Lys Asp Asp Ile Ala Glu Gly Glu Ala Ala Glu Met Met Lys Lys
            260                 265                 270

Val Asn Gln Leu Phe Pro Glu Asn Ser Val Asp Ile Val Phe Ala Gly
275 280 285

His Asn His Gln Tyr Thr Asn Gly Leu Val Gly Lys Thr Arg Ile Val
290 295 300

Gln Ala Leu Ser Gln Gly Lys Ala Tyr Ala Asp Val Arg Gly Val Leu
305 310 315 320

Asp Thr Asp Thr Gln Asp Phe Ile Glu Thr Pro Ser Ala Lys Val Val
325 330 335

Ala Val Ala Pro Gly Lys Lys Thr Gly Ser Ala Asp Ile Gln Ala Ile
340 345 350

Val Asp Gln Ala Asn Thr Ile Val Lys Gln Val Thr Glu Ala Lys Ile
355 360 365

Gly Thr Ala Glu Val Ser Gly Met Ile Thr Arg Ser Val Asp Gln Asp
370 375 380

Asn Val Ser Pro Val Gly Ser Leu Ile Thr Glu Ala Gln Leu Ala Ile
385 390 395 400

Ala Arg Lys Ser Trp Pro Asp Ile Asp Phe Ala Met Thr Asn Asn Gly
405 410 415

Gly Ile Arg Ala Asp Leu Leu Ile Lys Pro Asp Gly Thr Ile Thr Trp
420 425 430

Gly Ala Ala Gln Ala Val Gln Pro Phe Gly Asn Ile Leu Gln Val Val
435 440 445

Glu Ile Thr Gly Arg Asp Leu Tyr Lys Ala Leu Asn Glu Gln Tyr Asp
450 455 460

Gln Lys Gln Asn Phe Phe Leu Gln Ile Ala Gly Leu Arg Tyr Thr Tyr
465 470 475 480

Thr Asp Asn Lys Glu Gly Gly Glu Glu Thr Pro Phe Lys Val Val Lys
485 490 495

Ala Tyr Lys Ser Asn Gly Glu Glu Ile Asn Pro Asp Ala Lys Tyr Lys
500 505 510

Leu Val Ile Asn Asp Phe Leu Phe Gly Gly Gly Asp Gly Phe Ala Ser
515 520 525

Phe Arg Asn Ala Lys Leu Leu Gly Ala Ile Asn Pro Asp Thr Glu Val
530 535 540

Phe Met Ala Tyr Ile Thr Asp Leu Glu Lys Ala Gly Lys Lys Val Ser
545 550 555 560

Val Pro Asn Asn Lys Pro Lys Ile Tyr Val Thr Met Lys Met Val Asn
565 570 575

Glu Thr Ile Thr Gln Asn Asp Gly Thr His Ser Ile Ile Lys Lys Leu
580 585 590

Tyr Leu Asp Arg Gln Gly Asn Ile Val Ala Gln Glu Ile Val Ser Asp
595 600 605

Thr Leu Asn Gln Thr Lys Ser Lys Ser Thr Lys Ile Asn Pro Val Thr
610 615 620

Thr Ile His Lys Lys Gln Leu His Gln Phe Thr Ala Ile Asn Pro Met
625 630 635 640

Arg Asn Tyr Gly Lys Pro Ser Asn Ser Thr Thr Val Lys Ser Lys Gln
645 650 655

Leu Pro Lys Thr Asn Ser Glu Tyr Gly Gln Ser Phe Leu Met Ser Val
660 665 670

Phe Gly Val Gly Leu Ile Gly Ile Ala Leu Asn Thr Lys Lys Lys His
675 680 685

Met Lys
690

<210> 318

<211> 579

<212> PRT

<213> Streptococcus agalactiae

<400> 318

Met Ala Tyr Ile Trp Ser Tyr Leu Lys Arg Tyr Pro Asn Trp Leu Trp
1 5 10 15

Leu Asp Leu Leu Gly Ala Met Leu Phe Val Thr Val Ile Leu Gly Met
20 25 30

Pro Thr Ala Leu Ala Gly Met Ile Asp Asn Gly Val Thr Lys Gly Asp
35 40 45

Arg Thr Gly Val Tyr Leu Trp Thr Phe Ile Met Phe Ile Phe Val Val
50 55 60

Leu Gly Ile Ile Gly Arg Ile Thr Met Ala Tyr Ala Ser Ser Arg Leu
65                  70                  75                  80

Thr Thr Thr Met Ile Arg Asp Met Arg Asn Asp Met Tyr Ala Lys Leu
                85                  90                  95

Gln Glu Tyr Ser His His Glu Tyr Glu Gln Ile Gly Val Ser Ser Leu
            100                 105                 110

Val Thr Arg Met Thr Ser Asp Thr Phe Val Leu Met Gln Phe Ala Glu
        115                 120                 125

Met Ser Leu Arg Leu Gly Leu Val Thr Pro Met Val Met Ile Phe Ser
    130                 135                 140

Val Val Met Ile Leu Ile Thr Ser Pro Ser Leu Ala Trp Leu Val Ala
145                 150                 155                 160

Val Ala Met Pro Leu Leu Val Gly Val Val Leu Tyr Val Ala Ile Lys
                165                 170                 175

Thr Lys Pro Leu Ser Glu Arg Gln Gln Thr Met Leu Asp Lys Ile Asn
            180                 185                 190

Gln Tyr Val Arg Glu Asn Leu Thr Gly Leu Arg Val Val Arg Ala Phe
        195                 200                 205

Ala Arg Glu Asn Phe Gln Ser Gln Lys Phe Gln Val Ala Asn Gln Arg
    210                 215                 220

Tyr Thr Asp Thr Ser Thr Gly Leu Phe Lys Leu Thr Gly Leu Thr Glu
225                 230                 235                 240

Pro Leu Phe Val Gln Ile Ile Ile Ala Met Ile Val Ala Ile Val Trp
                245                 250                 255

Phe Ala Leu Asp Pro Leu Gln Arg Gly Ala Ile Lys Ile Gly Asp Leu
            260                 265                 270

Val Ala Phe Ile Glu Tyr Ser Phe His Ala Leu Phe Ser Phe Leu Leu
        275                 280                 285

Phe Ala Asn Leu Phe Thr Met Tyr Pro Arg Met Val Val Ser Ser His
    290                 295                 300

Arg Ile Arg Glu Val Met Asp Met Pro Ile Ser Ile Asn Pro Asn Ala
305                 310                 315                 320

Glu Gly Val Thr Asp Thr Lys Leu Lys Gly His Leu Glu Phe Asp Asn
                325                 330                 335

Val Thr Phe Ala Tyr Pro Gly Glu Thr Glu Ser Pro Val Leu His Asp
340 345 350

Ile Ser Phe Lys Ala Lys Pro Gly Glu Thr Ile Ala Phe Ile Gly Ser
355 360 365

Thr Gly Ser Gly Lys Ser Ser Leu Val Asn Leu Ile Pro Arg Phe Tyr
370 375 380

Asp Val Thr Leu Gly Lys Ile Leu Val Asp Gly Val Asp Val Arg Asp
385 390 395 400

Tyr Asn Leu Lys Ser Leu Arg Gln Lys Ile Gly Phe Ile Pro Gln Lys
405 410 415

Ala Leu Leu Phe Thr Gly Thr Ile Gly Glu Asn Leu Lys Tyr Gly Lys
420 425 430

Ala Asp Ala Thr Ile Asp Asp Leu Arg Gln Ala Val Asp Ile Ser Gln
435 440 445

Ala Lys Glu Phe Ile Glu Ser His Gln Glu Ala Phe Glu Thr His Leu
450 455 460

Ala Glu Gly Gly Ser Asn Leu Ser Gly Gly Gln Lys Gln Arg Leu Ser
465 470 475 480

Ile Ala Arg Ala Val Val Lys Asp Pro Asp Leu Tyr Ile Phe Asp Asp
485 490 495

Ser Phe Ser Ala Leu Asp Tyr Lys Thr Asp Ala Thr Leu Arg Ala Arg
500 505 510

Leu Lys Glu Val Thr Gly Asp Ser Thr Val Leu Ile Val Ala Gln Arg
515 520 525

Val Gly Thr Ile Met Asp Ala Asp Gln Ile Ile Val Leu Asp Glu Gly
530 535 540

Glu Ile Val Gly Arg Gly Thr His Ala Gln Leu Ile Glu Asn Asn Ala
545 550 555 560

Ile Tyr Arg Glu Ile Ala Glu Ser Gln Leu Lys Asn Gln Asn Leu Ser
565 570 575

Glu Gly Glu

<210> 319

<211> 543

<212> PRT

<213> Streptococcus agalactiae

<400> 319

Met Lys Lys Gly Gln Val Asn Asp Thr Lys Gln Ser Tyr Ser Leu Arg
1 5 10 15

Lys Tyr Lys Phe Gly Leu Ala Ser Val Ile Leu Gly Pro Phe Ile Met
20 25 30

Val Thr Ser Pro Val Phe Ala Asp Gln Thr Thr Ser Val Gln Val Asn
35 40 45

Asn Gln Thr Gly Thr Ser Val Asp Ala Asn Asn Ser Ser Asn Glu Thr
50 55 60

Ser Ala Ser Ser Val Ile Thr Ser Asn Asn Asp Ser Val Gln Ala Ser
65 70 75 80

Asp Lys Val Val Asn Ser Gln Asn Thr Ala Thr Lys Asp Ile Thr Thr
85 90 95

Pro Leu Val Glu Thr Lys Pro Met Val Glu Lys Thr Leu Pro Glu Gln
100 105 110

Gly Asn Tyr Val Tyr Ser Lys Glu Thr Glu Val Lys Asn Thr Pro Ser
115 120 125

Lys Ser Ala Pro Val Ala Phe Tyr Ala Lys Lys Gly Asp Lys Val Phe
130 135 140

Tyr Asp Gln Val Phe Asn Lys Asp Asn Val Lys Trp Ile Ser Tyr Lys
145 150 155 160

Ser Phe Cys Gly Val Arg Arg Tyr Ala Ala Ile Glu Ser Leu Asp Pro
165 170 175

Ser Gly Gly Ser Glu Thr Lys Ala Pro Thr Pro Val Thr Asn Ser Gly
180 185 190

Ser Asn Asn Gln Glu Lys Ile Ala Thr Gln Gly Asn Tyr Thr Phe Ser
195 200 205

His Lys Val Glu Val Lys Asn Glu Ala Lys Val Ala Ser Pro Thr Gln
210 215 220

Phe Thr Leu Asp Lys Gly Asp Arg Ile Phe Tyr Asp Gln Ile Leu Thr
225 230 235 240

Ile Glu Gly Asn Gln Trp Leu Ser Tyr Lys Ser Phe Asn Gly Val Arg
245 250 255

Arg Phe Val Leu Leu Gly Lys Ala Ser Ser Val Glu Lys Thr Glu Asp
260 265 270

Lys Glu Lys Val Ser Pro Gln Pro Gln Ala Arg Ile Thr Lys Thr Gly
275 280 285

Arg Leu Thr Ile Ser Asn Glu Thr Thr Thr Gly Phe Asp Ile Leu Ile
290 295 300

Thr Asn Ile Lys Asp Asp Asn Gly Ile Ala Ala Val Lys Val Pro Val
305 310 315 320

Trp Thr Glu Gln Gly Gly Gln Asp Asp Ile Lys Trp Tyr Thr Ala Val
325 330 335

Thr Thr Gly Asp Gly Asn Tyr Lys Val Ala Val Ser Phe Ala Asp His
340 345 350

Lys Asn Glu Lys Gly Leu Tyr Asn Ile His Leu Tyr Tyr Gln Glu Ala
355 360 365

Ser Gly Thr Leu Val Gly Val Thr Gly Thr Lys Val Thr Val Ala Gly
370 375 380

Thr Asn Ser Ser Gln Glu Pro Ile Glu Asn Gly Leu Ala Lys Thr Gly
385 390 395 400

Val Tyr Asn Ile Ile Gly Ser Thr Glu Val Lys Asn Glu Ala Lys Ile
405 410 415

Ser Ser Gln Thr Gln Phe Thr Leu Glu Lys Gly Asp Lys Ile Asn Tyr
420 425 430

Asp Gln Val Leu Thr Ala Asp Gly Tyr Gln Trp Ile Ser Tyr Lys Ser
435 440 445

Tyr Ser Gly Val Arg Arg Tyr Ile Pro Val Lys Lys Leu Thr Thr Ser
450 455 460

Ser Glu Lys Ala Lys Asp Glu Ala Thr Lys Pro Thr Ser Tyr Pro Asn
465 470 475 480

Leu Pro Lys Thr Gly Thr Tyr Thr Phe Thr Lys Thr Val Asp Val Lys
485 490 495

Ser Gln Pro Lys Val Ser Ser Pro Val Glu Phe Asn Phe Gln Lys Gly
500 505 510

Glu Lys Ile His Tyr Asp Gln Val Leu Val Val Asp Gly His Gln Trp
515 520 525

Ile Ser Tyr Lys Ser Tyr Ser Gly Ile Arg Arg Tyr Ile Glu Ile
530 535 540

<210> 320

<211> 415

<212> PRT

<213> Streptococcus agalactiae

<400> 320

Met Glu Asn Trp Lys Phe Ala Leu Ser Ser Ile Leu Gly His Lys Met
1 5 10 15

Arg Ala Phe Leu Thr Met Leu Gly Ile Ile Ile Gly Val Ala Ser Val
20 25 30

Val Leu Ile Met Ala Leu Gly Lys Gly Met Lys Asp Ser Val Thr Asn
35 40 45

Glu Ile Thr Lys Ser Gln Lys Asn Leu Gln Ile Tyr Tyr Lys Thr Lys
50 55 60

Glu Asp Gln Lys Asn Glu Asp Asn Phe Gly Ala Gln Gly Ala Phe Met
65 70 75 80

Gln Gly Ser Asp Thr Asn Arg Lys Glu Pro Ile Ile Gln Glu Ser Trp
85 90 95

Leu Lys Lys Ile Ala Lys Glu Val Asp Gly Val Ser Gly Tyr Tyr Val
100 105 110

Thr Asn Gln Thr Asn Ala Pro Val Ala Tyr Leu Glu Lys Lys Ala Lys
115 120 125

Thr Val Asn Ile Thr Gly Val Asn Arg Thr Tyr Leu Gly Ile Lys Lys
130 135 140

Phe Lys Ile Lys Ser Gly Arg Gln Phe Gln Glu Glu Asp Tyr Asn Gln
145 150 155 160

Phe Ser Arg Val Ile Leu Leu Glu Glu Lys Leu Ala Gln Arg Leu Phe
165 170 175

Gln Thr Asn Glu Ala Ala Leu Asn Lys Val Val Thr Val Lys Asn Lys
180 185 190

Ser Tyr Leu Val Val Gly Val Tyr Ser Asp Pro Glu Ala Gly Ser Gly
195 200 205

Leu Tyr Gly Ser Asn Ser Asp Gly Asn Ala Ile Leu Thr Asn Thr Gln
210 215 220

Leu Ala Ser Glu Phe Gly Ala Lys Glu Ala Glu Asn Ile Tyr Phe His
225 230 235 240

Leu Asn Asp Val Ser Gln Ser Asn Arg Ile Gly Lys Glu Ile Gly Lys
245 250 255

Arg Leu Thr Asp Ile Ser His Ala Lys Asp Gly Tyr Tyr Asp Asn Phe
260 265 270

Asp Met Thr Ser Ile Val Lys Ser Ile Asn Thr Gln Val Gly Ile Met
275 280 285

Thr Gly Val Ile Gly Ala Ile Ala Ala Ile Ser Leu Leu Val Gly Gly
290 295 300

Ile Gly Val Met Asn Ile Met Leu Val Ser Val Thr Glu Arg Thr Arg
305 310 315 320

Glu Ile Gly Leu Arg Lys Ala Leu Gly Ala Thr Arg Arg Lys Ile Leu
325 330 335

Ala Gln Phe Leu Ile Glu Ser Met Val Leu Thr Ile Leu Gly Gly Leu
340 345 350

Ile Gly Leu Leu Leu Ala Tyr Gly Gly Thr Met Leu Ile Ala Asn Ala
355 360 365

Gln Asp Lys Ile Thr Pro Ser Val Ser Leu Asn Val Ala Ile Gly Ser
370 375 380

Leu Ile Phe Ser Ala Phe Ile Gly Ile Ile Phe Gly Leu Leu Pro Ala
385 390 395 400

Asn Lys Ala Ser Lys Leu Asn Pro Ile Asp Ala Leu Arg Tyr Glu
405 410 415

<210> 321

<211> 404

<212> PRT

<213> Streptococcus agalactiae

<400> 321

Met Gln Tyr Ser Glu Ile Met Ile Arg Tyr Gly Glu Leu Ser Thr Lys
1 5 10 15

Lys Lys Asn Arg Met Arg Phe Ile Asn Lys Leu Lys Asn Asn Met Glu
20 25 30

His Val Leu Ser Ile Tyr Pro Asp Val Ser Val Lys Thr Asp Arg Asp
35 40 45

Arg Gly His Val Tyr Leu Asn Gly Thr Asp Tyr His Glu Val Ala Glu
50 55 60

Ser Leu Lys Glu Ile Phe Gly Ile Gln Ala Phe Ser Pro Ser Phe Lys
65 70 75 80

Val Glu Lys Asn Val Asp Thr Leu Val Lys Ala Val Gln Glu Ile Met
85 90 95

Thr Ser Val Tyr Lys Asp Gly Met Thr Phe Lys Ile Thr Ala Lys Arg
100 105 110

Ser Asp His Ser Phe Glu Leu Asp Ser Arg Ala Leu Asn His Thr Leu
115 120 125

Gly Asp Ala Val Phe Ser Val Leu Pro Asn Ile Lys Ala Gln Met Lys
130 135 140

Gln Pro Asp Ile Asn Leu Lys Val Glu Ile Arg Asp Glu Ala Ala Tyr
145 150 155 160

Ile Ser Tyr Glu Asn Ile Arg Gly Ala Gly Gly Leu Pro Val Gly Thr
165 170 175

Ser Gly Lys Gly Met Leu Met Leu Ser Gly Gly Ile Asp Ser Pro Val
180 185 190

Ala Gly Tyr Leu Ala Leu Lys Arg Gly Val Asp Ile Glu Ala Val His
195 200 205

Phe Ala Ser Pro Pro Tyr Thr Ser Pro Gly Ala Leu Lys Lys Ala His
210 215 220

Asp Leu Thr Arg Lys Leu Thr Lys Phe Gly Gly Asn Ile Gln Phe Ile
225 230 235 240

Glu Val Pro Phe Thr Glu Ile Gln Glu Glu Ile Lys Glu Lys Ala Pro
245 250 255

Glu Ala Tyr Leu Met Thr Leu Thr Arg Arg Phe Met Met Arg Ile Thr
260 265 270

Asp Arg Ile Arg Glu Asn Arg Asn Gly Leu Val Ile Ile Asn Gly Glu
275 280 285

Ser Leu Gly Gln Val Ala Ser Gln Thr Leu Glu Ser Met Gln Ala Ile
290 295 300

Asn Ala Val Thr Ala Thr Pro Ile Ile Arg Pro Val Val Thr Met Asp
305 310 315 320

Lys Leu Glu Ile Ile Asp Ile Ala Gln Lys Ile Asp Thr Phe Asp Ile
325 330 335

Ser Ile Gln Pro Phe Glu Asp Cys Cys Thr Ile Phe Ala Pro Asp Arg
340 345 350

Pro Lys Thr Asn Pro Lys Ile Lys Asn Thr Glu Gln Tyr Glu Lys Arg
355 360 365

Met Asp Val Glu Gly Leu Val Glu Arg Ala Val Ala Gly Ile Met Val
370 375 380

Thr Thr Ile Gln Pro Gln Ala Asp Ser Asp Asp Val Asp Asp Leu Ile
385 390 395 400

Asp Asp Leu Leu

<210> 322

<211> 119

<212> PRT

<213> Streptococcus agalactiae

<400> 322

Met Ala Arg Val Lys Gly Gly Val Val Ser Arg Lys Arg Arg Lys Arg
1 5 10 15

Val Leu Lys Leu Ala Lys Gly Tyr Tyr Gly Ala Lys His Ile Leu Phe
20 25 30

Arg Thr Ala Lys Glu Gln Val Met Asn Ser Tyr Tyr Tyr Ala Tyr Arg
35 40 45

Asp Arg Arg Gln Lys Lys Arg Asp Phe Arg Lys Leu Trp Ile Thr Arg
50 55 60

Ile Asn Ala Ala Ala Arg Met Asn Gly Leu Ser Tyr Ser Gln Leu Met
65 70 75 80

His Gly Leu Lys Leu Ala Glu Ile Glu Val Asn Arg Lys Met Leu Ala
85 90 95

Asp Leu Ala Val Asn Asp Ala Ala Ala Phe Thr Ala Leu Ala Asp Ala
100 105 110

Ala Lys Ala Lys Leu Gly Lys
115

<210> 323

<211> 341

<212> PRT

<213> Streptococcus agalactiae

<400> 323

Met Phe Lys Ala Ser Lys Lys Leu Val Gln Lys Asn Lys Ser Asn His
1 5 10 15

Phe Trp Leu Val Phe Phe Ile Thr Leu Ile Leu Phe Leu Ile Gly Cys
20 25 30

Tyr Ala Ser Leu Arg Phe Gly Ala Ile Asn Phe Lys Thr Ser Asp Leu
35 40 45

Ile Thr Val Leu Lys Asn Pro Leu Lys Asn Ser Asn Ala Gln Asp Val
50 55 60

Ile Phe Asp Ile Arg Leu Pro Arg Ile Ile Ala Ala Ile Leu Val Gly
65 70 75 80

Ala Ala Met Ser Gln Ala Gly Ala Ile Met Gln Gly Val Thr Arg Asn
85 90 95

Ala Ile Ala Asp Pro Gly Leu Leu Gly Ile Asn Ala Gly Ala Gly Leu
100 105 110

Ala Leu Val Val Ala Tyr Ala Phe Leu Gly Ser Met His Tyr Ser Thr
115 120 125

Ile Leu Ile Val Cys Leu Leu Gly Ser Val Ile Ser Tyr Leu Leu Val
130 135 140

Phe Thr Leu Ser Tyr Thr Lys Gln Lys Gly Tyr His Gln Leu Arg Leu
145 150 155 160

Ile Leu Ala Gly Ala Met Ile Ser Thr Leu Phe Thr Ser Val Gly Gln
165 170 175

Val Val Thr Leu Tyr Phe Lys Leu Asn Arg Thr Val Ile Gly Trp Gln
180 185 190

Ala Gly Gly Leu Ser Gln Ile Asn Trp Lys Met Leu Ile Ile Ile Ala
195 200 205

Pro Ile Ile Ile Leu Gly Leu Leu Ile Ser Gln Leu Leu Ala His Gln
210 215 220

Leu Thr Ile Leu Ser Leu Asn Glu Ser Val Ala Lys Ala Leu Gly Gln
225 230 235 240

Lys Thr Gln Leu Met Thr Ala Phe Leu Leu Leu Ile Val Leu Phe Leu
245 250 255

Ser Ala Ser Ser Val Ala Leu Ile Gly Thr Val Ser Phe Ile Gly Leu
260 265 270

Ile Ile Pro His Phe Ile Lys Leu Phe Ile Pro Lys Asp Tyr Arg Leu
275 280 285

Leu Leu Pro Leu Ile Gly Phe Ser Gly Ala Thr Phe Met Ile Trp Val
290 295 300

Asp Leu Ser Ser Arg Ile Ile Asn Pro Pro Ser Glu Thr Pro Ile Ser
305 310 315 320

Ser Ile Ile Ser Ile Val Gly Leu Pro Cys Phe Leu Trp Leu Ile Arg
325 330 335

Lys Gly Lys Asn Leu
340

<210> 324

<211> 188

<212> PRT

<213> Streptococcus agalactiae

<400> 324

Met Ile Lys Arg Pro Ile His Leu Ser His Asp Phe Leu Ala Glu Val
1 5 10 15

Ile Asp Lys Glu Ala Ile Thr Leu Asp Ala Thr Met Gly Asn Gly Asn
20 25 30

Asp Thr Val Phe Leu Ala Lys Ser Ser Lys Lys Val Tyr Ala Phe Asp
35 40 45

Ile Gln Glu Glu Ala Ile Ala Lys Thr Lys Ala Lys Leu Thr Glu Gln
50 55 60

Gly Ile Ser Asn Ala Glu Leu Ile Leu Asp Gly His Glu Asn Leu Glu
65 70 75 80

Gln Tyr Val His Thr Pro Leu Arg Ala Ala Ile Phe Asn Leu Gly Tyr
85 90 95

Leu Pro Ser Ala Asp Lys Thr Val Ile Thr Lys Pro His Thr Thr Ile
100 105 110

Lys Ala Ile Lys Asn Val Leu Asp Ile Leu Glu Val Gly Gly Arg Leu
115 120 125

Ser Leu Met Val Tyr Tyr Gly His Asp Gly Gly Lys Ser Glu Lys Asp
130 135 140

Ala Val Ile Ala Phe Val Glu Gln Leu Pro Gln Asn Asn Phe Ala Thr
145 150 155 160

Met Leu Tyr Gln Pro Leu Asn Gln Val Asn Thr Pro Pro Phe Leu Ile
165 170 175

Met Val Glu Lys Leu Gln Ser Tyr Glu Asn Glu Val
180 185

<210> 325

<211> 335

<212> PRT

<213> Streptococcus agalactiae

<400> 325

Met Arg Val His Ile Thr Ser Ile Tyr Gly Gln Ser Pro Arg Ser Ile
1 5 10 15

Ala Leu Ile Ser Gln Lys Leu Val Lys Asp Val Gly Arg Gln Leu Gly
20 25 30

Tyr Asp Glu Met Gly Ile Tyr Phe Tyr Asn Asp His Ala Glu Thr His
35 40 45

Gly Glu Arg Ser Thr Arg Met Asp Gly Ile Ile Ala Gly Leu Gly Arg
50 55 60

Gly Asp Ile Val Val Phe Gln Val Pro Thr Trp Asn Ser Thr Glu Phe
65 70 75 80

Asp Glu Leu Phe Leu Asp Lys Leu Gln Ala Tyr Gly Ala Arg Ile Ile
85 90 95

Thr Phe Val His Asp Ile Val Pro Leu Met Phe Glu Ser Asn Phe Tyr
100 105 110

Leu Leu Asp Arg Val Ile Asp Met Tyr Asn Arg Ser Asp Val Val Ile
115 120 125

Leu Pro Thr Lys Ala Met His Asp Tyr Leu Ile Glu Lys Gly Met Thr
130 135 140

Thr Ser Lys Val Leu Tyr Gln Glu Val Trp Asp His Pro Val Asn Ile
145 150 155 160

Asp Leu Pro Arg Pro Glu Cys Gln Lys Val Leu Ser Phe Ala Gly Asp
165 170 175

Ile Gln Arg Phe Pro Phe Val Asn Asp Trp Lys Glu Asn Ile Pro Leu
180 185 190

Ile Tyr Tyr Gly Asp Gly Ser Arg Leu Asn Ser Glu Ala Asn Val His
195 200 205

Ala Gln Gly Trp Lys Asp Asp Val Glu Leu Met Leu Ser Leu Ser Lys
210 215 220

Arg Gly Gly Phe Gly Leu Cys Trp Ser Glu Asp Arg Glu Glu Leu Val
225 230 235 240

Glu Arg Arg Tyr Ser Arg Met Asn Ala Ser Tyr Lys Leu Ser Thr Phe
245 250 255

Leu Ala Ala Gly Leu Pro Ile Ile Ala Asn His Asp Ile Ser Ser Arg
260 265 270

Asp Phe Ile Lys Gln His Gly Leu Gly Phe Thr Val Glu Thr Leu Glu
275 280 285

Glu Ala Val Glu Lys Ile Asn Asn Met Glu Lys Glu Thr Tyr Asp Ser
290 295 300

Tyr Val Glu Asn Val Glu Lys Ile Ala Thr Leu Leu Arg Asn Gly Tyr
305 310 315 320

Ile Thr Lys Lys Leu Leu Ile Asp Ala Val His Met Leu Tyr Arg
325 330 335

<210> 326

<211> 1310

<212> PRT

<213> Streptococcus agalactiae

<400> 326

Met Ser Gln Lys Thr Phe Gly Lys Gln Leu Thr Val Val Asp Thr Lys
1 5 10 15

Ser Arg Val Lys Met His Lys Ser Gly Lys Asn Trp Val Arg Thr Val
20 25 30

Met Ser His Phe Asn Leu Phe Lys Ala Ile Lys Gly Arg Ala Thr Val
35 40 45

Glu Ala Asp Val Cys Ile Gln Asp Val Glu Lys Glu Asp Arg Leu Ser
50 55 60

Ser Gly Asn Leu Thr Tyr Leu Lys Gly Ile Leu Ala Ala Gly Ala Leu
65 70 75 80

Val Gly Gly Ala Ser Leu Thr Ser Arg Val Tyr Ala Asp Glu Thr Pro
85 90 95

Val Val Gln Glu Gln Ser Ser Ser Val Pro Thr Leu Ala Glu Gln Thr
100 105 110

Glu Val Thr Val Lys Thr Thr Thr Val Gln Asn His Gln Asp Gly Thr
115 120 125

Val Ser Lys Asn Ile Ile Asp Ser Asn Ser Val Ser Met Ser Glu Ser
130 135 140

Ala Ser Thr Ser Thr Ser Glu Ser Val Ser Met Ser Met Ser Gly Ser
145 150 155 160

Thr Leu Thr Ser Val Ser Glu Ser Val Ser Thr Ser Ala Leu Thr Ser
165 170 175

Ala Ser Glu Ser Ile Ser Thr Ser Ala Ser Glu Ser Val Ser Lys Ser
180 185 190

Thr Ser Ile Ser Glu Val Ser Asn Ile Leu Glu Thr Gln Ala Ser Leu
195 200 205

Thr Asp Lys Gly Arg Glu Ser Phe Ser Ala Asn Gln Ile Val Thr Glu
210 215 220

Ser Ser Leu Val Thr Asp Ala Gly Lys Asn Ala Ser Val Ser Ser Leu
225 230 235 240

Ile Glu Ile Thr Lys Pro Lys Ser Glu Leu Gln Thr Ser Lys Met Ser
245 250 255

Asn Glu Ser Leu Ile Thr Pro Glu Lys Ser Gln Val Met Ile Ala Ser
260 265 270

Asp Lys Thr Gly Asn Glu Ser Leu Thr Pro Thr Ile Arg Leu Lys Ser
275 280 285

Val Ile Gln Pro Arg Ser Met Asn Leu Met Thr Leu Ser Ser Glu Met
290 295 300

Asp Leu Ile Pro Leu Glu Glu Val Ser Asp Thr Glu Met Leu Gly Lys
305 310 315 320

Asp Val Ser Ser Glu Leu Gln Lys Val Asn Ile Ala Leu Lys Asp Asn
325 330 335

Thr Leu Ser Glu Pro Gly Thr Val Lys Leu Asp Ser Ser Glu Asn Leu
340 345 350

Val Leu Asn Phe Ala Phe Ser Ile Ala Ser Val Asn Glu Gly Asp Val
355 360 365

Phe Thr Val Lys Leu Ser Asp Asn Leu Asp Thr Gln Gly Ile Gly Thr
370 375 380

Ile Leu Lys Val Gln Asp Ile Met Asp Glu Thr Gly Gln Leu Leu Ala
385 390 395 400

Thr Gly Ser Tyr Ser Pro Leu Thr His Asn Ile Thr Tyr Thr Trp Thr
405 410 415

Arg Tyr Ala Ser Thr Leu Asn Asn Ile Lys Ala Arg Val Asn Met Pro
420 425 430

Val Trp Pro Asp Gln Arg Ile Ile Ser Lys Thr Thr Ser Asp Lys Gln
435 440 445

Cys Phe Thr Ala Thr Leu Asn Asn Gln Val Ala Ser Ile Glu Glu Arg
450 455 460

Val Gln Tyr Asn Ser Pro Ser Val Thr Glu His Thr Asn Val Lys Thr
465 470 475 480

Asn Val Arg Ser Arg Ile Met Lys Leu Asp Asp Glu Arg Gln Thr Glu
485 490 495

Thr Tyr Ile Thr Gln Ile Asn Pro Glu Gly Lys Glu Met Tyr Phe Ala
500 505 510

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Ser Gly Leu Gly Asn Leu Tyr Thr Ile Ile Gly Ser Asp Gly Thr Ser
        515                 520                 525

Gly Ser Pro Val Asn Leu Leu Asn Ala Glu Val Lys Ile Leu Lys Thr
    530                 535                 540

Asn Ser Lys Asn Leu Thr Asp Ser Met Asp Gln Asn Tyr Asp Ser Pro
545                 550                 555                 560

Glu Phe Glu Asp Val Thr Ser Gln Tyr Ser Tyr Thr Asn Asp Gly Ser
                565                 570                 575

Lys Ile Thr Ile Asp Trp Lys Thr Asn Ser Ile Ser Ser Thr Thr Ser
            580                 585                 590

Tyr Val Val Leu Val Lys Ile Pro Lys Gln Ser Gly Val Leu Tyr Ser
        595                 600                 605

Thr Val Ser Asp Ile Asn Gln Thr Tyr Gly Ser Lys Tyr Ser Tyr Gly
    610                 615                 620

His Thr Asn Ile Ser Gly Asp Ser Asp Ala Asn Ala Glu Ile Lys Leu
625                 630                 635                 640

Leu Ser Glu Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
                645                 650                 655

Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser
            660                 665                 670

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser
        675                 680                 685

Ala Ser Thr Ser Ala Ser Thr Ser Thr Ser Thr Ser Ala Ser Thr Ser
    690                 695                 700

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser
705                 710                 715                 720

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
                725                 730                 735

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
            740                 745                 750

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
        755                 760                 765

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Met Ser
    770                 775                 780
```

Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Thr Ser
785 790 795 800

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
805 810 815

Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
820 825 830

Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
835 840 845

Ala Ser Thr Ser Ala Ser Thr Ser Thr Ser Thr Ser Ala Ser Thr Ser
850 855 860

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser
865 870 875 880

Ala Ser Thr Ser Pro Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
885 890 895

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser
900 905 910

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser
915 920 925

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser
930 935 940

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser
945 950 955 960

Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
965 970 975

Ala Ser Thr Ser Thr Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
980 985 990

Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Thr Ser
995 1000 1005

Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Ile
1010 1015 1020

Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser Ala Ser
1025 1030 1035

Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser Ala
1040 1045 1050

Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser
1055 1060 1065

Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr
1070 1075 1080

Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser
1085 1090 1095

Thr Ser Ala Ser Thr Ser Ser Ser Thr Ser Ala Ser Thr Ser Ala
1100 1105 1110

Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser
1115 1120 1125

Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Thr
1130 1135 1140

Ser Ala Ser Thr Ser Ala Ser Met Ser Ala Ser Thr Ser Ser Ser
1145 1150 1155

Thr Ser Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Met Ser Ala
1160 1165 1170

Ser Thr Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser Met Ser
1175 1180 1185

Ala Ser Thr Ser Ser Ser Thr Ser Ala Ser Met Ser Ala Ser Thr
1190 1195 1200

Ser Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Thr Ser Ala Ser
1205 1210 1215

Thr Ser Ala Ser Met Ser Ala Ser Thr Ser Ala Ser Met Ser Ala
1220 1225 1230

Thr Thr Ser Ala Ser Thr Ser Val Ser Thr Ser Ala Ser Thr Ser
1235 1240 1245

Ala Ser Thr Ser Ala Ser Thr Ser Ser Ser Ser Ser Val Thr Ser
1250 1255 1260

Asn Ser Ser Lys Glu Lys Val Tyr Ser Ala Leu Pro Ser Thr Gly
1265 1270 1275

Asp Gln Asp Tyr Ser Val Thr Ala Thr Ala Leu Gly Leu Gly Leu
1280 1285 1290

Met Thr Gly Ala Thr Leu Leu Gly Arg Lys Lys Ser Lys Lys Asp
1295 1300 1305

Lys Asp
1310

<210> 327

<211> 663

<212> PRT

<213> Streptococcus agalactiae

<400> 327

Met Ile Asp Arg Lys Asp Thr Asn Arg Phe Lys Leu Val Ser Lys Tyr
1 5 10 15

Ser Pro Ser Gly Asp Gln Pro Gln Ala Ile Glu Thr Leu Val Asp Asn
20 25 30

Ile Glu Gly Gly Glu Lys Ala Gln Ile Leu Lys Gly Ala Thr Gly Thr
35 40 45

Gly Lys Thr Tyr Thr Met Ser Gln Val Ile Ala Gln Val Asn Lys Pro
50 55 60

Thr Leu Val Ile Ala His Asn Lys Thr Leu Ala Gly Gln Leu Tyr Gly
65 70 75 80

Glu Phe Lys Glu Phe Phe Pro Asp Asn Ala Val Glu Tyr Phe Val Ser
85 90 95

Tyr Tyr Asp Tyr Tyr Gln Pro Glu Ala Tyr Val Pro Ser Ser Asp Thr
100 105 110

Tyr Ile Glu Lys Asp Ser Ser Val Asn Asp Glu Ile Asp Lys Leu Arg
115 120 125

His Ser Ala Thr Ser Ser Leu Leu Glu Arg Asn Asp Val Ile Val Val
130 135 140

Ala Ser Val Ser Cys Ile Tyr Gly Leu Gly Ser Pro Lys Glu Tyr Ala
145 150 155 160

Asp Ser Val Val Ser Leu Arg Pro Gly Gln Glu Ile Ser Arg Asp Gln
165 170 175

Leu Leu Asn Asn Leu Val Asp Ile Gln Phe Glu Arg Asn Asp Ile Asp
180 185 190

Phe Gln Arg Gly Lys Phe Arg Val Arg Gly Asp Val Val Glu Val Phe
195 200 205

Pro Ala Ser Arg Asp Glu His Ala Phe Arg Ile Glu Phe Phe Gly Asp
210 215 220

Glu Ile Asp Arg Ile Arg Glu Ile Glu Ser Leu Thr Gly Arg Val Leu
225 230 235 240

Gly Glu Val Glu His Leu Ala Ile Phe Pro Ala Thr His Phe Met Thr
245 250 255

Asn Asp Glu His Met Glu Glu Ala Ile Ser Lys Ile Gln Ala Glu Met
260 265 270

Glu Asn Gln Val Glu Leu Phe Glu Lys Glu Gly Lys Leu Ile Glu Ala
275 280 285

Gln Arg Ile Arg Gln Arg Thr Glu Tyr Asp Ile Glu Met Leu Arg Glu
290 295 300

Met Gly Tyr Thr Asn Gly Val Glu Asn Tyr Ser Arg His Met Asp Gly
305 310 315 320

Arg Ser Glu Gly Glu Pro Pro Phe Thr Leu Leu Asp Phe Phe Pro Glu
325 330 335

Asp Phe Leu Ile Met Ile Asp Glu Ser His Met Thr Met Gly Gln Ile
340 345 350

Lys Gly Met Tyr Asn Gly Asp Arg Ser Arg Lys Glu Met Leu Val Asn
355 360 365

Tyr Gly Phe Arg Leu Pro Ser Ala Leu Asp Asn Arg Pro Leu Arg Arg
370 375 380

Glu Glu Phe Glu Ser His Val His Gln Ile Val Tyr Val Ser Ala Thr
385 390 395 400

Pro Gly Asp Tyr Glu Met Glu Gln Thr Asp Thr Val Val Glu Gln Ile
405 410 415

Ile Arg Pro Thr Gly Leu Leu Asp Pro Glu Val Glu Val Arg Pro Ser
420 425 430

Met Gly Gln Met Asp Asp Leu Leu Gly Glu Ile Asn Leu Arg Thr Glu
435 440 445

Lys Gly Glu Arg Thr Phe Ile Thr Thr Leu Thr Lys Arg Met Ala Glu
450 455 460

Asp Leu Thr Asp Tyr Leu Lys Glu Met Gly Val Lys Val Lys Tyr Met
465 470 475 480

His Ser Asp Ile Lys Thr Leu Glu Arg Thr Glu Ile Ile Arg Asp Leu
485 490 495

Arg Leu Gly Val Phe Asp Val Leu Ile Gly Ile Asn Leu Leu Arg Glu
500 505 510

Gly Ile Asp Val Pro Glu Val Ser Leu Val Ala Ile Leu Asp Ala Asp
515 520 525

Lys Glu Gly Phe Leu Arg Asn Glu Arg Gly Leu Ile Gln Thr Ile Gly
530 535 540

Arg Ala Ala Arg Asn Ser Asn Gly His Val Ile Met Tyr Ala Asp Lys
545 550 555 560

Ile Thr Asp Ser Met Gln Arg Ala Met Asp Glu Thr Ala Arg Arg Arg
565 570 575

Arg Leu Gln Met Asp Tyr Asn Glu Lys His Gly Ile Val Pro Gln Thr
580 585 590

Ile Lys Lys Glu Ile Arg Asp Leu Ile Ala Ile Thr Lys Ser Asn Asp
595 600 605

Ser Asp Lys Pro Glu Lys Val Val Asp Tyr Ser Ser Leu Ser Lys Lys
610 615 620

Glu Arg Gln Ala Glu Ile Lys Ala Leu Gln Gln Gln Met Gln Glu Ala
625 630 635 640

Ala Glu Leu Leu Asp Phe Glu Leu Ala Ala Gln Ile Arg Asp Val Ile
645 650 655

Leu Glu Leu Lys Ala Ile Asp
660

<210> 328

<211> 727

<212> PRT

<213> Streptococcus agalactiae

<400> 328

Met Lys His Lys Leu Lys Ala Phe Thr Leu Ala Leu Leu Ser Ile Phe
1 5 10 15

Phe Val Phe Gly Gly Lys Val Ser Ala Glu Thr Val Asn Ile Val Ser
20 25 30

Asp Thr Ala Tyr Ala Pro Phe Glu Phe Lys Asp Ser Asp Gln Thr Tyr
        35                  40                  45

Lys Gly Ile Asp Val Asp Ile Val Asn Glu Val Ala Lys Arg Ala Gly
    50                  55                  60

Trp Asn Val Asn Met Thr Tyr Pro Gly Phe Asp Ala Ala Val Asn Ala
65                  70                  75                  80

Val Gln Ser Gly Gln Ala Asp Ala Leu Met Ala Gly Thr Thr Val Thr
                85                  90                  95

Glu Ala Arg Lys Lys Val Phe Asn Phe Ser Asp Thr Tyr Tyr Asp Thr
            100                 105                 110

Ser Val Ile Leu Tyr Thr Lys Asn Asn Asn Lys Val Thr Asn Tyr Lys
        115                 120                 125

Gln Leu Lys Gly Lys Val Val Gly Val Lys Asn Gly Thr Ala Ala Gln
    130                 135                 140

Ser Phe Leu Glu Glu Asn Lys Ser Lys Tyr Gly Tyr Lys Val Lys Thr
145                 150                 155                 160

Phe Asp Thr Ser Asp Leu Met Asn Asn Ser Leu Asp Ser Gly Ser Ile
                165                 170                 175

Tyr Ala Ala Met Asp Asp Gln Pro Val Val Gln Phe Ala Ile Asn Gln
            180                 185                 190

Gly Lys Ala Tyr Ala Ile Asn Met Glu Gly Glu Ala Val Gly Ser Phe
        195                 200                 205

Ala Phe Ala Val Lys Lys Gly Ser Gly His Asp Asn Leu Ile Lys Glu
    210                 215                 220

Phe Asn Thr Ala Phe Ala Gln Met Lys Ser Asp Gly Thr Tyr Asn Asp
225                 230                 235                 240

Ile Met Asp Lys Trp Leu Gly Lys Asp Ala Thr Lys Thr Ser Gly Lys
                245                 250                 255

Ala Thr Gly Asn Ala Asn Glu Lys Ala Thr Pro Val Lys Pro Ser Tyr
            260                 265                 270

Lys Ile Val Ser Asp Ser Ser Phe Ala Pro Phe Glu Tyr Gln Asn Gly
        275                 280                 285

Lys Gly Lys Tyr Thr Gly Phe Asp Met Glu Leu Ile Lys Lys Ile Ala
    290                 295                 300

Lys Gln Gln Gly Phe Lys Leu Asp Ile Ser Asn Pro Gly Phe Asp Ala
305                 310                 315                 320

Ala Leu Asn Ala Val Gln Ser Gly Gln Ala Asp Gly Val Ile Ala Gly
                325                 330                 335

Ala Thr Ile Thr Glu Ala Arg Gln Lys Ile Phe Asp Phe Ser Asp Pro
            340                 345                 350

Tyr Tyr Thr Ser Ser Val Ile Leu Ala Val Lys Lys Gly Ser Asn Val
        355                 360                 365

Lys Ser Tyr Gln Asp Leu Lys Gly Lys Thr Val Gly Ala Lys Asn Gly
    370                 375                 380

Thr Ala Ser Tyr Thr Trp Leu Ser Asp His Ala Asp Lys Tyr Asn Tyr
385                 390                 395                 400

His Val Lys Ala Phe Asp Glu Ala Ser Thr Met Tyr Asp Ser Met Asn
                405                 410                 415

Ser Gly Ser Ile Asp Ala Leu Met Asp Asp Glu Ala Val Leu Ala Tyr
            420                 425                 430

Ala Ile Asn Gln Gly Arg Lys Phe Glu Thr Pro Ile Lys Gly Glu Lys
        435                 440                 445

Ser Gly Asp Ile Gly Phe Ala Val Lys Lys Gly Ala Asn Pro Glu Leu
    450                 455                 460

Ile Lys Met Phe Asn Asn Gly Leu Ala Ser Leu Lys Lys Ser Gly Glu
465                 470                 475                 480

Tyr Asp Lys Leu Val Lys Lys Tyr Leu Ser Thr Ala Ser Thr Ser Ser
                485                 490                 495

Asn Asp Lys Ala Ala Lys Pro Val Asp Glu Ser Thr Ile Leu Gly Leu
            500                 505                 510

Ile Ser Asn Asn Tyr Lys Gln Leu Leu Ser Gly Ile Gly Thr Thr Leu
        515                 520                 525

Ser Leu Thr Leu Ile Ser Phe Ala Ile Ala Met Val Ile Gly Ile Ile
    530                 535                 540

Phe Gly Met Met Ser Val Ser Pro Ser Asn Thr Leu Arg Thr Ile Ser
545                 550                 555                 560

Met Ile Phe Val Asp Ile Val Arg Gly Ile Pro Leu Met Ile Val Ala
                565                 570                 575

Ala Phe Ile Phe Trp Gly Ile Pro Asn Leu Ile Glu Ser Ile Thr Gly
580 585 590

His Gln Ser Pro Ile Asn Asp Phe Val Ala Ala Thr Ile Ala Leu Ser
595 600 605

Leu Asn Gly Gly Ala Tyr Ile Ala Glu Ile Val Arg Gly Gly Ile Glu
610 615 620

Ala Val Pro Ser Gly Gln Met Glu Ala Ser Arg Ser Leu Gly Ile Ser
625 630 635 640

Tyr Gly Lys Thr Met Gln Lys Val Ile Leu Pro Gln Ala Val Arg Leu
645 650 655

Met Leu Pro Asn Phe Ile Asn Gln Phe Val Ile Ser Leu Lys Asp Thr
660 665 670

Thr Ile Val Ser Ala Ile Gly Leu Val Glu Leu Phe Gln Thr Gly Lys
675 680 685

Ile Ile Ile Ala Arg Asn Tyr Gln Ser Phe Arg Met Tyr Ala Ile Leu
690 695 700

Ala Ile Met Tyr Leu Val Ile Ile Thr Leu Leu Thr Arg Leu Ala Lys
705 710 715 720

Arg Leu Glu Lys Arg Leu Lys
725

<210> 329

<211> 52

<212> PRT

<213> Streptococcus agalactiae

<400> 329

Met Gly Asp Lys Pro Ile Ser Phe Arg Asp Lys Asp Gly Asn Phe Val
1 5 10 15

Ser Ala Ala Asp Val Trp Asn Ala Glu Lys Leu Glu Glu Leu Phe Asn
20 25 30

Thr Leu Asn Pro Asn Arg Lys Leu Arg Leu Glu Arg Glu Lys Leu Ala
35 40 45

Lys Glu Lys Gly
50

<210> 330

<211> 280

<212> PRT

<213> Streptococcus agalactiae

<400> 330

Met Glu Thr Tyr Thr Leu Ser Asn Thr Leu Asn Ile Pro Lys Ile Gly
1 5 10 15

Phe Gly Thr Trp Gln Leu Thr Glu Gly Glu Glu Ala Tyr Lys Ala Val
20 25 30

Thr His Ala Leu Lys Val Gly Tyr Thr His Ile Asp Thr Ala Gln Ile
35 40 45

Tyr Gly Asn Glu His Ser Val Gly Arg Ala Ile Arg Asp Ser Gly Leu
50 55 60

Ala Arg Glu Ser Ile Phe Leu Thr Thr Lys Ile Trp Asn Asp Lys His
65 70 75 80

Asp Tyr His Leu Ala Lys Ala Ser Ile Asp Glu Ser Leu Gln Lys Leu
85 90 95

Gly Val Asp Tyr Ile Asp Leu Leu Leu Ile His Trp Pro Asn Pro Lys
100 105 110

Ala Leu Arg Glu Asn Asp Ala Trp Lys Ala Gly Asn Ala Gly Thr Trp
115 120 125

Lys Ala Met Glu Glu Ala Tyr Lys Glu Gly Lys Val Lys Ala Ile Gly
130 135 140

Val Ser Asn Phe Met Lys His His Leu Glu Ala Leu Phe Glu Thr Ala
145 150 155 160

Glu Ile Lys Pro Met Val Asn Gln Ile Ile Leu Ala Pro Gly Cys Ala
165 170 175

Gln Glu Asp Leu Val Arg Phe Cys Lys Gly Asn Asp Ile Leu Leu Glu
180 185 190

Ala Tyr Ser Pro Phe Gly Thr Gly Ala Ile Phe Glu Asn Glu Ser Ile
195 200 205

Lys Ala Ile Ala Glu Lys Tyr Gly Lys Ser Val Ala Gln Val Ala Leu
210 215 220

Arg Trp Ser Leu Asp Asn Gly Phe Leu Pro Leu Pro Lys Ser Ala Thr
225 230 235 240

Pro Lys Asn Ile Glu Ala Asn Leu Asp Ile Phe Asp Phe Gln Leu Asn
245 250 255

Glu Asp Asp Ile Thr Thr Leu Ile Gln Leu Asp Ser Gly Ile Lys Pro
260 265 270

Lys Asp Pro Asp Asn Val Ser Phe
275 280

<210> 331

<211> 155

<212> PRT

<213> Streptococcus agalactiae

<400> 331

Met Val Lys Gly Gln Gly Asn Val Val Ala Gln Asn Lys Lys Ala His
1 5 10 15

His Asp Tyr Thr Ile Val Glu Thr Ile Glu Ala Gly Ile Val Leu Thr
20 25 30

Gly Thr Glu Ile Lys Ser Val Arg Ala Ala Arg Ile Thr Leu Lys Asp
35 40 45

Gly Tyr Ala Gln Ile Lys Asn Gly Glu Ala Trp Leu Ile Asn Val His
50 55 60

Ile Thr Pro Tyr Asp Gln Gly Asn Ile Trp Asn Gln Asp Pro Asp Arg
65 70 75 80

Thr Arg Lys Leu Leu Leu Lys Lys Arg Glu Ile Glu Lys Ile Ser Asn
85 90 95

Glu Leu Lys Gly Thr Gly Met Thr Leu Val Pro Leu Lys Val Tyr Leu
100 105 110

Lys Asp Gly Phe Ala Lys Val Leu Leu Gly Leu Ala Lys Gly Lys His
115 120 125

Asp Tyr Asp Lys Arg Glu Ser Ile Lys Arg Arg Glu Gln Asn Arg Asp
130 135 140

Ile Ala Arg Gln Leu Lys Asn Tyr Asn Ser Arg
145 150 155

<210> 332

<211> 267

<212> PRT

<213> Streptococcus agalactiae

<400> 332

Met Asp His Phe Thr Lys Leu Trp Gln Asp Phe Ser Lys Leu Pro Asn
1               5                   10                  15

Val Val Ala Ile Ala Leu Gly Gly Ser Arg Ser Gly Asp Ser Phe Asp
            20                  25                  30

Gln Ser Ser Asp Tyr Asp Leu Tyr Val Tyr Cys Ala Ala Thr Pro Asp
        35                  40                  45

Ile Thr Ser Arg Lys Arg Ile Leu Asn Lys His Cys His Tyr Ile Glu
    50                  55                  60

Leu Asn Asn His Tyr Trp Glu Leu Glu Asp Asn Gly Thr Leu Asn Asp
65                  70                  75                  80

Gly Thr Asp Ile Asp Ile Leu Tyr Arg Asn Ile Asp Asn Phe Leu Ser
                85                  90                  95

Asp Leu Glu Asp Val Val Glu His His Asn Ser Arg Ile Gly Tyr Thr
            100                 105                 110

Thr Cys Phe Trp His Asn Leu Ile Asn Cys Gln Ile Leu Tyr Asp Pro
        115                 120                 125

Glu Asn Gln Leu Gln Ser Leu Lys Glu Arg Phe Glu Val Ser Tyr Pro
    130                 135                 140

Ser Gln Leu Gln Lys Gln Ile Ile Ile Gln Asn Arg Asn Leu Leu Thr
145                 150                 155                 160

Gly Lys Leu Pro Ser Tyr Asp Lys Gln Ile Ile Lys Ala Leu Lys Arg
                165                 170                 175

Gln Asp Phe Val Ser Thr His His Arg Thr Thr Ala Phe Leu Asp Ser
            180                 185                 190

Tyr Phe Asp Ile Ile Phe Ala Leu Asn Lys Leu Thr His Pro Gly Glu
        195                 200                 205

Lys Arg Met Ile Ser Tyr Ala Lys Lys Asn Ala Thr Leu Leu Pro Lys
    210                 215                 220

His Phe Glu Glu Asn Ile Ile Lys Leu Cys His His Asn Ser Asn Glu
225 230 235 240

His Thr Val Lys Glu Thr Leu Asn Asp Ile Ile Met His Leu Asp Val
245 250 255

Met Leu Lys Glu Asn Phe Gln His Phe Ile Gly
260 265

<210> 333

<211> 267

<212> PRT

<213> Streptococcus agalactiae

<400> 333

Met Lys Lys Ile Ile Tyr Leu Gly Leu Ala Cys Val Ser Ile Leu Thr
1 5 10 15

Leu Ser Gly Cys Glu Ser Ile Glu Arg Ser Leu Lys Gly Asp Arg Tyr
20 25 30

Val Asp Gln Lys Leu Ala Glu Asn Ser Ser Lys Glu Ala Thr Glu Gln
35 40 45

Leu Asn Lys Lys Thr Lys Gln Ala Leu Lys Ala Asp Lys Lys Ala Phe
50 55 60

Pro Gln Leu Asp Lys Ala Val Ala Lys Asn Glu Ala Gln Val Leu Ile
65 70 75 80

Lys Thr Ser Lys Gly Asp Ile Asn Ile Lys Leu Phe Pro Lys Tyr Ala
85 90 95

Pro Leu Ala Val Glu Asn Phe Leu Thr His Ala Lys Glu Gly Tyr Tyr
100 105 110

Asn Gly Leu Ser Phe His Arg Val Ile Lys Asp Phe Met Ile Gln Ser
115 120 125

Gly Asp Pro Asn Gly Asp Gly Thr Gly Gly Lys Ser Ile Trp Asn Ser
130 135 140

Lys Asp Lys Lys Lys Asp Ser Gly Asn Gly Phe Val Asn Glu Ile Ser
145 150 155 160

Pro Tyr Leu Tyr Asn Ile Arg Gly Ser Leu Ala Met Ala Asn Ala Gly
165 170 175

Ala Asp Thr Asn Gly Ser Gln Phe Phe Ile Asn Gln Ser Gln Gln Asp
180 185 190

His Ser Lys Gln Leu Ser Asp Lys Lys Val Pro Lys Val Ile Ile Lys
195 200 205

Ala Tyr Ser Glu Gly Gly Asn Pro Ser Leu Asp Gly Gly Tyr Thr Val
210 215 220

Phe Gly Gln Val Ile Ser Gly Met Glu Thr Val Asp Lys Ile Ala Ser
225 230 235 240

Val Glu Val Thr Lys Ser Asp Gln Pro Lys Glu Lys Ile Thr Ile Thr
245 250 255

Ser Ile Lys Val Ile Lys Asp Tyr Lys Phe Lys
260 265

<210> 334

<211> 229

<212> PRT

<213> Streptococcus agalactiae

<400> 334

Met Lys Ile Gly Ile Ile Ala Ala Met Glu Glu Glu Leu Lys Leu Leu
1 5 10 15

Val Glu Asn Leu Glu Asp Lys Ser Gln Glu Thr Val Leu Ser Asn Val
20 25 30

Tyr Tyr Ser Gly Arg Tyr Gly Glu His Glu Leu Val Leu Val Gln Ser
35 40 45

Gly Val Gly Lys Val Met Ser Ala Met Ser Val Ala Ile Leu Val Glu
50 55 60

Ser Phe Lys Val Asp Ala Ile Ile Asn Thr Gly Ser Ala Gly Ala Val
65 70 75 80

Ala Thr Gly Leu Asn Val Gly Asp Val Val Val Ala Asp Thr Leu Val
85 90 95

Tyr His Asp Val Asp Leu Thr Ala Phe Gly Tyr Asp Tyr Gly Gln Met
100 105 110

Ser Met Gln Pro Leu Tyr Phe His Ser Asp Lys Thr Phe Val Ser Thr
115 120 125

Phe Glu Ala Val Leu Ser Lys Glu Glu Met Thr Ser Lys Val Gly Leu
130 135 140

Ile Ala Thr Gly Asp Ser Phe Ile Ala Gly Gln Glu Lys Ile Asp Val
145 150 155 160

Ile Lys Gly His Phe Pro Gln Val Leu Ala Val Glu Met Glu Gly Ala
165 170 175

Ala Ile Ala Gln Ala Ala Gln Ala Thr Gly Lys Pro Phe Val Val Val
180 185 190

Arg Ala Met Ser Asp Thr Ala Ala His Asp Ala Asn Ile Thr Phe Asp
195 200 205

Glu Phe Ile Ile Glu Ala Gly Lys Arg Ser Ala Gln Val Leu Met Ala
210 215 220

Phe Leu Lys Ala Leu
225

<210> 335

<211> 388

<212> PRT

<213> Streptococcus agalactiae

<400> 335

Met Glu Lys Arg Leu Ser Leu Gly Ala Leu Val Leu Ala Ser Thr Val
1 5 10 15

Leu Leu Ala Ala Cys Gly Asn Val Gly Gly Gly Ala Ser Ser Thr Gly
20 25 30

Thr Lys Ile Gly Lys Asp Ile Lys Val Gly Tyr Asn Trp Glu Leu Ser
35 40 45

Gly Asn Val Ser Ser Tyr Gly Asn Ser Met Lys Asn Gly Ala Asp Leu
50 55 60

Ala Val Lys Glu Ile Asn Ala Ala Gly Gly Val Gly Gly Lys Lys Leu
65 70 75 80

Lys Val Leu Ser Gln Asp Asn Lys Ser Glu Asn Ala Glu Ala Ala Thr
85 90 95

Val Ala Thr Asn Leu Val Thr Lys Gly Ala Asn Val Ile Ile Gly Pro
100 105 110

Ala Thr Ser Gly Ala Ala Ala Ser Ser Thr Pro Lys Val Asn Ala Ala
115 120 125

Ala Val Pro Met Ile Ala Pro Ala Ala Thr Gln Asp Asn Leu Val Tyr
130 135 140

Gly Ser Asp Gly Lys Thr Leu Asn Gln Tyr Phe Phe Arg Ala Thr Phe
145 150 155 160

Val Asp Asn Tyr Gln Gly Lys Leu Leu Ser Gln Tyr Ala Thr Asp Asn
165 170 175

Leu Lys Ala Lys Lys Val Val Leu Phe Tyr Asp Asn Ser Ser Asp Tyr
180 185 190

Ser Lys Gly Val Ala Lys Ser Phe Lys Glu Ser Tyr Ser Gly Lys Ile
195 200 205

Val Asp Ser Met Thr Phe Ser Ala Gly Asp Thr Asp Phe Gln Ala Ser
210 215 220

Leu Thr Lys Leu Lys Gly Lys Glu Tyr Asp Ala Ile Val Met Pro Gly
225 230 235 240

Tyr Tyr Thr Glu Thr Gly Leu Ile Val Lys Gln Ala Arg Asp Leu Gly
245 250 255

Ile Ser Lys Pro Val Leu Gly Pro Asp Gly Phe Asp Ser Pro Lys Phe
260 265 270

Val Gln Ser Ala Thr Pro Val Gly Ala Ser Asn Val Tyr Tyr Leu Thr
275 280 285

Gly Phe Thr Thr Gln Gly Ser Thr Lys Ala Lys Ala Phe His Asp His
290 295 300

Tyr Val Lys Ala Tyr Gly Glu Glu Pro Ser Met Phe Ser Ala Leu Ser
305 310 315 320

Tyr Asp Ala Val Tyr Met Ala Ala Lys Ser Ala Lys Gly Ala Lys Thr
325 330 335

Ser Ile Asp Leu Lys Lys Ala Leu Ala Lys Leu Lys Asp Phe Lys Gly
340 345 350

Val Thr Gly Lys Met Ser Ile Asp Lys Asn His Asn Val Val Lys Ser
355 360 365

Ala Tyr Val Val Lys Leu Asp Asp Gly Lys Thr Ser Ser Val Asn Ile
370 375 380

Ile Ser Ala Lys
385

<210> 336

<211> 450

<212> PRT

<213> Streptococcus agalactiae

<400> 336

Met Glu Asn His Asn Ser Ile Lys Gln Thr Tyr Gly Leu Met Thr Thr
1 5 10 15

Ile Ala Met Ile Val Gly Val Val Ile Gly Ser Gly Ile Tyr Phe Lys
20 25 30

Val Asp Asp Ile Leu Lys Phe Thr Gly Gly Asp Val Phe Leu Gly Met
35 40 45

Val Ile Leu Val Leu Gly Ser Phe Ser Ile Val Phe Gly Ser Leu Ser
50 55 60

Ile Ser Glu Leu Ala Ile Arg Thr Ser Glu Ser Gly Gly Ile Phe Ser
65 70 75 80

Tyr Tyr Glu Lys Tyr Val Ser Pro Ala Leu Ala Ala Thr Leu Gly Leu
85 90 95

Phe Ala Ser Phe Leu Tyr Leu Pro Thr Leu Thr Ala Ile Val Ser Trp
100 105 110

Val Ala Ala Phe Tyr Thr Leu Gly Glu Ser Ser Ser Leu Glu Ser Gln
115 120 125

Ile Ile Leu Ala Ala Val Tyr Ile Leu Ala Leu Ser Leu Met Asn Ile
130 135 140

Phe Ala Lys Arg Ile Ala Gly Gly Phe Gln Ser Leu Thr Thr Phe Val
145 150 155 160

Lys Met Ile Pro Leu Val Leu Ile Ala Leu Ile Gly Ala Phe Trp Ser
165 170 175

Asp Lys Ala Pro Gln Leu Pro Gln His Leu Thr Ala Ile Gln Pro Ser
180 185 190

Asn Val Gly Trp Ser Trp Val Ser Gly Leu Val Pro Leu Tyr Phe Ala
195 200 205

Tyr Asp Gly Trp Thr Ile Phe Val Ser Ile Ala Pro Glu Val Lys Asn
    210                 215                 220

Pro Lys Lys Asn Leu Pro Leu Ala Phe Val Ile Gly Pro Ala Leu Ile
225                 230                 235                 240

Leu Leu Ser Tyr Leu Ala Phe Phe Tyr Gly Leu Thr Gln Ile Leu Gly
                245                 250                 255

Ala Ser Phe Ile Met Thr Thr Gly Asn Asp Ala Ile Asn Tyr Ala Ala
            260                 265                 270

Asn Ile Ile Phe Gly Pro Ser Val Gly Arg Leu Leu Ser Phe Ile Val
        275                 280                 285

Ile Leu Ser Val Leu Gly Val Ala Asn Gly Leu Leu Leu Gly Thr Met
    290                 295                 300

Arg Leu Pro Gln Ala Phe Ala Glu Arg Gly Trp Ile Lys Ser Glu Arg
305                 310                 315                 320

Met Ala Asn Ile Asn Leu Lys Tyr Gln Met Ser Leu Pro Ala Ser Leu
                325                 330                 335

Thr Val Thr Ala Val Ala Ile Phe Trp Leu Phe Val His Phe Met Val
            340                 345                 350

Thr Lys Phe Asn Leu Leu Pro Gly Ser Asp Ile Ser Glu Ile Ala Val
        355                 360                 365

Val Phe Asn Asn Thr Ser Leu Ile Ile Leu Tyr Val Leu Val Leu Ser
    370                 375                 380

Leu Tyr Leu Lys Lys Asp Ile Lys Asn Lys Phe Thr Gly Leu Val Ser
385                 390                 395                 400

Pro Ile Leu Ala Ile Leu Gly Gly Leu Ile Leu Phe Ile Gly Ser Leu
                405                 410                 415

Leu Ser Asn Phe Phe Thr Val Leu Ile Phe Gln Cys Phe Cys Leu Leu
            420                 425                 430

Phe Cys Leu Ile Cys His Tyr Ile Tyr Gln Lys Asn Asn Pro Lys Thr
        435                 440                 445

His Glu
    450

<210> 337

<211> 600

<212> PRT

<213> Streptococcus agalactiae

<400> 337

Leu Thr Glu Phe Asn Asp Asp Gln His Ser Asn His Asp Gln Lys Ser
1 5 10 15

Phe Lys Glu Gln Ile Leu Ala Glu Leu Glu Glu Ala Asn Arg Leu Arg
20 25 30

Lys Leu Arg Glu Glu Glu Leu Tyr Gln Lys Glu Gln Glu Ala Lys Glu
35 40 45

Ala Ala Arg Arg Thr Ala Gln Leu Met Ala Asp Tyr Glu Ala Gln Arg
50 55 60

Leu Lys Asp Glu Gln Glu Ala Arg Ala Lys Ala Leu Glu Thr Lys Gln
65 70 75 80

Arg Leu Glu Glu Gln Glu Lys Ala Arg Ile Glu Ala Lys Leu Leu Ala
85 90 95

Glu Ala Ala Arg Glu Glu Glu Arg Arg Gln Ala Glu Gln Ala Leu Ala
100 105 110

Ser Gln Glu Glu Gln Val Ile Asn Gln Gly Met Glu Pro Ser Arg Glu
115 120 125

Leu Asp Ser Gly Ser Lys Ser Ser Glu Phe Arg Thr Thr Glu Asn Val
130 135 140

Pro Asp Ile Asp Leu Lys Ala Asp Lys Thr Asp Val Ala Thr Ala Val
145 150 155 160

Pro Asn Gln Glu Thr Glu Glu Ile Phe Leu Val Arg Ala Thr Asp Ile
165 170 175

Pro Thr Glu Gly Glu Asn Val Lys Leu Gly Glu Thr Ser Glu Leu Glu
180 185 190

Pro Val Ala Lys Glu Pro Ile Arg Val Glu Asp Leu Ser Lys Glu Glu
195 200 205

Glu Asp Ile Ala Leu Ser Ala Lys Asn Lys His Asn Lys Arg Glu Arg
210 215 220

Arg Gln Lys Ala Asp Asn Val Ala Lys Arg Ile Ala Arg Ile Leu Ile
225 230 235 240

Ser Ile Ile Ile Leu Val Leu Leu Leu Thr Ala Phe Val Gly Tyr Arg
245 250 255

Phe Val Asp Ser Ala Ile Lys Pro Val Asp Ser Asn Ser Asn Lys Phe
260 265 270

Val Gln Val Glu Ile Pro Ile Gly Ser Gly Asn Lys Leu Ile Gly Gln
275 280 285

Ile Leu Glu Lys Ala Gly Val Ile Lys Ser Ala Thr Val Phe Asn Tyr
290 295 300

Tyr Ser Lys Phe Lys Asn Tyr Ser Asn Phe Gln Ser Gly Tyr Tyr Asn
305 310 315 320

Leu Lys Lys Ser Met Thr Leu Asp Gln Ile Ala Ala Glu Leu Glu Lys
325 330 335

Gly Gly Thr Ala Glu Pro Thr Lys Pro Ala Leu Gly Lys Ile Leu Ile
340 345 350

Thr Glu Gly Tyr Thr Ile Lys Gln Ile Ala Lys Ala Ile Glu Ser Asn
355 360 365

Lys Ile Asp Thr Lys Thr Thr Ser Thr Pro Tyr Lys Ala Asp Asp Phe
370 375 380

Leu Lys Leu Val Gln Asp Glu Thr Phe Ile Lys Lys Met Val Ala Lys
385 390 395 400

Tyr Pro Asn Leu Leu Gly Ser Leu Pro Asp Lys Ser Lys Ala Ile Tyr
405 410 415

Gln Leu Glu Gly Tyr Leu Phe Pro Ala Thr Tyr Asn Tyr Tyr Lys Asp
420 425 430

Thr Thr Leu Glu Gly Leu Val Glu Asp Met Ile Ser Thr Met Asn Thr
435 440 445

Lys Met Ala Pro Tyr Tyr Asn Thr Ile Lys Ala Lys Asn Met Ser Val
450 455 460

Asn Asp Val Leu Thr Leu Ser Ser Leu Val Glu Lys Glu Gly Ser Thr
465 470 475 480

Asp Glu Asp Arg Arg Lys Ile Ala Ser Val Phe Tyr Asn Arg Leu Ser
485 490 495

Ala Gly Gln Ala Leu Gln Ser Asn Ile Ala Ile Leu Tyr Ala Met Gly
500 505 510

Lys Leu Gly Asp Lys Thr Ser Leu Ala Glu Asp Ala Gln Ile Asn Thr
515 520 525

Ser Ile Lys Ser Pro Tyr Asn Ile Tyr Thr Asn Thr Gly Leu Met Pro
530 535 540

Gly Pro Val Asp Ser Pro Ser Ile Ser Ala Ile Glu Ala Thr Ile Lys
545 550 555 560

Pro Ala Ser Thr Asp Tyr Leu Tyr Phe Val Ala Asp Val Lys Thr Gly
565 570 575

Asn Val Tyr Tyr Ala Lys Asp Phe Glu Thr His Lys Ala Asn Val Glu
580 585 590

Lys Tyr Ile Asn Ser Gln Ile Asn
595 600

<210> 338

<211> 1032

<212> PRT

<213> Streptococcus agalactiae

<400> 338

Met Ser Arg Met Ile Pro Gly Arg Ile Arg Asn Gln Gly Ile Glu Leu
1 5 10 15

Tyr Glu Gln Gly Leu Val Ser Leu Ile Ser Gln Glu Gly Asn Leu Leu
20 25 30

Lys Ala Lys Val Gly Asp Cys Gln Ile Glu Tyr Ser Leu Val Thr Glu
35 40 45

Glu Thr Lys Cys Ser Cys Asp Phe Phe Ala Arg Lys Gly Tyr Cys Gln
50 55 60

His Leu Ala Ala Leu Glu His Phe Leu Lys Asn Asp Pro Glu Gly Lys
65 70 75 80

Ala Ile Leu Ser Lys Val Gln Val Gln Gln Glu Ser Gln Gln Glu Thr
85 90 95

Lys Lys Lys Thr Ser Phe Gly Ser Val Phe Leu Asp Ser Leu Ile Ile
100 105 110

Asn Glu Asp Asp Thr Ile Lys Tyr Gln Leu Ser Ala Gln Gly Glu Gln
115 120 125

Asn Pro Tyr Ala Asn Asp Ile Trp Trp Thr Leu Lys Ile Arg Arg Leu
130 135 140

Pro Asp Asp Arg Ser Tyr Val Ile Arg Asp Ile Lys Ala Phe Leu Asn
145 150 155 160

Thr Val Arg Lys Glu Ala Tyr Tyr Gln Ile Gly Lys Gln Tyr Phe Glu
165 170 175

Thr Leu Ser Leu Ile Gln Phe Asp Glu Thr Ser Gln Glu Leu Ile Glu
180 185 190

Phe Leu Trp Arg Leu Ile Pro Ser His Ser Ser Lys Ile Asp Leu Glu
195 200 205

Phe Ile Leu Pro Asn Gln Gly Arg His Leu Ser Leu Thr Arg Gly Phe
210 215 220

Phe Glu Glu Gly Val Thr Leu Met Asn Ala Leu Glu Asn Phe Ser Phe
225 230 235 240

Glu Ser Asp Phe His Gln Phe Asn His Leu Tyr Phe Lys Glu Leu Glu
245 250 255

Gly Glu Asp His Leu Tyr Gln Phe Lys Val Ile Val His Arg Gln Ser
260 265 270

Ile Glu Leu Glu Ile Lys Glu Lys Asp Leu Lys Pro Leu Phe Ala Asn
275 280 285

Ser Tyr Leu Phe Tyr Arg Asp Thr Phe Tyr His Leu Asn Leu Lys Gln
290 295 300

Glu Lys Met Val Thr Ala Ile Arg Ser Leu Pro Ile Glu Gly Asp Leu
305 310 315 320

Ala Lys His Ile His Phe Asp Leu Asp Asp Gln Asp Lys Leu Ala Ala
325 330 335

His Leu Leu Asp Phe Lys Glu Ile Gly Leu Val Asp Ala Pro Arg Ser
340 345 350

Phe Ser Ile His Asp Phe Lys Val Asn Phe Glu Phe Asp Ile Asn Ser
355 360 365

Gln Asn Glu Ile Leu Leu Gln Met Val Phe Asp Tyr Gly Asn Asp Leu
370 375 380

Thr Val His Asn Arg Gln Glu Leu Glu Gln Leu Thr Phe Ala Ser His
385 390 395 400

Phe Lys His Glu Glu Lys Ile Phe Lys Leu Leu Glu Arg Tyr Gly Phe
405 410 415

Ala Pro His Phe Ser Thr Ser His Pro Ala Tyr Ser Ala Gln Glu Leu
420 425 430

Tyr Asp Phe Tyr Thr Tyr Met Leu Pro Gln Phe Lys Lys Met Gly Thr
435 440 445

Val Ser Leu Ser Ala Lys Leu Glu Ser Tyr Arg Leu Ile Glu Arg Pro
450 455 460

Gln Ile Asp Ile Glu Ala Lys Gly Ser Leu Leu Asp Ile Ser Phe Asp
465 470 475 480

Phe Ser Asp Leu Leu Glu Asn Asp Val Asp Gln Ala Leu Val Ala Leu
485 490 495

Phe Asp Asn Asn Pro Tyr Phe Val Asn Lys Ser Gly Gln Leu Val Ile
500 505 510

Phe Asp Glu Glu Thr Lys Lys Val Ser Ala Thr Leu Gln Gly Leu Arg
515 520 525

Ala Arg Arg Ala Lys Asn Gly His Ile Glu Leu Asp Asn Ile Ala Ala
530 535 540

Phe Gln Leu Ser Glu Leu Phe Ala Asn Gln Asp Asn Val Ser Phe Ser
545 550 555 560

Gln His Phe Tyr Gln Leu Ile Glu Asp Leu Arg His Pro Glu Lys Phe
565 570 575

Lys Ile Pro Gly Leu Ser Val Ser Ala Ser Leu Arg Asp Tyr Gln Leu
580 585 590

Thr Gly Val Arg Trp Leu Ser Met Leu Asp His Tyr Gly Phe Ala Gly
595 600 605

Ile Leu Ala Asp Asp Met Gly Leu Gly Lys Thr Leu Gln Thr Ile Ser
610 615 620

Phe Leu Ser Thr Lys Leu Thr Arg Asp Ser Arg Val Leu Ile Leu Ser
625 630 635 640

Pro Ser Ser Leu Ile Tyr Asn Trp Gln Asp Glu Phe His Lys Phe Ala
645 650 655

Pro Asp Val Asp Val Ala Val Ala Tyr Gly Ser Lys Ile Arg Arg Asp
660 665 670

Glu Ile Ile Ala Glu Arg His Gln Val Ile Ile Thr Ser Tyr Ser Ser
675 680 685

Phe Arg Gln Asp Phe Glu Thr Tyr Ser Glu Gly Asn Tyr Asp Tyr Leu
690 695 700

Ile Leu Asp Glu Ala Gln Val Met Lys Asn Ala Gln Thr Lys Ile Ala
705 710 715 720

His Ser Leu Arg Ser Phe Glu Val Lys Asn Cys Phe Ala Leu Ser Gly
725 730 735

Thr Pro Ile Glu Asn Lys Leu Leu Glu Ile Trp Ser Ile Phe Gln Ile
740 745 750

Ile Leu Pro Gly Leu Leu Pro Gly Lys Lys Glu Phe Leu Lys Leu Asn
755 760 765

Pro Lys Gln Val Ala Arg Tyr Ile Lys Pro Phe Val Met Arg Arg Arg
770 775 780

Lys Glu Glu Val Leu Pro Glu Leu Pro Asp Leu Ile Glu Met Asn Tyr
785 790 795 800

Pro Asn Glu Met Thr Asp Ser Gln Lys Val Ile Tyr Leu Ala Gln Leu
805 810 815

Arg Gln Ile Gln Glu Ser Ile Gln His Ser Ser Asp Ala Asp Leu Asn
820 825 830

Arg Arg Lys Ile Glu Ile Leu Ser Gly Ile Thr Arg Leu Arg Gln Ile
835 840 845

Cys Asp Thr Pro Arg Leu Phe Met Asp Tyr Asp Gly Glu Ser Gly Lys
850 855 860

Leu Glu Ser Leu His Gln Leu Leu Thr Gln Ile Lys Glu Asn Gly His
865 870 875 880

Arg Ala Leu Ile Phe Ser Gln Phe Arg Gly Met Leu Asp Ile Ala Glu
885 890 895

Arg Glu Met Val Ala Met Gly Leu Thr Thr Tyr Lys Ile Thr Gly Ser
900 905 910

Thr Pro Ala Asn Glu Arg His Glu Met Thr Arg Ala Phe Asn Ala Gly
915 920 925

Ser Lys Asp Ala Phe Leu Ile Ser Leu Lys Ala Gly Gly Val Gly Leu
930 935 940

Asn Leu Thr Gly Ala Asp Thr Val Val Leu Ile Asp Leu Trp Trp Asn
945 950 955 960

Pro Ala Val Glu Met Gln Ala Ile Ser Arg Ala His Arg Leu Gly Gln
965 970 975

Lys Glu Asn Val Glu Val Tyr Arg Leu Ile Thr Arg Gly Thr Ile Glu
980 985 990

Glu Lys Ile Leu Glu Met Gln Glu Thr Lys Lys His Leu Val Thr Thr
995 1000 1005

Val Leu Asp Gly Asn Glu Thr His Ala Ser Met Ser Val Asp Asp
1010 1015 1020

Ile Arg Glu Ile Leu Gly Val Ser Lys
1025 1030

<210> 339

<211> 177

<212> PRT

<213> Streptococcus agalactiae

<400> 339

Val Leu Leu Thr Glu Ile Lys Lys Ser Pro Glu Gly Leu Tyr Phe Asp
1 5 10 15

Lys Lys Ile Asp Ile Lys Glu Ser Leu Met Glu Arg His Ser Glu Ile
20 25 30

Met Asp Ile Ser Asp Ile Gln Val Ser Gly His Val Val Tyr Glu Asp
35 40 45

Gly Leu Tyr Leu Leu Asp Tyr Asn Met Ala Tyr Asp Ile Thr Leu Pro
50 55 60

Ser Ser Arg Ser Met Lys Pro Val Val Leu Ser Glu Lys Gln Thr Ile
65 70 75 80

Asn Glu Val Phe Ile Glu Ala Glu Asn Val Ser Thr Lys Lys Glu Leu
85 90 95

Val Asp Gln Asp Leu Val Leu Ile Leu Glu Glu Asp Asp Ile Asn Leu
100 105 110

Glu Glu Ser Val Ile Asp Asn Ile Leu Leu Asn Ile Pro Leu Arg Val
115 120 125

Leu Ala Ala Asp Glu Val Gly Val Glu Ala Asp Leu Ser Gly Lys Asn
    130                 135                 140

Trp Ser Leu Met Thr Glu Lys Gln Tyr Glu Glu Lys Gln Ala Lys Glu
145                 150                 155                 160

Lys Glu Lys Ser Asn Pro Phe Ala Ala Leu Glu Gly Met Phe Asp Ser
                165                 170                 175

Asp

<210> 340

<211> 192

<212> PRT

<213> Streptococcus agalactiae

<400> 340

Met Glu Val Lys Thr Ala Ile Glu Trp Met His Thr Phe Asn Gln Lys
1               5                   10                  15

Ile Gln Ser Asn Lys Asp Tyr Leu Ser Glu Leu Asp Thr Pro Ile Gly
            20                  25                  30

Asp Gly Asp His Gly Gly Asn Met Ala Arg Gly Met Thr Ala Val Ile
        35                  40                  45

Glu Asn Leu Asp Asn Asn Glu Phe Ser Ser Ala Ala Asp Val Phe Lys
    50                  55                  60

Thr Val Ser Met Gln Leu Leu Ser Lys Val Gly Gly Ala Ser Gly Pro
65                  70                  75                  80

Leu Tyr Gly Ser Ala Phe Met Gly Ile Thr Lys Ala Glu Gln Ser Glu
                85                  90                  95

Ser Thr Ile Ser Glu Ala Leu Gly Ala Gly Leu Glu Met Ile Gln Lys
            100                 105                 110

Arg Gly Lys Ala Glu Leu Asn Glu Lys Thr Met Val Asp Val Trp His
        115                 120                 125

Gly Val Ile Glu Ala Ile Glu Lys Asn Glu Leu Thr Glu Asp Arg Ile
    130                 135                 140

Asp Ser Leu Val Asp Ala Thr Lys Gly Met Lys Ala Thr Lys Gly Arg
145                 150                 155                 160

Ala Ser Tyr Val Gly Glu Arg Ser Leu Gly His Ile Asp Pro Gly Ser
165 170 175

Phe Ser Ser Gly Leu Leu Phe Lys Ala Leu Leu Glu Val Gly Gly Val
180 185 190

<210> 341

<211> 942

<212> PRT

<213> Streptococcus agalactiae

<400> 341

Met Gln Asp Lys Leu Met Ile Arg Gly Ala Arg Ala His Asn Leu Lys
1 5 10 15

Asn Ile Ser Val Asp Ile Pro Arg Asp Lys Leu Val Val Val Thr Gly
20 25 30

Leu Ser Gly Ser Gly Lys Ser Ser Leu Ala Phe Asp Thr Ile Tyr Ala
35 40 45

Glu Gly Gln Arg Arg Tyr Val Glu Ser Leu Ser Ala Tyr Ala Arg Gln
50 55 60

Phe Leu Gly Asn Met Glu Lys Pro Asp Val Asp Ser Ile Asp Gly Leu
65 70 75 80

Ser Pro Ala Ile Ser Ile Asp Gln Lys Thr Thr Ser Lys Asn Pro Arg
85 90 95

Ser Thr Val Gly Thr Val Thr Glu Ile Asn Asp Tyr Leu Arg Leu Leu
100 105 110

Tyr Ala Arg Val Gly Thr Pro Tyr Cys Ile Asn Gly His Gly Ala Ile
115 120 125

Thr Ala Ser Ser Val Glu Gln Ile Val Asp Lys Val Leu Ala Leu Pro
130 135 140

Glu Arg Thr Lys Met Gln Ile Leu Ala Pro Ile Ile Arg Arg Lys Lys
145 150 155 160

Gly Gln His Lys Ser Thr Phe Glu Lys Ile Gln Lys Asp Gly Tyr Val
165 170 175

Arg Val Arg Ile Asp Gly Asp Ile His Asp Val Thr Glu Val Pro Glu
180 185 190

Leu Ser Lys Ser Lys Met His Asn Ile Asp Ile Val Val Asp Arg Leu
195 200 205

Ile Asn Lys Glu Gly Ile Arg Ser Arg Leu Phe Asp Ser Val Glu Ala
210 215 220

Ala Leu Arg Leu Ser Asp Gly Tyr Val Val Ile Asp Thr Met Asp Gly
225 230 235 240

Asn Glu Leu Leu Phe Ser Glu His Tyr Ser Cys Pro Glu Cys Gly Phe
245 250 255

Thr Val Pro Glu Leu Glu Pro Arg Leu Phe Ser Phe Asn Ala Pro Phe
260 265 270

Gly Ser Cys Thr Thr Cys Asp Gly Leu Gly Ile Lys Leu Glu Val Asp
275 280 285

Ile Asp Leu Val Ile Pro Asp Lys Ser Lys Thr Leu Arg Glu Gly Ala
290 295 300

Leu Val Pro Trp Asn Pro Ile Ser Ser Asn Tyr Tyr Pro Thr Met Leu
305 310 315 320

Glu Gln Ala Met Thr Gln Phe Asp Val Asp Met Asp Thr Pro Phe Glu
325 330 335

Lys Leu Ser Lys Ala Glu Gln Asp Leu Ala Leu Tyr Gly Ser Gly Glu
340 345 350

Arg Glu Phe His Phe His Tyr Ile Asn Asp Phe Gly Gly Glu Arg Asn
355 360 365

Ile Asp Leu Pro Phe Glu Gly Val Val Asn Asn Ile Asn Arg Arg Tyr
370 375 380

His Glu Thr Asn Ser Asp Tyr Thr Arg Asn Val Met Arg Glu Tyr Met
385 390 395 400

Asn Glu Leu Lys Cys Asn Thr Cys His Gly Tyr Arg Leu Asn Asp Gln
405 410 415

Ala Leu Cys Val Arg Val Gly Gly Glu Glu Gly Leu Asn Ile Gly Gln
420 425 430

Val Ser Asp Leu Ser Ile Ala Asp His Leu Glu Leu Leu Glu Thr Leu
435 440 445

Arg Leu Ser Ser Asn Glu Gln Leu Ile Ala Arg Pro Ile Ile Lys Glu
450 455 460

Ile His Asp Arg Leu Ser Phe Leu Asn Asn Val Gly Leu Asn Tyr Leu
465 470 475 480

Asn Leu Ser Arg Ser Ala Gly Thr Leu Ser Gly Gly Glu Ser Gln Arg
485 490 495

Ile Arg Leu Ala Thr Gln Ile Gly Ser Asn Leu Ser Gly Val Leu Tyr
500 505 510

Val Leu Asp Glu Pro Ser Ile Gly Leu His Gln Arg Asp Asn Asp Arg
515 520 525

Leu Ile Asp Ser Leu Lys Lys Met Arg Asp Leu Gly Asn Thr Leu Ile
530 535 540

Val Val Glu His Asp Glu Asp Thr Met Met Ala Ala Asp Trp Leu Ile
545 550 555 560

Asp Val Gly Pro Gly Ala Gly Ala Phe Gly Gly Glu Ile Val Ala Ser
565 570 575

Gly Thr Pro Lys Gln Val Ala Lys Asn Thr Lys Ser Ile Thr Gly Gln
580 585 590

Tyr Leu Ser Gly Lys Lys Val Ile Pro Val Pro Ser Glu Arg Arg Val
595 600 605

Gly Asn Gly Arg Phe Leu Glu Ile Lys Gly Ala Ala Glu Asn Asn Leu
610 615 620

Gln Asn Leu Asp Val Lys Phe Pro Leu Gly Lys Phe Ile Ala Val Thr
625 630 635 640

Gly Val Ser Gly Ser Gly Lys Ser Thr Leu Ile Asn Ser Ile Leu Lys
645 650 655

Lys Ala Val Ala Gln Lys Leu Asn Arg Asn Ser Asp Lys Pro Gly Lys
660 665 670

Tyr Val Ser Leu Glu Gly Ile Glu Tyr Val Asp Arg Leu Ile Asp Ile
675 680 685

Asp Gln Ser Pro Ile Gly Arg Thr Pro Arg Ser Asn Pro Ala Thr Tyr
690 695 700

Thr Gly Val Phe Asp Asp Ile Arg Asp Leu Phe Ala Gln Thr Asn Glu
705 710 715 720

Ala Lys Ile Arg Gly Tyr Lys Lys Gly Arg Phe Ser Phe Asn Val Lys
725 730 735

Gly Gly Arg Cys Glu Ser Cys Ser Gly Asp Gly Ile Ile Lys Ile Glu
740 745 750

Met His Phe Leu Pro Asp Val Tyr Val Pro Cys Glu Val Cys His Gly
755 760 765

Thr Arg Tyr Asn Ser Glu Thr Leu Glu Val His Tyr Lys Glu Lys Asn
770 775 780

Ile Ala Gln Ile Leu Asp Met Thr Val Asn Asp Ala Val Thr Phe Phe
785 790 795 800

Ala Ala Ile Pro Lys Ile Ala Arg Lys Leu Gln Thr Ile Lys Asp Val
805 810 815

Gly Leu Gly Tyr Val Thr Leu Gly Gln Pro Ala Thr Thr Leu Ser Gly
820 825 830

Gly Glu Ala Gln Arg Met Lys Leu Ala Ser Glu Leu His Lys Arg Ser
835 840 845

Thr Gly Lys Ser Leu Tyr Ile Leu Asp Glu Pro Thr Thr Gly Leu His
850 855 860

Ala Asp Asp Ile Ala Arg Leu Leu Lys Val Leu Asp Arg Phe Val Asp
865 870 875 880

Asp Gly Asn Thr Val Leu Val Ile Glu His Asn Leu Asp Val Ile Lys
885 890 895

Thr Ala Asp His Ile Ile Asp Leu Gly Pro Glu Gly Gly Ile Gly Gly
900 905 910

Gly Gln Ile Val Ala Ile Gly Thr Pro Glu Glu Val Ala Glu Asn Pro
915 920 925

Lys Ser Tyr Thr Gly Tyr Tyr Leu Lys Glu Lys Leu Ala Arg
930 935 940

<210> 342

<211> 374

<212> PRT

<213> Streptococcus agalactiae

<400> 342

Met Trp Pro Glu Asp Arg Ile Ala Ser Phe Arg Arg Thr Leu Leu Gly
1 5 10 15

Trp Tyr Asp Gln Glu Lys Arg Asp Leu Pro Trp Arg Arg Thr Thr Asn
20 25 30

Pro Tyr Tyr Ile Trp Val Ser Glu Ile Met Leu Gln Gln Thr Gln Val
35 40 45

Asn Thr Val Ile Pro Tyr Tyr Lys Arg Phe Leu Glu Trp Phe Pro Gln
50 55 60

Ile Lys Asp Leu Ala Asp Ala Pro Glu Glu Gln Leu Leu Lys Ala Trp
65 70 75 80

Glu Gly Leu Gly Tyr Tyr Ser Arg Val Arg Asn Met Gln Lys Ala Ala
85 90 95

Gln Gln Val Met Val Asp Phe Gly Gly Ile Phe Pro His Thr Tyr Asp
100 105 110

Asp Ile Ala Ser Leu Lys Gly Ile Gly Pro Tyr Thr Ala Gly Ala Ile
115 120 125

Ala Ser Ile Ser Phe Asn Leu Pro Glu Pro Ala Val Asp Gly Asn Val
130 135 140

Met Arg Val Met Ala Arg Leu Phe Glu Val Asn Tyr Asp Ile Gly Asp
145 150 155 160

Pro Lys Asn Arg Lys Ile Phe Gln Ala Ile Met Glu Ile Leu Ile Asp
165 170 175

Pro Asp Arg Pro Gly Asp Phe Asn Gln Ala Leu Met Asp Leu Gly Thr
180 185 190

Asp Ile Glu Ser Ala Lys Thr Pro Arg Pro Asp Glu Ser Pro Ile Arg
195 200 205

Phe Phe Asn Ala Ala Tyr Leu Asn Gly Thr Tyr Ser Lys Tyr Pro Ile
210 215 220

Lys Asn Pro Lys Lys Lys Pro Lys Pro Met Arg Ile Gln Ala Phe Val
225 230 235 240

Ile Arg Asn Gln Asn Gly Gln Tyr Leu Leu Glu Lys Asn Thr Lys Gly
245 250 255

Arg Leu Leu Gly Gly Phe Trp Ser Phe Pro Ile Ile Glu Thr Ser Pro
260 265 270

Leu Ser Gln Gln Leu Asp Leu Phe Asp Asp Asn Gln Ser Asn Pro Ile
275 280 285

Ile Trp Gln Thr Gln Asn Glu Thr Phe Gln Arg Glu Tyr Gln Leu Lys
290 295 300

Pro Gln Trp Thr Asp Asn His Phe Pro Asn Ile Lys His Thr Phe Ser
305 310 315 320

His Gln Lys Trp Thr Ile Glu Leu Ile Glu Gly Val Val Lys Ala Thr
325 330 335

Asp Leu Pro Asn Ala Pro His Leu Lys Trp Ala Ala Ile Glu Asp Phe
340 345 350

Ser Leu Tyr Pro Phe Ala Thr Pro Gln Lys Lys Met Leu Glu Thr Tyr
355 360 365

Leu Lys Gln Lys Asn Ala
370

<210> 343

<211> 282

<212> PRT

<213> Streptococcus agalactiae

<400> 343

Leu Ile Glu Ile Thr Trp Thr Val Lys Tyr Ile Thr Glu Phe Ile Ala
1 5 10 15

Thr Ala Phe Leu Ile Ile Leu Gly Asn Gly Ala Val Ala Asn Val Asp
20 25 30

Leu Lys Gly Thr Lys Gly Asn Asn Ser Gly Trp Ile Ile Ile Ala Ile
35 40 45

Gly Tyr Gly Leu Gly Val Met Met Pro Ala Leu Met Phe Gly Asn Val
50 55 60

Ser Gly Asn His Ile Asn Pro Ala Phe Thr Leu Gly Leu Ala Phe Ser
65 70 75 80

Gly Leu Phe Pro Trp Ala His Val Gly Gln Tyr Ile Leu Ala Gln Ile
85 90 95

Leu Gly Ala Met Phe Gly Gln Leu Val Val Val Met Val Tyr Gln Pro
100 105 110

Tyr Phe Val Lys Thr Glu Asn Pro Asn His Val Leu Gly Ser Phe Ser
115 120 125

Thr Ile Ser Ala Leu Asp Asp Gly Gln Lys Ser Ser Arg Lys Ala Ala
130 135 140

Tyr Ile Asn Gly Phe Leu Asn Glu Phe Val Gly Ser Phe Val Leu Phe
145 150 155 160

Phe Gly Ala Leu Ala Leu Thr Lys Asn Tyr Phe Gly Val Glu Leu Val
165 170 175

Gly Lys Leu Val Gln Ala Gly Tyr Asp Gln Thr Thr Ala Ala Thr Arg
180 185 190

Ile Ser Pro Tyr Val Thr Gly Ser Leu Ala Val Ala His Leu Gly Ile
195 200 205

Gly Phe Leu Val Met Thr Leu Val Ala Ser Leu Gly Gly Pro Thr Gly
210 215 220

Pro Ala Leu Asn Pro Ala Arg Asp Leu Gly Pro Arg Ile Val His Arg
225 230 235 240

Leu Leu Pro Lys Gln Ile Leu Gly Gln Ala Lys Glu Asp Ser Lys Trp
245 250 255

Trp Tyr Ala Trp Val Pro Val Leu Ala Pro Ile Val Ala Ser Ile Leu
260 265 270

Ala Val Ala Leu Phe Lys Leu Leu Tyr Leu
275 280

<210> 344

<211> 326

<212> PRT

<213> Streptococcus agalactiae

<400> 344

Met Ser Ser Tyr Trp Asn Asn Tyr Pro Glu Leu Lys Lys Asn Ile Asp
1 5 10 15

Glu Thr Asn Gln Leu Ile Gln Glu Arg Ile Gln Val Arg Asn Lys Asp
20 25 30

Ile Glu Ala Ala Leu Ser Gln Leu Thr Ala Ala Gly Gly Lys Gln Leu
35 40 45

Arg Pro Ala Phe Phe Tyr Leu Phe Ser Gln Leu Gly Asn Lys Glu Asn
50 55 60

Gln Asp Thr Gln Gln Leu Lys Lys Ile Ala Ala Ser Leu Glu Ile Leu
65 70 75 80

His Val Ala Thr Leu Ile His Asp Asp Val Ile Asp Asp Ser Pro Leu
85 90 95

Arg Arg Gly Asn Met Thr Ile Gln Ser Lys Phe Gly Lys Asp Ile Ala
100 105 110

Val Tyr Thr Gly Asp Leu Leu Phe Thr Val Phe Phe Asp Leu Ile Leu
115 120 125

Glu Ser Met Ala Asp Thr Pro Phe Met Arg Ile Asn Ala Lys Ser Met
130 135 140

Arg Lys Ile Leu Met Gly Glu Leu Asp Gln Met His Leu Arg Tyr Asn
145 150 155 160

Gln Gln Gln Gly Ile His His Tyr Leu Arg Ala Ile Ser Gly Lys Thr
165 170 175

Ala Glu Leu Phe Lys Leu Ala Ser Lys Glu Gly Ala Tyr Phe Gly Gly
180 185 190

Ala Glu Lys Glu Val Val Arg Leu Ala Gly His Ile Gly Phe Asn Ile
195 200 205

Gly Met Thr Phe Gln Ile Leu Asp Asp Ile Leu Asp Tyr Thr Ala Asp
210 215 220

Lys Lys Thr Phe Asn Lys Pro Val Leu Glu Asp Leu Thr Gln Gly Val
225 230 235 240

Tyr Ser Leu Pro Leu Leu Leu Ala Ile Glu Glu Asn Pro Asp Ile Phe
245 250 255

Lys Pro Ile Leu Asp Lys Lys Thr Asp Met Ala Thr Glu Asp Met Glu
260 265 270

Lys Ile Ala Tyr Leu Val Val Ser His Arg Gly Val Asp Lys Ala Arg
275 280 285

His Leu Ala Arg Lys Phe Thr Glu Lys Ala Ile Ser Asp Ile Asn Lys
290 295 300

Leu Pro Gln Asn Ser Ala Lys Lys Gln Leu Leu Gln Leu Thr Asn Tyr
305 310 315 320

Leu Leu Lys Arg Lys Ile
325

<210> 345

<211> 582

<212> PRT

<213> Streptococcus agalactiae

<400> 345

Met Phe Lys Ile Pro Leu Phe Lys Glu Leu Lys Thr Asp Gln Trp Val
1               5                   10                  15

Lys Pro Phe Phe Lys Gln Tyr Lys Val Ser Leu Val Ile Ala Leu Phe
            20                  25                  30

Leu Gly Phe Met Thr Phe Phe Ser Ala Ser Ala Leu Met Phe Asn Ser
        35                  40                  45

Gly Tyr Leu Ile Ser Lys Ser Ala Ser Leu Pro Ser Asn Ile Leu Leu
    50                  55                  60

Val Tyr Val Pro Ile Val Leu Thr Arg Ala Phe Gly Ile Gly Arg Pro
65                  70                  75                  80

Val Phe Arg Tyr Ile Glu Arg Leu Thr Ser His Asn Trp Val Leu Arg
                85                  90                  95

Met Thr Ser Gln Leu Arg Leu Lys Leu Tyr His Ser Leu Glu Ser Asn
            100                 105                 110

Ala Ile Phe Met Lys Arg Asp Phe Arg Leu Gly Asp Val Met Gly Leu
        115                 120                 125

Leu Ala Glu Asp Ile Asn Tyr Leu Gln Asn Leu Tyr Leu Arg Thr Ile
    130                 135                 140

Phe Pro Thr Ile Ile Ala Trp Leu Leu Tyr Ser Phe Ile Ile Ile Ala
145                 150                 155                 160

Thr Gly Phe Phe Ser Leu Trp Phe Ala Leu Met Met Leu Leu Tyr Leu
                165                 170                 175

Ala Ile Met Ile Phe Leu Phe Pro Leu Trp Ser Ile Leu Ala Asn Gly
            180                 185                 190

Ala Arg Gln Thr Arg Glu Lys Glu Leu Lys Asn His Leu Tyr Thr Asp
        195                 200                 205

Leu Thr Asp Asn Val Leu Gly Ile Ser Asp Trp Ile Phe Ser Gln Arg
    210                 215                 220

Gly Gln Glu Tyr Val Ala Leu His Glu Arg Ser Glu Ser Glu Leu Met
225 230 235 240

Ala Ile Gln Lys Lys Ile Arg Ser Phe Asn Asn Arg Arg Ala Leu Ile
245 250 255

Val Glu Leu Val Phe Gly Phe Leu Ala Ile Leu Val Ile Ile Trp Ala
260 265 270

Ser Asn Gln Phe Ile Gly His Arg Gly Gly Glu Ala Asn Trp Ile Ala
275 280 285

Ala Phe Val Leu Thr Val Phe Pro Leu Ser Glu Ala Phe Ala Gly Leu
290 295 300

Ser Ala Ala Ala Gln Glu Thr Asn Lys Tyr Ser Asp Ser Ile His Arg
305 310 315 320

Leu Asn Glu Leu Ser Glu Thr Tyr Phe Glu Thr Thr Gln Asn Gln Leu
325 330 335

Pro Asn Lys Pro Tyr Asp Phe Ser Val Lys Asn Leu Ser Phe Gln Tyr
340 345 350

Lys Pro Gln Glu Lys Trp Val Leu His His Leu Asp Leu Asp Ile Lys
355 360 365

Glu Gly Glu Lys Ile Ala Ile Leu Gly Arg Ser Gly Ser Gly Lys Ser
370 375 380

Thr Leu Ala Ser Leu Leu Arg Gly Asp Leu Lys Ala Ser Gln Gly Lys
385 390 395 400

Ile Thr Leu Gly Gly Ala Asp Val Ser Ile Val Gly Asp Cys Ile Ser
405 410 415

Asn Tyr Ile Gly Val Ile Gln Gln Ala Pro Tyr Leu Phe Asn Thr Thr
420 425 430

Leu Leu Asn Asn Ile Arg Ile Gly Asn Gln Asp Ala Ser Glu Glu Asp
435 440 445

Val Trp Lys Val Leu Glu Arg Val Gly Leu Lys Glu Met Val Thr Asp
450 455 460

Leu Ser Asp Gly Leu Tyr Thr Met Val Asp Glu Ala Gly Leu Arg Phe
465 470 475 480

Ser Gly Gly Glu Arg His Arg Ile Ala Leu Ala Arg Ile Leu Leu Lys
485 490 495

Asp Val Pro Ile Val Ile Leu Asp Glu Pro Thr Val Gly Leu Asp Pro
500 505 510

Ile Thr Glu Gln Ala Leu Leu Arg Val Phe Met Lys Glu Leu Glu Gly
515 520 525

Lys Thr Leu Val Trp Ile Thr His His Leu Lys Gly Ile Glu His Ala
530 535 540

Asp Arg Ile Leu Phe Ile Glu Asn Gly Gln Leu Glu Leu Glu Gly Ser
545 550 555 560

Pro Gln Glu Leu Ser Gln Ser Ser Gln Arg Tyr Arg Gln Leu Lys Ala
565 570 575

Ala Asp Asp Gly Asp Leu
580

<210> 346

<211> 148

<212> PRT

<213> Streptococcus agalactiae

<400> 346

Met Lys Lys Leu Ile Thr Glu Lys Lys Val Asn Asn Val Ser Thr Val
1 5 10 15

Asn Tyr Leu Lys Leu Gly Leu Val Ser Ala Met Phe Ala Gly Gly Ala
20 25 30

Phe Val Ala Leu Gly Ser Thr Gln Gly Val Ser Ala Ser Thr Phe Thr
35 40 45

Ala Pro Gln Ala Thr His Pro Lys Ala Glu Arg Gln Leu Thr Asp Ser
50 55 60

Glu Ile Tyr Glu Arg Ala Gln Lys Gln Val Leu Pro Lys Tyr Ile Gln
65 70 75 80

Gly Ser Leu Ser Gly Ile Leu Asn Gln His Ser Thr Leu Tyr Lys Gln
85 90 95

Gln Asn Ala Ala Val Thr Pro Gln Val Ser Ser Pro Lys Ala Glu Arg
100 105 110

Gln Leu Thr Asp Ser Glu Ile Tyr Glu Arg Ala Gln Lys Gln Val Leu
115 120 125

Pro Lys Tyr Ile Gln Gly Ser Leu Ser Gly Ile Leu Asn Gln His Ser
130 135 140

Thr Leu Asn Ala
145

<210> 347

<211> 169

<212> PRT

<213> Streptococcus agalactiae

<400> 347

Met Glu Glu Asn Met Asn Ile Lys Gln Leu Lys Ser Lys Thr Met Leu
1 5 10 15

Gly Thr Val Ala Leu Val Ser Ala Phe Ser Phe Ala Ser Thr Asn Ala
20 25 30

Asp Ala Asn Thr Tyr Asn Tyr Ala Val Asp Val Asp Tyr Leu Ala Ser
35 40 45

Ala Glu Glu Ile Ala Gln Ala His Pro Ala Ser Asn Thr Phe Pro Leu
50 55 60

Gly Gln Cys Thr Trp Gly Val Lys Glu Met Ala Thr Trp Ala Gly Asn
65 70 75 80

Trp Trp Gly Asn Gly Gly Asp Trp Ala Ala Ser Ala Ala Ser Ala Gly
85 90 95

Tyr Thr Val Gly Thr Gln Pro Arg Val Gly Ser Ile Val Cys Trp Thr
100 105 110

Asp Gly Ser Tyr Gly His Val Ala Tyr Val Thr Ala Val Asp Pro Val
115 120 125

Thr Asn Lys Ile Gln Val Leu Glu Ser Asn Tyr Ala Gly His Gln Trp
130 135 140

Ile Asp Asn Tyr Arg Gly Trp Phe Asp Pro Gln Asn Thr Ala Thr Pro
145 150 155 160

Gly Val Val Ser Tyr Ile Tyr Pro Asn
165

<210> 348

<211> 313

<212> PRT

<213> Streptococcus agalactiae

<400> 348

Met Lys Ile Asn Gln Met Lys Lys Asp Glu Leu Phe Glu Gly Phe Tyr
1               5                   10                  15

Leu Ile Lys Lys Ala Glu Val Arg Lys Thr Arg Ala Gly Lys Asp Phe
            20                  25                  30

Ile Ala Phe Thr Phe Arg Asp Asp Thr Gly Glu Ile Ser Gly Asn Met
        35                  40                  45

Trp Asp Ala Gln Thr Tyr Asn Val Glu Glu Phe Val Ala Gly Lys Ile
    50                  55                  60

Val His Met Lys Gly Arg Arg Glu Val Tyr Asn Gly Thr Pro Gln Val
65                  70                  75                  80

Asn Gln Ile Thr Leu Arg Asn Ile Lys Asp Gly Glu Pro Asn Asp Pro
                85                  90                  95

Arg Asp Phe Lys Glu Lys Pro Pro Ile Asn Val Asp Asn Val Arg Glu
            100                 105                 110

Tyr Met Glu Gln Met Leu Phe Lys Ile Glu Asn Ala Thr Trp Gln Arg
        115                 120                 125

Val Val Arg Ala Leu Tyr Arg Lys Tyr Asn Lys Glu Phe Phe Thr Tyr
    130                 135                 140

Pro Ala Ala Lys Thr Asn His His Ala Phe Glu Ser Gly Leu Ala Tyr
145                 150                 155                 160

His Thr Ala Thr Met Val Arg Leu Ala Asp Ser Ile Gly Asp Ile Tyr
                165                 170                 175

Pro Glu Leu Asn Lys Ser Leu Met Phe Ala Gly Ile Met Leu His Asp
            180                 185                 190

Leu Ala Lys Val Ile Glu Leu Ser Gly Pro Asp Asn Thr Glu Tyr Thr
        195                 200                 205

Ile Arg Gly Asn Leu Ile Gly His Ile Ser Leu Ile Asp Glu Glu Leu
    210                 215                 220

Thr Lys Ile Leu Ala Glu Leu Asn Ile Asp Asp Thr Lys Glu Glu Val
225                 230                 235                 240

Thr Val Leu Arg His Val Ile Leu Ser His His Gly Gln Leu Glu Tyr
245 250 255

Gly Ser Pro Val Arg Pro Arg Ile Met Glu Ala Glu Ile Ile His Met
260 265 270

Ile Asp Asn Ile Asp Ala Asn Met Met Met Met Thr Thr Ala Leu Asn
275 280 285

Arg Val Asn Glu Gly Glu Met Thr Asn Arg Ile Phe Ala Met Asp Asn
290 295 300

Arg Ser Phe Tyr Lys Pro Asn Ile Lys
305 310

<210> 349

<211> 283

<212> PRT

<213> Streptococcus agalactiae

<400> 349

Met Leu Val Asp Lys Lys Trp Arg Phe Glu Asp Ser Ala Ser Tyr Phe
1 5 10 15

Ala Cys Pro Lys Cys Gln Asn Pro Leu Ile Lys Glu Ser Asn Ser Leu
20 25 30

Lys Cys Ser Asp Asn His Cys Phe Asp Leu Ser Lys Phe Gly Tyr Val
35 40 45

Asn Leu Leu Gly Gly Lys Lys Ile Asp Glu His Tyr Asp Lys Lys Ser
50 55 60

Phe Glu Asn Arg Gln Leu Val Leu Glu Asn Gly Tyr Tyr Asn His Ile
65 70 75 80

Leu Glu Ala Ile Ser Lys Val Leu Glu Asn Asn Ser Gln Phe His Ser
85 90 95

Val Leu Asp Ile Gly Cys Gly Glu Gly Phe Tyr Ser Arg Gln Leu Val
100 105 110

Asn Lys Tyr Glu Lys Thr Phe Leu Ala Phe Asp Ile Ser Lys Asp Ser
115 120 125

Ile Gln Leu Ala Ala Lys Ser Asp Gln Ser Arg Leu Val Lys Trp Phe
130 135 140

Val Ser Asp Leu Ala Asn Leu Pro Ile Gln Asp Ser Ser Ile Asp Ile
145 150 155 160

Ile Leu Asp Ile Phe Ser Pro Ala Asn Tyr Lys Glu Phe Arg Arg Val
165 170 175

Leu Ser Asp Asp Gly Ile Leu Val Lys Val Val Pro Val Ala Glu His
180 185 190

Val Gln Glu Leu Arg Glu Lys Ala Ser Gln Tyr Leu Lys Gln Lys Asp
195 200 205

Tyr Ser Asn Gln Lys Ile Leu Asp His Phe Arg Glu Asn Phe Glu Ile
210 215 220

Ile Ser Glu Gln Lys Val Val Gln Ser Tyr Asn Cys Ser Gln Gln Glu
225 230 235 240

Arg Gln Ala Phe Ile Asp Met Thr Pro Leu Leu Phe Ser Val Asp Lys
245 250 255

Thr Thr Ile Asp Trp Ala Ser Ile Ser Glu Ile Thr Val Gly Ala Leu
260 265 270

Ile Val Ile Gly Lys Lys Arg Ser Val Ser Lys
275 280

<210> 350

<211> 149

<212> PRT

<213> Streptococcus agalactiae

<400> 350

Met Cys Leu Ile Cys Gln Arg Ile Glu Met Ile Glu Arg Asn Glu Asn
1 5 10 15

Pro Tyr Phe Val Lys Glu Tyr Glu Thr Gly Tyr Leu Val Leu Gly Asp
20 25 30

His Gln Tyr Phe Gln Gly Tyr Cys Leu Phe Leu Ser Lys Lys His Val
35 40 45

Thr Glu Leu His Glu Leu Pro Arg Asp Trp Arg Asn Gln Tyr Leu Ser
50 55 60

Glu Met Ala Asp Ala Ser Glu Ile Val Ala Lys Ala Phe Arg Ala Asp
65 70 75 80

Lys Met Asn Ile Glu Ser Leu Gly Asn Gly Asp Ala His Leu His Phe
85 90 95

His Leu Phe Pro Arg Lys Thr Gly Asp Leu Arg Asn Tyr Gly His Asn
100 105 110

Gly Lys Gly Pro Val Trp Trp Tyr Pro Phe Glu Lys Met Tyr Ala Asp
115 120 125

Ser Val Arg Ala Thr Gly Ala Glu Ile Glu Lys Leu Lys Glu Lys Leu
130 135 140

Leu Asp Val Leu Gly
145

<210> 351

<211> 395

<212> PRT

<213> Streptococcus agalactiae

<400> 351

Met Phe Ser Asp Leu Arg Lys Lys Phe Val Phe Leu Thr Met Ser Ile
1 5 10 15

Leu Ile Val Val Val Leu Phe Leu Phe Ala Val Ser Asn Arg Tyr Asn
20 25 30

Gln Tyr Trp Asp Glu Tyr Asp Ala Tyr Arg Ile Val Lys Leu Val Ala
35 40 45

Lys Asn Asp Tyr Leu Gly Ile Pro Gly Asp Glu Pro Ile Ala Leu Val
50 55 60

Thr Ile Asp Asn Gln Lys Met Val Lys Ile Gln Ser Asn Asn Thr Asp
65 70 75 80

Leu Thr Asn Asp Val Ile Glu Lys Ser Ser Leu Lys Leu Leu Glu Gln
85 90 95

Gly Lys Lys Ser Arg Lys Trp Lys Ser Phe Ile Tyr Ser Ile Lys Glu
100 105 110

Tyr Lys Asp Lys Thr Tyr Thr Ile Ala Ile Met Asp Leu Ala Ser Tyr
115 120 125

Glu Val Pro Tyr Ala Arg Arg Phe Leu Ile Leu Val Phe Thr Ile Phe
130 135 140

Gly Phe Cys Leu Leu Ala Ala Val Ser Leu Tyr Leu Ser Arg Phe Ile
145 150 155 160

Val Gly Pro Val Glu Thr Glu Met Thr Arg Glu Lys Gln Phe Val Ser
165 170 175

Asp Ala Ser His Glu Leu Lys Thr Pro Ile Ala Ala Ile Arg Ala Asn
180 185 190

Val Gln Val Leu Glu Gln Gln Ile Pro Gly Asn Arg Tyr Leu Asp His
195 200 205

Val Val Ser Glu Thr Lys Arg Met Glu Phe Leu Ile Glu Asp Leu Leu
210 215 220

Asn Leu Ser Arg Leu Asp Glu Lys Arg Ser Lys Val Asn Phe Lys Lys
225 230 235 240

Leu Asn Leu Ser Val Leu Cys Gln Glu Val Leu Leu Thr Tyr Glu Ser
245 250 255

Leu Ala Tyr Glu Glu Glu Lys Cys Leu Asn Asp Thr Ile Glu Asp Asp
260 265 270

Val Trp Ile Val Gly Glu Glu Ser Gln Ile Lys Gln Ile Leu Ile Ile
275 280 285

Leu Leu Asp Asn Ala Ile Arg His Ser Leu Ser Lys Ser Glu Ile Gln
290 295 300

Phe Ser Leu Lys Gln Ala Arg Arg Lys Ala Ile Leu Thr Ile Ser Asn
305 310 315 320

Pro Ser Ala Ile Tyr Ser Lys Glu Val Met Asp Asn Leu Phe Glu Arg
325 330 335

Phe Tyr Gln Ala Lys Asp Asp His Ala Asp Ser Leu Ser Phe Gly Leu
340 345 350

Gly Leu Ser Ile Ala Lys Ala Ile Val Glu Arg His Lys Gly Arg Ile
355 360 365

Arg Ala Tyr Gln Glu Lys Asp Gln Leu Arg Leu Glu Val Gln Leu Pro
370 375 380

Ile Asp Gly Phe Trp Thr Asn Thr Met Ile Asn
385 390 395

<210> 352

<211> 559

<212> PRT

<213> Streptococcus agalactiae

<400> 352

Leu Ile Ile Leu Asp Lys Lys Ser Tyr Asp Leu Leu Phe Tyr Leu Leu
1               5                   10                  15

Lys Leu Glu Glu Pro Glu Thr Val Met Ala Ile Ala Asn Ala Leu Asn
            20                  25                  30

Gln Ser Arg Arg Lys Val Tyr Tyr His Leu Glu Lys Ile Asn Asp Ala
        35                  40                  45

Leu Pro Ser Asp Val Pro Gln Ile Val Ser Tyr Pro Arg Val Gly Ile
    50                  55                  60

Leu Leu Thr Glu Lys Gln Lys Ala Ala Cys Arg Leu Leu Leu Asp Glu
65                  70                  75                  80

Val Thr Asp Tyr Ser Tyr Val Met Lys Ser Ser Glu Arg Leu Gln Leu
                85                  90                  95

Ser Leu Val Ser Ile Val Val Ala Lys Asp Arg Ile Thr Ile Asp Arg
            100                 105                 110

Leu Met Gln Leu Asn Asp Val Ser Arg Asn Thr Ile Leu Asn Asp Leu
        115                 120                 125

Asn Glu Leu Arg Ser Glu Leu Ala Glu Lys Glu Tyr Asn Leu Gln Leu
    130                 135                 140

Gln Ser Thr Lys Cys Arg Gly Tyr Phe Leu Asp Gly His Pro Leu Ser
145                 150                 155                 160

Ile Ile Gln Tyr Leu Tyr Lys Leu Leu Asp Asp Ile Tyr His Asn Gly
                165                 170                 175

Ser Ser Ser Phe Ile Asp Leu Phe Asn His Lys Leu Ser Gln Ala Phe
            180                 185                 190

Gly Ala Ser Thr Tyr Phe Ser Lys Glu Val Leu Asp Tyr Phe His His
        195                 200                 205

Tyr Leu Phe Ile Ser Gln Arg Ser Leu Gly Lys Lys Ile Asn Ser Gln
    210                 215                 220

Asp Gly Gln Phe Met Ile Gln Ile Leu Pro Phe Ile Leu Met Ala Tyr
225                 230                 235                 240

Arg Lys Met Arg Leu Ser Pro Glu Val Gln Thr Ser Leu Asn Ser Asp
245 250 255

Phe Ser Leu Val Trp Gln Arg Lys Glu Tyr Glu Ile Ala Lys Glu Leu
260 265 270

Ala Asp Glu Leu Glu Glu Asn Phe Gln Leu Ser Leu Asp Glu Ile Glu
275 280 285

Val Gly Leu Val Ala Met Leu Met Leu Ser Phe Arg Lys Asp Arg Asp
290 295 300

Asn His Leu Glu Ser Gln Asp Tyr Asp Asp Met Arg Ala Thr Leu Thr
305 310 315 320

Ser Phe Leu Lys Glu Leu Glu Glu Arg Tyr His Leu His Phe Val His
325 330 335

Lys Lys Asp Leu Leu Arg Gln Leu Leu Thr His Cys Lys Ala Leu Leu
340 345 350

Tyr Arg Lys Arg Tyr Gly Ile Phe Ser Val Asn Pro Leu Thr Glu His
355 360 365

Ile Lys Asp Lys Tyr Glu Glu Leu Phe Ala Ile Thr Ser Ser Ser Val
370 375 380

Lys Leu Leu Glu Lys Ala Trp Gln Ile Lys Leu Thr Asp Asp Asp Val
385 390 395 400

Ala Tyr Leu Thr Ile His Leu Gly Gly Glu Leu Arg Asn Ser Gln Gln
405 410 415

Ser Pro Asn Lys Leu Lys Leu Val Ile Val Ser Asp Glu Gly Ile Ala
420 425 430

Ile Gln Lys Leu Leu Leu Lys Gln Cys Gln Arg Tyr Leu Thr Asn Ser
435 440 445

Asp Ile Glu Ala Val Phe Thr Thr Glu Gln Tyr Gln Ser Val Ser Asp
450 455 460

Leu Met His Val Asp Met Val Val Ser Thr Ser Asp Ala Leu Glu Ser
465 470 475 480

Arg Phe Pro Met Leu Val Val His Pro Val Leu Thr Asp Asp Asp Ile
485 490 495

Ile Arg Leu Ile Arg Phe Ser Lys Lys Gly Asn Cys Ala Asn Ser Asn
500 505 510

Gln Phe Thr Asn Glu Leu Glu Lys Thr Ile Ala Gln Tyr Val Lys Glu
515 520 525

Asp Ser Glu Arg Tyr Val Leu Lys Ser Lys Ile Glu Lys Leu Ile His
530 535 540

Gln Glu Leu Leu Gln Asp Val Leu Pro Leu Gln Ser Thr Val Cys
545 550 555

<210> 353

<211> 215

<212> PRT

<213> Streptococcus agalactiae

<400> 353

Met Lys Tyr Phe Leu Asp Thr Ala Asp Val Ser Glu Ile Arg Arg Leu
1 5 10 15

Asn Arg Leu Gly Ile Val Asp Gly Val Thr Thr Asn Pro Thr Ile Ile
20 25 30

Ser Arg Glu Gly Arg Asp Phe Lys Glu Val Ile Asn Glu Ile Cys Gln
35 40 45

Ile Val Asp Gly Pro Val Ser Ala Glu Val Thr Gly Leu Thr Cys Asp
50 55 60

Glu Met Val Thr Glu Ala Arg Glu Ile Ala Lys Trp Ser Pro Asn Val
65 70 75 80

Val Val Lys Ile Pro Met Thr Glu Glu Gly Leu Ala Ala Val Ser Gln
85 90 95

Leu Ser Lys Glu Gly Ile Lys Thr Asn Val Thr Leu Ile Phe Thr Val
100 105 110

Ala Gln Gly Leu Ser Ala Met Lys Ala Gly Ala Thr Phe Ile Ser Pro
115 120 125

Phe Val Gly Arg Leu Glu Asp Ile Gly Thr Asp Ala Tyr Ala Leu Ile
130 135 140

Arg Asp Leu Arg His Ile Ile Asp Phe Tyr Gly Phe Gln Ser Glu Ile
145 150 155 160

Ile Ala Ala Ser Ile Arg Gly Leu Ala His Val Glu Gly Val Ala Lys
165 170 175

Cys Gly Ala His Ile Ala Thr Ile Pro Asp Lys Thr Phe Ala Ser Leu
180 185 190

Phe Thr His Pro Leu Thr Asp Lys Gly Ile Glu Thr Phe Leu Lys Asp
195 200 205

Trp Asp Ser Phe Lys Lys Lys
210 215

<210> 354

<211> 815

<212> PRT

<213> Streptococcus agalactiae

<400> 354

Met Ser His Tyr Ser Ile Lys Leu Gln Glu Val Phe Arg Leu Ala Gln
1 5 10 15

Phe Gln Ala Ala Arg Tyr Glu Ser His Tyr Leu Glu Ser Trp His Leu
20 25 30

Leu Leu Ala Met Val Leu Val His Asp Ser Val Ala Gly Leu Thr Phe
35 40 45

Ala Glu Tyr Glu Ser Glu Val Ala Ile Glu Glu Tyr Glu Ala Ala Thr
50 55 60

Ile Leu Ala Leu Gly Arg Ala Pro Lys Glu Glu Ile Thr Asn Tyr Gln
65 70 75 80

Phe Leu Glu Gln Ser Pro Ala Leu Lys Lys Ile Leu Lys Leu Ala Glu
85 90 95

Asn Ile Ser Ile Val Val Gly Ala Glu Asp Val Gly Thr Glu His Val
100 105 110

Leu Leu Ala Met Leu Val Asn Lys Asp Leu Leu Ala Thr Arg Ile Leu
115 120 125

Glu Leu Val Gly Phe Arg Gly Gln Asp Asp Gly Glu Ser Val Arg Met
130 135 140

Val Asp Leu Arg Lys Ala Leu Glu Arg His Ala Gly Phe Thr Lys Asp
145 150 155 160

Asp Ile Lys Ala Ile Tyr Glu Leu Arg Asn Pro Lys Lys Ala Lys Ser
165 170 175

Gly Ala Ser Phe Ser Asp Met Met Lys Pro Pro Ser Thr Ala Gly Asp
180 185 190

Leu Ala Asp Phe Thr Arg Asp Leu Ser Gln Met Ala Val Asp Gly Glu
195 200 205

Ile Glu Pro Val Ile Gly Arg Asp Lys Glu Ile Ser Arg Met Val Gln
210 215 220

Val Leu Ser Arg Lys Thr Lys Asn Asn Pro Val Leu Val Gly Asp Ala
225 230 235 240

Gly Val Gly Lys Thr Ala Leu Ala Tyr Gly Leu Ala Gln Arg Ile Ala
245 250 255

Asn Gly Asn Ile Pro Tyr Glu Leu Arg Asp Met Arg Val Leu Glu Leu
260 265 270

Asp Met Met Ser Val Val Ala Gly Thr Arg Phe Arg Gly Asp Phe Glu
275 280 285

Glu Arg Met Asn Gln Ile Ile Ala Asp Ile Glu Glu Asp Gly His Ile
290 295 300

Ile Leu Phe Ile Asp Glu Leu His Thr Ile Met Gly Ser Gly Ser Gly
305 310 315 320

Ile Asp Ser Thr Leu Asp Ala Ala Asn Ile Leu Lys Pro Ala Leu Ala
325 330 335

Arg Gly Thr Leu Arg Thr Val Gly Ala Thr Thr Gln Glu Glu Tyr Gln
340 345 350

Lys His Ile Glu Lys Asp Ala Ala Leu Ser Arg Arg Phe Ala Lys Val
355 360 365

Leu Val Glu Glu Pro Asn Leu Glu Asp Ala Tyr Glu Ile Leu Leu Gly
370 375 380

Leu Lys Pro Ala Tyr Glu Ala Phe His Asn Val Thr Ile Ser Asp Glu
385 390 395 400

Ala Val Met Thr Ala Val Lys Val Ala His Arg Tyr Leu Thr Ser Lys
405 410 415

Asn Leu Pro Asp Ser Ala Ile Asp Leu Leu Asp Glu Ala Ser Ala Thr
420 425 430

Val Gln Met Met Ile Lys Lys Asn Ala Pro Ser Leu Leu Thr Glu Val
435 440 445

Asp Gln Ala Ile Leu Asp Asp Asp Met Lys Ser Ala Ser Lys Ala Leu
450 455 460

Lys Ala Ser Tyr Lys Gly Lys Lys Arg Lys Pro Ile Ala Val Thr Glu
465 470 475 480

Asp His Ile Met Ala Thr Leu Ser Arg Leu Ser Gly Ile Pro Val Glu
485 490 495

Lys Leu Thr Gln Ala Asp Ser Lys Lys Tyr Leu Asn Leu Glu Lys Glu
500 505 510

Leu His Lys Arg Val Ile Gly Gln Asp Asp Ala Val Thr Ala Ile Ser
515 520 525

Arg Ala Ile Arg Arg Asn Gln Ser Gly Ile Arg Thr Gly Lys Arg Pro
530 535 540

Ile Gly Ser Phe Met Phe Leu Gly Pro Thr Gly Val Gly Lys Thr Glu
545 550 555 560

Leu Ala Lys Ala Leu Ala Glu Val Leu Phe Asp Asp Glu Ser Ala Leu
565 570 575

Ile Arg Phe Asp Met Ser Glu Tyr Met Glu Lys Phe Ala Ala Ser His
580 585 590

Leu Asn Gly Ala Pro Pro Gly Tyr Val Gly Tyr Asp Glu Gly Gly Glu
595 600 605

Leu Thr Glu Lys Val Arg Asn Lys Pro Tyr Ser Val Leu Leu Phe Asp
610 615 620

Glu Val Glu Lys Ala His Pro Asp Ile Phe Asn Val Leu Leu Gln Val
625 630 635 640

Leu Asp Asp Gly Val Leu Thr Asp Ser Arg Gly Arg Lys Val Asp Phe
645 650 655

Ser Asn Thr Ile Ile Ile Met Thr Ser Asn Leu Gly Ala Thr Ala Leu
660 665 670

Arg Asp Asp Lys Thr Val Gly Phe Gly Ala Lys Asp Ile Ser His Asp
675 680 685

Tyr Thr Ala Met Gln Lys Arg Ile Met Glu Glu Leu Lys Lys Ala Tyr
690 695 700

Arg Pro Glu Phe Ile Asn Arg Ile Asp Glu Lys Val Val Phe His Ser
705 710 715 720

Leu Ser Gln Asp Asn Met Arg Glu Val Val Lys Ile Met Val Lys Pro
725 730 735

Leu Ile Leu Ala Leu Lys Asp Lys Gly Met Asp Leu Lys Phe Gln Pro
740 745 750

Ser Ala Leu Lys His Leu Ala Glu Asp Gly Tyr Asp Ile Glu Met Gly
755 760 765

Ala Arg Pro Leu Arg Arg Thr Ile Gln Thr Gln Val Glu Asp His Leu
770 775 780

Ser Glu Leu Leu Leu Ala Asn Gln Val Lys Glu Gly Gln Val Ile Lys
785 790 795 800

Ile Gly Val Ser Lys Gly Lys Leu Lys Phe Asp Ile Ala Lys Ser
805 810 815

<210> 355

<211> 510

<212> PRT

<213> Streptococcus agalactiae

<400> 355

Met Val Leu Asp Lys Glu Ile Lys Ala Gln Leu Ala Gln Tyr Leu Asp
1 5 10 15

Leu Leu Glu Ser Asp Ile Val Leu Gln Ala Asp Leu Gly Asp Asn Asp
20 25 30

Asn Ser Gln Lys Val Lys Asp Phe Leu Asp Glu Ile Val Ala Met Ser
35 40 45

Asp Arg Ile Ser Leu Glu Ser Thr His Leu Lys Arg Gln Pro Ser Phe
50 55 60

Gly Ile Ala Lys Lys Gly His Glu Ser Arg Val Ile Phe Ser Gly Leu
65 70 75 80

Pro Met Gly His Glu Phe Thr Ser Phe Ile Leu Ala Leu Leu Gln Val
85 90 95

Ser Gly Arg Ala Pro Lys Val Asp Glu Asp Ile Ile Lys Arg Ile Lys
100 105 110

Gly Ile Glu Lys Thr Ile Asn Leu Glu Thr Tyr Val Ser Leu Thr Cys
115 120 125

His Asn Cys Pro Asp Val Val Gln Ala Phe Asn Ile Met Ala Val Leu
130 135 140

Asn Pro Asn Ile Thr His Thr Met Ile Glu Gly Gly Met Tyr Gln Asp
145 150 155 160

Glu Val Lys Ser Lys Gly Ile Met Ser Val Pro Thr Val Tyr Lys Asp
165 170 175

Gln Glu Glu Phe Thr Ser Gly Arg Ala Thr Ile Glu Gln Leu Leu Glu
180 185 190

Gln Leu Asp Gly Pro Leu Asp Ala Glu Ala Phe Ala Asp Lys Gly Val
195 200 205

Tyr Asp Val Leu Val Ile Gly Gly Gly Pro Ala Gly Asn Ser Ala Ala
210 215 220

Ile Tyr Ala Ala Arg Lys Gly Leu Lys Thr Gly Ile Leu Ala Glu Thr
225 230 235 240

Phe Gly Gly Gln Val Ile Glu Thr Val Gly Ile Glu Asn Met Ile Gly
245 250 255

Thr Leu Tyr Thr Glu Gly Pro Lys Leu Met Ala Gln Ile Glu Glu His
260 265 270

Thr Lys Ser Tyr Asp Ile Asp Ile Ile Lys Ser Gln Leu Ala Thr Gly
275 280 285

Ile Glu Lys Lys Glu Leu Val Glu Val Thr Leu Ala Asn Gly Ala Ile
290 295 300

Leu Gln Ala Lys Thr Ala Ile Leu Ala Leu Gly Ala Lys Trp Arg Asn
305 310 315 320

Ile Asn Val Pro Gly Glu Glu Glu Phe Arg Asn Lys Gly Val Thr Tyr
325 330 335

Cys Pro His Cys Asp Gly Pro Leu Phe Glu Gly Lys Asp Val Ala Val
340 345 350

Ile Gly Gly Gly Asn Ser Gly Met Glu Ala Ala Leu Asp Leu Ala Gly
355 360 365

Val Thr Lys His Val Thr Val Leu Glu Phe Leu Pro Glu Leu Lys Ala
370 375 380

Asp Gln Val Leu Gln Glu Arg Ala Ala Lys Thr Asp Asn Leu Thr Ile
385 390 395 400

Leu Lys Asn Val Ala Thr Lys Asp Ile Val Gly Glu Asp His Val Thr
405 410 415

Gly Leu Asn Tyr Thr Asp Arg Asp Thr Asn Glu Glu Lys His Ile Asp
420 425 430

Leu Glu Gly Val Phe Val Gln Ile Gly Leu Val Pro Ser Thr Ser Trp
435 440 445

Leu Lys Asp Ser Gly Ile Glu Leu Asn Glu Arg Gln Glu Ile Val Val
450 455 460

Asp Lys Phe Gly Ser Thr Asn Ile Pro Gly Ile Phe Ala Ala Gly Asp
465 470 475 480

Cys Thr Asp Ala Ala Tyr Lys Gln Ile Ile Ile Ser Met Gly Ser Gly
485 490 495

Ala Thr Ala Ala Ile Gly Ala Phe Asp Tyr Leu Ile Arg Gln
500 505 510

<210> 356

<211> 631

<212> PRT

<213> Streptococcus agalactiae

<400> 356

Met Ile Lys Tyr Gln Asp Asp Phe Tyr Gln Ala Val Asn Gly Glu Trp
1 5 10 15

Ala Lys Thr Ala Val Ile Pro Asp Asp Lys Pro Arg Thr Gly Gly Phe
20 25 30

Ser Asp Leu Ala Asp Asp Ile Glu Ala Leu Met Leu Ser Thr Thr Asp
35 40 45

Lys Trp Leu Ala Asp Glu Asn Lys Pro Ser Asp Thr Ile Leu Asn His
50 55 60

Phe Ile Ala Phe His Lys Met Thr Ala Asp Tyr Gln Lys Arg Glu Glu
65 70 75 80

Val Gly Val Ser Pro Val Leu Pro Leu Ile Glu Glu Tyr Lys Gly Leu
85 90 95

Gln Ser Phe Ser Glu Phe Ala Ser Lys Val Ala Glu Tyr Glu Leu Glu
100 105 110

Gly Lys Pro Asn Glu Phe Pro Phe Gly Val Ala Pro Asp Phe Met Asn
115 120 125

Ala Gln Leu Asn Val Leu Trp Ala Glu Ala Pro Gly Ile Ile Leu Pro
130 135 140

Asp Thr Thr Tyr Tyr Ser Glu Asp Asn Glu Lys Gly Lys Glu Leu Leu
145 150 155 160

Ala Phe Trp Arg Lys Ser Gln Glu Asp Leu Leu Pro Leu Phe Gly Leu
165 170 175

Ser Glu Gln Glu Ile Lys Asp Ile Leu Asp Lys Val Leu Ala Leu Asp
180 185 190

Ala Lys Leu Ala Gln Tyr Val Leu Ser Arg Glu Glu Ser Ser Glu Tyr
195 200 205

Val Lys Leu Tyr His Pro Tyr Asn Trp Glu Asp Phe Thr Lys Leu Ala
210 215 220

Pro Glu Leu Pro Leu Asp Ala Ile Phe Gln Lys Ile Leu Gly Gln Lys
225 230 235 240

Pro Asp Lys Val Ile Val Pro Glu Glu Arg Phe Trp Thr Glu Phe Ala
245 250 255

Ser Asp Tyr Tyr Ser Glu Ser Asn Trp Glu Leu Leu Lys Ala Asp Leu
260 265 270

Ile Leu Ser Ala Ala Asn Ala Tyr Asn Ala Tyr Leu Thr Asp Asp Ile
275 280 285

Arg Ile Lys Ser Gly Val Tyr Ser Arg Ala Leu Ser Gly Thr Pro Gln
290 295 300

Ala Met Asp Lys Lys Lys Ala Ala Tyr Tyr Leu Ala Ser Gly Pro Tyr
305 310 315 320

Asn Gln Ala Leu Gly Leu Trp Tyr Ala Gly Glu Lys Phe Ser Pro Glu
325 330 335

Ala Lys Ala Asp Val Glu His Lys Ile Ala Thr Met Ile Asp Val Tyr
340 345 350

Lys Ser Arg Leu Glu Lys Ala Asp Trp Leu Ala Gln Ser Thr Arg Glu
355 360 365

Lys Ala Ile Met Lys Leu Asn Val Ile Thr Pro His Ile Gly Tyr Pro
370 375 380

Glu Lys Leu Pro Glu Thr Tyr Thr Lys Lys Ile Ile Asp Pro Lys Leu
385                 390                 395                 400

Ser Leu Val Glu Asn Ala Thr Asn Leu Asp Lys Ile Ser Ile Ala Tyr
                405                 410                 415

Gly Trp Ser Lys Trp Asn Lys Pro Val Asp Arg Ser Glu Trp His Met
            420                 425                 430

Pro Ala His Met Val Asn Ala Tyr Tyr Asp Pro Gln Gln Asn Gln Ile
        435                 440                 445

Val Phe Pro Ala Ala Ile Leu Gln Glu Pro Phe Tyr Ala Leu Glu Gln
    450                 455                 460

Ser Ser Ser Ala Asn Tyr Gly Gly Ile Gly Ala Val Ile Ala His Glu
465                 470                 475                 480

Ile Ser His Ala Phe Asp Thr Asn Gly Ala Ser Phe Asp Glu His Gly
                485                 490                 495

Ser Leu Asn Asn Trp Trp Thr Asp Glu Asp Phe Glu Ala Phe Lys Lys
            500                 505                 510

Leu Thr Asp Lys Val Val Glu Gln Phe Asp Gly Leu Glu Ser Tyr Gly
        515                 520                 525

Ala Lys Val Asn Gly Lys Leu Thr Val Ser Glu Asn Val Ala Asp Leu
    530                 535                 540

Gly Gly Val Ala Cys Ala Leu Glu Ala Ala Gln Arg Glu Ser Asp Phe
545                 550                 555                 560

Ser Ala Arg Asp Phe Phe Ile Asn Phe Ala Thr Ile Trp Arg Met Lys
                565                 570                 575

Ala Arg Asp Glu Tyr Met Gln Met Leu Ala Ser Val Asp Val His Ala
            580                 585                 590

Pro Ala Gln Trp Arg Thr Asn Ile Thr Val Thr Asn Phe Glu Glu Phe
        595                 600                 605

His Lys Glu Phe Asp Val Lys Asp Gly Asp Asn Met Trp Arg Pro Val
    610                 615                 620

Glu Lys Arg Val Ile Ile Trp
625                 630

<210>  357

<211> 335

<212> PRT

<213> Streptococcus agalactiae

<400> 357

Met Ser Lys Ile Leu Phe Phe Gly Glu Pro Leu Ile Arg Ile Thr Pro
1               5                   10                  15

Lys Glu Asn Asp Tyr Phe Ala Asp Ser Ile Ser Thr Lys Leu Phe Tyr
            20                  25                  30

Gly Gly Ser Glu Val Asn Thr Ala Arg Ala Leu Gln Gly Phe Gly Gln
        35                  40                  45

Asp Thr Lys Leu Leu Ser Ala Leu Pro Asn Asn Pro Ile Gly Asn Ser
    50                  55                  60

Phe Leu Gln Phe Leu Lys Ala Gln Gly Ile Asp Thr His Ser Ile Gln
65                  70                  75                  80

Trp Val Gly Glu Arg Val Gly Leu Tyr Phe Leu Glu Asp Ser Phe Ala
                85                  90                  95

Cys Arg Lys Gly Glu Val Val Tyr Asp Arg Asp His Ser Ser Leu His
            100                 105                 110

Asp Phe Arg Ile Asn Gln Ile Asp Phe Asp Gln Leu Phe Glu Gly Val
        115                 120                 125

Ser Leu Phe His Phe Ser Gly Ile Thr Leu Ser Leu Asp Glu Ser Ile
    130                 135                 140

Gln Glu Ile Thr Leu Leu Leu Leu Lys Glu Ala Lys Lys Arg Glu Ile
145                 150                 155                 160

Thr Ile Ser Leu Asp Leu Asn Phe Arg Ser Lys Leu Ile Ser Pro Lys
                165                 170                 175

Asn Ala Lys Ile Leu Phe Ser Gln Phe Ala Thr Phe Ala Asp Ile Cys
            180                 185                 190

Phe Gly Ile Glu Pro Leu Met Val Asp Ser Gln Asp Thr Thr Phe Phe
        195                 200                 205

Asn Arg Asp Glu Ala Thr Ile Glu Asp Val Lys Glu Arg Met Ile Ser
    210                 215                 220

Leu Ile Asn His Phe Asp Phe Gln Val Ile Phe His Thr Lys Arg Leu
225                 230                 235                 240

Gln Asp Glu Trp Gly Arg Asn His Tyr Gln Ala Tyr Ile Ala Asn Arg
245 250 255

Lys Gln Glu Phe Val Thr Ser Lys Glu Ile Thr Thr Ala Val Asn Gln
260 265 270

Arg Ile Gly Ser Gly Asp Ala Phe Val Ala Gly Ala Leu Tyr Gln Leu
275 280 285

Leu Gln His Ser Asp Ser Lys Thr Val Ile Asp Phe Ala Val Ala Ser
290 295 300

Ala Ser Leu Lys Cys Ala Leu Glu Gly Asp Asn Met Phe Glu Thr Val
305 310 315 320

Thr Ala Val Asn Lys Val Leu Asn Gln Ser Lys Asp Ile Ile Arg
325 330 335

<210> 358

<211> 194

<212> PRT

<213> Streptococcus agalactiae

<400> 358

Met Lys Ser Arg Lys Lys Asp Lys Leu Val Leu Arg Leu Thr Thr Thr
1 5 10 15

Leu Leu Val Phe Gly Leu Gly Gly Val Trp Phe Tyr Asn Tyr Lys Asn
20 25 30

Asp Asn Val Glu Pro Thr Val Thr Ser Ala Ser Asp Gln Thr Thr Thr
35 40 45

Phe Ile Gln Thr Ile Ser Pro Thr Ala Ile Glu Ile Ser Lys Thr Tyr
50 55 60

Asp Leu Tyr Ala Ser Val Leu Leu Ala Gln Ala Ile Leu Glu Ser Ser
65 70 75 80

Ser Gly Gln Ser Asp Leu Ser Lys Ala Pro Asn Tyr Asn Leu Phe Gly
85 90 95

Ile Lys Gly Glu Tyr Lys Gly Lys Ser Val Gln Met Pro Thr Leu Glu
100 105 110

Asp Asp Gly Lys Gly Asn Met Thr Gln Ile Gln Ala Pro Phe Arg Ala
115 120 125

Tyr Pro Asn Tyr Ser Ala Ser Leu Tyr Asp Tyr Ala Glu Leu Val Ser
130 135 140

Ser Gln Lys Tyr Ala Ser Val Trp Lys Ser Asn Thr Ser Ser Tyr Lys
145 150 155 160

Asp Ala Thr Ala Ala Leu Thr Gly Leu Tyr Ala Thr Asp Thr Ala Tyr
165 170 175

Ala Ser Lys Leu Asn Gln Ile Ile Glu Thr Tyr Ser Leu Asp Ala Tyr
180 185 190

Asp Lys

<210> 359

<211> 445

<212> PRT

<213> Streptococcus agalactiae

<400> 359

Met Ala Asp Val Lys Val Val Asn Asn Glu Asp Ser Arg Gly Gln Lys
1 5 10 15

Gln Asp Leu Lys Ala Lys Leu Phe His Ile Lys Ile Gly Ser Val Pro
20 25 30

Leu Pro Val Tyr Val Cys Leu Ala Leu Leu Ile Leu Leu Ala Gly Phe
35 40 45

Leu Gln Lys Leu Pro Val Asn Met Leu Gly Gly Phe Ala Val Ile Leu
50 55 60

Thr Met Gly Trp Phe Leu Gly Thr Ile Gly Ala Ser Ile Pro Gly Phe
65 70 75 80

Lys Asn Phe Gly Gly Pro Ala Ile Leu Ser Leu Leu Val Pro Ser Ile
85 90 95

Leu Val Phe Phe Asn Leu Ile Asn Lys Asn Val Leu Glu Ser Thr Asn
100 105 110

Met Leu Met Lys Gln Ala Asn Phe Leu Tyr Phe Tyr Ile Ala Cys Leu
115 120 125

Val Ser Gly Ser Ile Leu Gly Met Asn Arg Lys Met Leu Ile Gln Gly
130 135 140

Leu Leu Arg Met Ile Phe Pro Met Leu Leu Gly Met Val Cys Ala Met
145 150 155 160

Met Val Gly Thr Phe Val Gly Val Ile Leu Gly Leu Glu Trp Arg His
165 170 175

Thr Leu Phe Tyr Ile Val Thr Pro Val Leu Ala Gly Gly Ile Gly Glu
180 185 190

Gly Ile Leu Pro Leu Ser Leu Gly Tyr Ser Ser Ile Thr Gly Val Ala
195 200 205

Ser Glu Gln Leu Val Ala Gln Leu Ile Pro Ala Thr Ile Ile Gly Asn
210 215 220

Phe Phe Ala Ile Leu Cys Thr Ala Leu Leu Asn Arg Leu Gly Glu Lys
225 230 235 240

Lys Pro His Leu Ser Gly Gln Gly Gln Leu Val Arg Leu Asn Lys Gly
245 250 255

Glu Asp Met Ser Asp Ile Ile Ala Asp His Ser Gly Pro Ile Asp Val
260 265 270

Lys Lys Met Gly Gly Gly Val Leu Thr Ala Cys Ser Leu Phe Ile Phe
275 280 285

Gly His Leu Leu Gln Gln Leu Thr Gly Phe Pro Gly Pro Val Leu Met
290 295 300

Ile Val Ala Ala Ala Ile Leu Lys Tyr Ile Asn Val Ile Pro Arg Glu
305 310 315 320

Thr Gln Asn Gly Ala Lys Gln Leu Tyr Lys Phe Ile Ser Gly Asn Phe
325 330 335

Thr Phe Pro Leu Met Ala Gly Leu Gly Leu Leu Tyr Ile Pro Leu Lys
340 345 350

Asp Val Val Ala Thr Leu Ser Ile Gln Tyr Phe Ile Val Val Ile Ser
355 360 365

Val Val Phe Thr Val Ile Ser Val Gly Phe Phe Val Ser Arg Phe Leu
370 375 380

Asn Met Asn Pro Val Glu Ala Gly Ile Ile Ser Ala Cys Gln Ser Gly
385 390 395 400

Met Gly Gly Thr Gly Asp Val Ala Ile Leu Ser Thr Ala Asp Arg Met
405 410 415

Asn Leu Met Pro Phe Ala Gln Val Ala Thr Arg Leu Gly Gly Ala Ile
420 425 430

Thr Val Ile Thr Met Thr Ala Ile Leu Arg Met Leu Phe
435 440 445

<210> 360

<211> 412

<212> PRT

<213> Streptococcus agalactiae

<400> 360

Arg Gly Lys Lys Ala Gly Lys Tyr Thr Thr Ser Asp Gly Tyr Ile Phe
1 5 10 15

Asp Ala Lys Asp Ile Lys Lys Asp Thr Gly Thr Gly Tyr Val Ile Pro
20 25 30

His Met Thr His Glu His Trp Val Pro Lys Lys Asp Leu Ser Glu Ser
35 40 45

Glu Leu Lys Ala Ala Gln Glu Phe Leu Ser Gly Lys Ser Glu Ala Asn
50 55 60

Gln Asp Lys Pro Lys Thr Gly Lys Thr Ala Gln Glu Ile Tyr Glu Ala
65 70 75 80

Ile Glu Pro Lys Ala Ile Val Lys Pro Glu Asp Leu Leu Phe Gly Ile
85 90 95

Ala Gln Ala Thr Asp Tyr Lys Asn Gly Thr Phe Val Ile Pro His Lys
100 105 110

Asp His Tyr His Tyr Val Glu Leu Lys Trp Phe Asp Glu Glu Lys Asp
115 120 125

Leu Leu Ala Asp Ser Asp Lys Thr Tyr Ser Leu Glu Asp Tyr Leu Ala
130 135 140

Thr Ala Lys Tyr Tyr Met Met His Pro Glu Lys Arg Pro Lys Val Glu
145 150 155 160

Gly Trp Gly Lys Asp Ala Glu Ile Tyr Lys Glu Lys Asp Ser Asn Lys
165 170 175

Ala Asp Lys Pro Ser Pro Ala Pro Thr Asp Asn Lys Ser Thr Ser Asn
180 185 190

Ser Ser Asp Lys Asn Leu Ser Ala Ala Glu Val Phe Lys Gln Ala Lys
195 200 205

Pro Glu Lys Ile Val Pro Leu Asp Lys Ile Ala Ala His Met Ala Tyr
210 215 220

Ala Val Gly Phe Glu Asp Asp Gln Leu Ile Val Pro His His Asp His
225 230 235 240

Tyr His Asn Val Pro Met Ala Trp Phe Asp Lys Gly Gly Leu Trp Lys
245 250 255

Ala Pro Glu Gly Tyr Thr Leu Gln Gln Leu Phe Ser Thr Ile Lys Tyr
260 265 270

Tyr Met Glu His Pro Asn Glu Leu Pro Lys Glu Lys Gly Trp Gly His
275 280 285

Asp Ser Asp His Asn Lys Gly Ser Asn Lys Asp Asn Lys Ala Lys Asn
290 295 300

Tyr Ala Pro Asp Glu Glu Pro Glu Asp Ser Gly Lys Val Thr His Asn
305 310 315 320

Tyr Gly Phe Tyr Asp Val Asn Lys Gly Ser Asp Glu Glu Glu Pro Glu
325 330 335

Lys Gln Glu Asp Glu Ser Glu Leu Asp Glu Tyr Glu Leu Gly Met Ala
340 345 350

Gln Asn Ala Lys Lys Tyr Gly Met Asp Arg Gln Ser Phe Glu Lys Gln
355 360 365

Leu Ile Gln Leu Ser Asn Lys Tyr Ser Val Ser Phe Glu Ser Phe Asn
370 375 380

Tyr Ile Asn Gly Ser Gln Val Gln Val Thr Lys Lys Asp Gly Ser Lys
385 390 395 400

Val Leu Val Asp Ile Lys Thr Leu Thr Glu Val Lys
405 410

<210> 361

<211> 481

<212> PRT

<213> Streptococcus agalactiae

<400> 361

Met Asn Arg Lys Lys Thr Val Ile Ile Ser Ala Leu Ser Val Ala Leu
1               5                   10                  15

Phe Gly Thr Gly Val Gly Ala Tyr Gln Leu Gly Ser Tyr Asn Ala Gln
            20                  25                  30

Lys Ser Asp Asn Ser Val Ser Tyr Val Lys Thr Asp Lys Ser Asp Ser
        35                  40                  45

Lys Ala Gln Ala Thr Ala Val Asn Lys Thr Pro Asp Gln Ile Ser Lys
    50                  55                  60

Glu Glu Gly Ile Ser Ala Glu Gln Ile Val Val Lys Ile Thr Asp Asp
65                  70                  75                  80

Gly Tyr Val Thr Ser His Gly Asp His Tyr His Tyr Tyr Asn Gly Lys
                85                  90                  95

Val Pro Tyr Asp Ala Ile Ile Ser Glu Glu Leu Ile Met Lys Asp Pro
            100                 105                 110

Ser Tyr Val Phe Asn Lys Ala Asp Val Ile Asn Glu Val Lys Asp Gly
        115                 120                 125

Tyr Ile Ile Lys Val Asn Gly Lys Tyr Tyr Leu Tyr Leu Lys Glu Gly
    130                 135                 140

Ser Lys Arg Thr Asn Val Arg Thr Lys Glu Gln Ile Gln Lys Gln Arg
145                 150                 155                 160

Glu Glu Trp Ser Lys Gly Gly Ser Lys Gly Glu Ser Gly Lys His Ser
                165                 170                 175

Ser Ala Lys Thr Gln Ala Leu Ser Ala Ser Val Arg Glu Ala Lys Ala
            180                 185                 190

Ser Gly Arg Tyr Thr Thr Asp Asp Gly Tyr Val Phe Ser Pro Thr Asp
        195                 200                 205

Val Ile Asp Asp Met Gly Asp Ala Phe Leu Val Pro His Gly Asp His
    210                 215                 220

Phe His Tyr Ile Pro Lys Ala Asp Leu Ser Pro Ser Glu Leu Ser Ala
225                 230                 235                 240

Ala Gln Ala Tyr Trp Asn Arg Lys Thr Gly Arg Ser Gly Asn Ser Ser
                245                 250                 255

Lys Pro Ser Asn Ser Ser Ser Tyr Ile His Ala Ser Ala Pro Ser Gly
            260                 265                 270

Asn Val Ser Thr Gly Arg His Ala Asn Ala Pro Ile Ser Ile Pro Arg
275 280 285

Val Thr His Ala Asn His Trp Ser Lys Pro Ala Gly Asn His Ala Thr
290 295 300

Ala Pro Lys His His Ala Pro Thr Thr Lys Pro Ile Asn Lys Asp Ser
305 310 315 320

Ala Leu Asp Lys Met Leu Lys Arg Leu Tyr Ala Gln Pro Leu Tyr Ala
325 330 335

Arg His Val Glu Ser Asp Gly Leu Val Tyr Asp Pro Ala Gln Val Asn
340 345 350

Ala Phe Thr Ala Ile Gly Val Ser Ile Pro His Gly Asn His Phe His
355 360 365

Phe Ile His Tyr Lys Asp Met Ser Pro Leu Glu Leu Glu Ala Thr Arg
370 375 380

Met Val Ala Glu His Arg Gly His His Ile Asp Ala Leu Gly Lys Lys
385 390 395 400

Asp Ser Thr Glu Lys Pro Lys His Ile Ser His Glu Pro Asn Lys Glu
405 410 415

Pro His Thr Glu Glu Glu His His Ala Val Thr Pro Lys Asp Gln Arg
420 425 430

Lys Gly Lys Pro Asn Ser Gln Ile Val Tyr Ser Ala Gln Glu Ile Glu
435 440 445

Glu Ala Lys Lys Leu Val Asn Thr Gln His Leu Met Val Thr Phe Leu
450 455 460

Met Pro Lys Ile Leu Lys Lys Ile Gln Val Gln Val Met Ser Phe His
465 470 475 480

Ile

<210> 362

<211> 156

<212> PRT

<213> Streptococcus agalactiae

<400> 362

Met Ala Lys Phe Gly Phe Leu Ser Val Leu Glu Glu Glu Leu Asp Lys
1 5 10 15

His Leu Gln Tyr Asp Phe Ala Met Asp Trp Asp Lys Lys Asn His Thr
20 25 30

Val Glu Val Thr Phe Ile Leu Glu Ala Gln Asn Ser Ser Ala Ile Glu
35 40 45

Thr Val Asp Asp Gln Gly Glu Thr Ser Ser Glu Asp Ile Val Phe Glu
50 55 60

Asp Tyr Val Leu Phe Tyr Asn Pro Val Lys Ser Arg Phe Asp Ala Glu
65 70 75 80

Asp Tyr Leu Val Thr Ile Pro Tyr Glu Pro Lys Lys Gly Leu Ser Arg
85 90 95

Glu Phe Leu Ala Tyr Phe Ala Glu Thr Leu Asn Glu Val Ala Thr Glu
100 105 110

Gly Leu Ser Asp Leu Met Asp Phe Leu Thr Asp Asp Ser Ile Glu Glu
115 120 125

Phe Gly Leu Ser Trp Asp Thr Asp Ala Phe Glu Asn Gly Arg Ala Glu
130 135 140

Leu Lys Glu Thr Glu Phe Tyr Pro Tyr Pro Arg Tyr
145 150 155

<210> 363

<211> 1570

<212> PRT

<213> Streptococcus agalactiae

<400> 363

Met Asn Thr Lys Gln Arg Phe Ser Ile Arg Lys Tyr Lys Leu Gly Ala
1 5 10 15

Val Ser Val Leu Leu Gly Thr Leu Phe Phe Leu Gly Gly Ile Thr Asn
20 25 30

Val Ala Ala Asp Ser Val Ile Asn Lys Pro Ser Asp Ile Ala Val Glu
35 40 45

Gln Gln Val Lys Asp Ser Pro Thr Ser Ile Ala Asn Glu Thr Pro Thr
50 55 60

Asn Asn Thr Ser Ser Ala Leu Ala Ser Thr Ala Gln Asp Asn Leu Val
65 70 75 80

Thr Lys Ala Asn Asn Ser Pro Thr Glu Thr Gln Pro Val Ala Glu Ser
85 90 95

His Ser Gln Ala Thr Glu Thr Phe Ser Pro Val Ala Asn Gln Pro Val
100 105 110

Glu Ser Thr Gln Glu Val Ser Lys Thr Pro Leu Thr Lys Gln Asn Leu
115 120 125

Ala Val Lys Ser Thr Pro Ala Ile Ser Lys Glu Thr Pro Gln Asn Ile
130 135 140

Asp Ser Asn Lys Ile Ile Thr Val Pro Lys Val Trp Asn Thr Gly Tyr
145 150 155 160

Lys Gly Glu Gly Thr Val Val Ala Ile Ile Asp Ser Gly Leu Asp Ile
165 170 175

Asn His Asp Ala Leu Gln Leu Asn Asp Ser Thr Lys Ala Lys Tyr Gln
180 185 190

Asn Glu Gln Gln Met Asn Ala Ala Lys Ala Lys Ala Gly Ile Asn Tyr
195 200 205

Gly Lys Trp Tyr Asn Asn Lys Val Ile Phe Gly His Asn Tyr Val Asp
210 215 220

Val Asn Thr Glu Leu Lys Glu Val Lys Ser Thr Ser His Gly Met His
225 230 235 240

Val Thr Ser Ile Ala Thr Ala Asn Pro Ser Lys Lys Asp Thr Asn Glu
245 250 255

Leu Ile Tyr Gly Val Ala Pro Glu Ala Gln Val Met Phe Met Arg Val
260 265 270

Phe Ser Asp Glu Lys Arg Gly Thr Gly Pro Ala Leu Tyr Val Lys Ala
275 280 285

Ile Glu Asp Ala Val Lys Leu Gly Ala Asp Ser Ile Asn Leu Ser Leu
290 295 300

Gly Gly Ala Asn Gly Ser Leu Val Asn Ala Asp Asp Arg Leu Ile Lys
305 310 315 320

Ala Leu Glu Met Ala Arg Leu Ala Gly Val Ser Val Val Ile Ala Ala
325 330 335

Gly Asn Asp Gly Thr Phe Gly Ser Gly Ala Ser Lys Pro Ser Ala Leu
340 345 350

Tyr Pro Asp Tyr Gly Leu Val Gly Ser Pro Ser Thr Ala Arg Glu Ala
355 360 365

Ile Ser Val Ala Ser Tyr Asn Asn Thr Thr Leu Val Asn Lys Val Phe
370 375 380

Asn Ile Ile Gly Leu Glu Asn Asn Arg Asn Leu Asn Asn Gly Leu Ala
385 390 395 400

Ala Tyr Ala Asp Pro Lys Val Ser Asp Lys Thr Phe Glu Val Gly Lys
405 410 415

Gln Tyr Asp Tyr Val Phe Val Gly Lys Gly Asn Asp Asn Asp Tyr Lys
420 425 430

Asp Lys Thr Leu Asn Gly Lys Ile Ala Leu Ile Glu Arg Gly Asp Ile
435 440 445

Thr Phe Thr Lys Lys Val Val Asn Ala Ile Asn His Gly Ala Val Gly
450 455 460

Ala Ile Ile Phe Asn Asn Lys Ala Gly Glu Ala Asn Leu Thr Met Ser
465 470 475 480

Leu Asp Pro Glu Ala Ser Ala Ile Pro Ala Ile Phe Thr Gln Lys Glu
485 490 495

Phe Gly Asp Val Leu Ala Lys Asn Asn Tyr Lys Ile Val Phe Asn Asn
500 505 510

Ile Lys Asn Lys Gln Ala Asn Pro Asn Ala Gly Val Leu Ser Asp Phe
515 520 525

Ser Ser Trp Gly Leu Thr Ala Asp Gly Gln Leu Lys Pro Asp Leu Ser
530 535 540

Ala Pro Gly Gly Ser Ile Tyr Ala Ala Ile Asn Asp Asn Glu Tyr Asp
545 550 555 560

Met Met Ser Gly Thr Ser Met Ala Ser Pro His Val Ala Gly Ala Thr
565 570 575

Ala Leu Val Lys Gln Tyr Leu Leu Lys Glu His Pro Glu Leu Lys Lys
580 585 590

Gly Asp Ile Glu Arg Thr Val Lys Tyr Leu Leu Met Ser Thr Ala Lys
595 600 605

Ala His Leu Asn Lys Asp Thr Gly Ala Tyr Thr Ser Pro Arg Gln Gln
    610                 615                 620

Gly Ala Gly Ile Ile Asp Val Ala Ala Ala Val Gln Thr Gly Leu Tyr
625                 630                 635                 640

Leu Thr Gly Gly Glu Asn Asn Tyr Gly Ser Val Thr Leu Gly Asn Ile
                645                 650                 655

Lys Asp Lys Ile Ser Phe Asp Val Thr Val His Asn Ile Asn Lys Val
            660                 665                 670

Ala Lys Asp Leu His Tyr Thr Thr Tyr Leu Asn Thr Asp Gln Val Lys
        675                 680                 685

Asp Gly Phe Val Thr Leu Ala Pro Gln Gln Leu Gly Thr Phe Thr Gly
    690                 695                 700

Lys Thr Ile Arg Ile Glu Pro Gly Gln Thr Gln Thr Ile Thr Ile Asp
705                 710                 715                 720

Ile Asp Val Ser Lys Tyr His Asp Met Leu Lys Lys Val Met Pro Asn
                725                 730                 735

Gly Tyr Phe Leu Glu Gly Tyr Val Arg Phe Thr Asp Pro Val Asp Gly
            740                 745                 750

Gly Glu Val Leu Ser Ile Pro Tyr Val Gly Phe Lys Gly Glu Phe Gln
        755                 760                 765

Asn Leu Glu Val Leu Glu Lys Ser Ile Tyr Lys Leu Val Ala Asn Lys
    770                 775                 780

Glu Lys Gly Phe Tyr Phe Gln Pro Lys Gln Thr Asn Glu Val Pro Gly
785                 790                 795                 800

Ser Glu Asp Tyr Thr Ala Leu Met Thr Thr Ser Ser Glu Pro Ile Tyr
                805                 810                 815

Ser Thr Asp Gly Thr Ser Pro Ile Gln Leu Lys Ala Leu Gly Ser Tyr
            820                 825                 830

Lys Ser Ile Asp Gly Lys Trp Ile Leu Gln Leu Asp Gln Lys Gly Gln
        835                 840                 845

Pro His Leu Ala Ile Ser Pro Asn Asp Asp Gln Asn Gln Asp Ala Val
    850                 855                 860

Ala Val Lys Gly Val Phe Leu Arg Asn Phe Asn Asn Leu Arg Ala Lys
865                 870                 875                 880

Val Tyr Arg Ala Asp Asp Val Asn Leu Gln Lys Pro Leu Trp Val Ser
885 890 895

Ala Pro Gln Ala Gly Asp Lys Asn Tyr Tyr Ser Gly Asn Thr Glu Asn
900 905 910

Pro Lys Ser Thr Phe Leu Tyr Asp Thr Glu Trp Lys Gly Thr Thr Thr
915 920 925

Asp Gly Ile Pro Leu Glu Asp Gly Lys Tyr Lys Tyr Val Leu Thr Tyr
930 935 940

Tyr Ser Asp Val Pro Gly Ser Lys Pro Gln Gln Met Val Phe Asp Ile
945 950 955 960

Thr Leu Asp Arg Gln Ala Pro Thr Leu Thr Thr Ala Thr Tyr Asp Lys
965 970 975

Asp Arg Arg Ile Phe Lys Ala Arg Pro Ala Val Glu His Gly Glu Ser
980 985 990

Gly Ile Phe Arg Glu Gln Val Cys Tyr Leu Lys Lys Asp Lys Asp Gly
995 1000 1005

His Tyr Asn Ser Val Leu Arg Gln Gln Gly Glu Asp Gly Ile Leu
1010 1015 1020

Val Glu Asp Asn Lys Val Phe Ile Lys Gln Glu Lys Asn Gly Ser
1025 1030 1035

Phe Ile Leu Pro Lys Glu Val Asn Asp Phe Ser His Val Tyr Tyr
1040 1045 1050

Thr Val Glu Asp Tyr Ala Gly Asn Leu Val Ser Ala Lys Leu Glu
1055 1060 1065

Asp Leu Ile Asn Ile Gly Asn Lys Asn Gly Leu Val Asn Val Lys
1070 1075 1080

Val Phe Ser Pro Glu Leu Asn Ser Asn Val Asp Ile Asp Phe Ser
1085 1090 1095

Tyr Ser Val Lys Asp Asp Lys Gly Asn Ile Ile Lys Lys Gln His
1100 1105 1110

His Gly Lys Asp Leu Asn Leu Leu Lys Leu Pro Phe Gly Thr Tyr
1115 1120 1125

Thr Phe Asp Leu Phe Leu Tyr Asp Glu Glu Arg Ala Asn Leu Ile
1130 1135 1140

Ser Pro Lys Ser Val Thr Val Thr Ile Ser Glu Lys Asp Ser Leu
1145 1150 1155

Lys Asp Val Leu Phe Lys Val Asn Leu Leu Lys Lys Ala Ala Leu
1160 1165 1170

Leu Val Glu Phe Asp Lys Leu Leu Pro Lys Gly Ala Thr Val Gln
1175 1180 1185

Leu Val Thr Lys Thr Asn Thr Val Val Asp Leu Pro Lys Ala Thr
1190 1195 1200

Tyr Ser Pro Thr Asp Tyr Gly Lys Asn Ile Pro Val Gly Asp Tyr
1205 1210 1215

Arg Leu Asn Val Thr Leu Pro Ser Gly Tyr Ser Thr Leu Glu Asn
1220 1225 1230

Leu Asp Asp Leu Leu Val Ser Val Lys Glu Asp Gln Val Asn Leu
1235 1240 1245

Thr Lys Leu Thr Leu Ile Asn Lys Ala Pro Leu Ile Asn Ala Leu
1250 1255 1260

Ala Glu Gln Thr Asp Ile Ile Thr Gln Pro Val Phe Tyr Asn Ala
1265 1270 1275

Gly Thr His Leu Lys Asn Asn Tyr Leu Ala Asn Leu Glu Lys Ala
1280 1285 1290

Gln Thr Leu Ile Lys Asn Arg Val Glu Gln Thr Ser Ile Asp Asn
1295 1300 1305

Ala Ile Ala Ala Leu Arg Glu Ser Arg Gln Ala Leu Asn Gly Lys
1310 1315 1320

Glu Thr Asp Thr Ser Leu Leu Ala Lys Ala Ile Leu Ala Glu Thr
1325 1330 1335

Glu Ile Lys Gly Asn Tyr Gln Phe Val Asn Ala Ser Pro Leu Ser
1340 1345 1350

Gln Ser Thr Tyr Ile Asn Gln Val Gln Leu Ala Lys Asn Leu Leu
1355 1360 1365

Gln Lys Pro Asn Val Thr Gln Ser Glu Val Asp Lys Ala Leu Glu
1370 1375 1380

Asn Leu Asp Ile Ala Lys Asn Gln Leu Asn Gly His Glu Thr Asp
1385 1390 1395

Tyr Ser Gly Leu His His Met Ile Ile Lys Ala Asn Val Leu Lys
1400 1405 1410

Gln Thr Ser Ser Lys Tyr Gln Asn Ala Ser Gln Phe Ala Lys Glu
1415 1420 1425

Asn Tyr Asn Asn Leu Ile Lys Lys Ala Glu Leu Leu Leu Ser Asn
1430 1435 1440

Arg Gln Ala Thr Gln Ala Gln Val Glu Glu Leu Leu Asn Gln Ile
1445 1450 1455

Lys Ala Thr Glu Gln Glu Leu Asp Gly Arg Asp Arg Val Ser Ser
1460 1465 1470

Ala Glu Asn Tyr Ser Gln Ser Leu Asn Asp Asn Asp Ser Leu Asn
1475 1480 1485

Thr Thr Pro Ile Asn Pro Pro Asn Gln Pro Gln Ala Leu Ile Phe
1490 1495 1500

Lys Lys Gly Met Thr Lys Glu Ser Glu Val Ala Gln Lys Arg Val
1505 1510 1515

Leu Gly Val Thr Ser Gln Thr Asp Asn Gln Lys Val Lys Thr Asn
1520 1525 1530

Lys Leu Pro Lys Thr Gly Glu Ser Thr Pro Lys Ile Thr Tyr Thr
1535 1540 1545

Ile Leu Leu Phe Ser Leu Ser Met Leu Gly Leu Ala Thr Ile Lys
1550 1555 1560

Leu Lys Ser Ile Lys Arg Glu
1565 1570

<210> 364

<211> 643

<212> PRT

<213> Streptococcus agalactiae

<400> 364

Met Asn Asn Asn Glu Lys Lys Val Lys Tyr Phe Leu Arg Lys Thr Ala
1 5 10 15

Tyr Gly Leu Ala Ser Met Ser Ala Ala Phe Ala Val Cys Ser Gly Ile
20 25 30

Val His Ala Asp Thr Ser Ser Gly Ile Ser Ala Ser Ile Pro His Lys
35 40 45

Lys Gln Val Asn Leu Gly Ala Val Thr Leu Lys Asn Leu Ile Ser Lys
50 55 60

Tyr Arg Gly Asn Asp Lys Ala Ile Ala Ile Leu Leu Ser Arg Val Asn
65 70 75 80

Asp Phe Asn Arg Ala Ser Gln Asp Thr Leu Pro Gln Leu Ile Asn Ser
85 90 95

Thr Glu Ala Glu Ile Arg Asn Ile Leu Tyr Gln Gly Gln Ile Gly Lys
100 105 110

Gln Asn Lys Pro Ser Val Thr Thr His Ala Lys Val Ser Asp Gln Glu
115 120 125

Leu Gly Lys Gln Ser Arg Arg Ser Gln Asp Ile Ile Lys Ser Leu Gly
130 135 140

Phe Leu Ser Ser Asp Gln Lys Asp Ile Leu Val Lys Ser Ile Ser Ser
145 150 155 160

Ser Lys Asp Ser Gln Leu Ile Leu Lys Phe Val Thr Gln Ala Thr Gln
165 170 175

Leu Asn Asn Ala Glu Ser Thr Lys Ala Lys Gln Met Ala Gln Asn Asp
180 185 190

Val Ala Leu Ile Lys Asn Ile Ser Pro Glu Val Leu Glu Glu Tyr Lys
195 200 205

Glu Lys Ile Gln Arg Ala Ser Thr Lys Ser Gln Val Asp Glu Phe Val
210 215 220

Ala Glu Ala Lys Lys Val Val Asn Ser Asn Lys Glu Thr Leu Val Asn
225 230 235 240

Gln Ala Asn Gly Lys Lys Gln Glu Ile Ala Lys Leu Glu Asn Leu Ser
245 250 255

Asn Asp Glu Met Leu Arg Tyr Asn Thr Ala Ile Asp Asn Val Val Lys
260 265 270

Gln Tyr Asn Glu Gly Lys Leu Asn Ile Thr Ala Ala Met Asn Ala Leu
275 280 285

Asn Ser Ile Lys Gln Ala Ala Gln Glu Val Ala Gln Lys Asn Leu Gln
290 295 300

Lys Gln Tyr Ala Lys Lys Ile Glu Arg Ile Ser Ser Lys Gly Leu Ala
305 310 315 320

Leu Ser Lys Lys Ala Lys Glu Ile Tyr Glu Lys His Lys Ser Ile Leu
325 330 335

Pro Thr Pro Gly Tyr Tyr Ala Asp Ser Val Gly Thr Tyr Leu Asn Arg
340 345 350

Phe Arg Asp Lys Gln Thr Phe Gly Asn Arg Ser Val Trp Thr Gly Gln
355 360 365

Ser Gly Leu Asp Glu Ala Lys Lys Met Leu Asp Glu Val Lys Lys Leu
370 375 380

Leu Lys Glu Leu Gln Asp Leu Thr Arg Gly Thr Lys Glu Asp Lys Lys
385 390 395 400

Pro Asp Val Lys Pro Glu Ala Lys Pro Glu Ala Lys Pro Asn Ile Gln
405 410 415

Val Pro Lys Gln Ala Pro Thr Glu Ala Ala Lys Pro Ala Leu Ser Pro
420 425 430

Glu Ala Leu Thr Arg Leu Thr Thr Trp Tyr Asn Gln Ala Lys Asp Leu
435 440 445

Leu Lys Asp Asp Gln Val Lys Asp Lys Tyr Val Asp Ile Leu Ala Val
450 455 460

Gln Lys Ala Val Asp Gln Ala Tyr Asp His Val Glu Glu Gly Lys Phe
465 470 475 480

Ile Thr Thr Asp Gln Ala Asn Gln Leu Ala Asn Lys Leu Arg Asp Ala
485 490 495

Leu Gln Ser Leu Glu Leu Lys Asp Lys Lys Val Ala Lys Pro Glu Ala
500 505 510

Lys Pro Glu Ala Lys Pro Glu Ala Lys Pro Glu Ala Lys Pro Glu Ala
515 520 525

Lys Pro Glu Ala Lys Pro Glu Ala Lys Pro Glu Ala Lys Pro Asp Val
530 535 540

Lys Pro Glu Ala Lys Pro Asp Val Lys Pro Glu Ala Lys Pro Glu Ala
545 550 555 560

Lys Pro Glu Ala Lys Ser Glu Ala Lys Pro Glu Ala Lys Leu Glu Ala
565 570 575

Lys Pro Glu Ala Lys Pro Ala Thr Lys Lys Ser Val Asn Thr Ser Gly
580 585 590

Asn Leu Ala Ala Lys Lys Ala Ile Glu Asn Lys Lys Tyr Ser Lys Lys
595 600 605

Leu Pro Ser Thr Gly Glu Ala Ala Ser Pro Leu Leu Ala Ile Val Ser
610 615 620

Leu Ile Val Met Leu Ser Ala Gly Leu Ile Thr Ile Val Leu Lys His
625 630 635 640

Lys Lys Asn

<210> 365

<211> 540

<212> PRT

<213> Streptococcus agalactiae

<400> 365

Met Ala Lys Asp Ile Lys Phe Ser Ala Asp Ala Arg Ser Ala Met Val
1 5 10 15

Arg Gly Val Asp Ile Leu Ala Asp Thr Val Lys Val Thr Leu Gly Pro
20 25 30

Lys Gly Arg Asn Val Val Leu Glu Lys Ala Phe Gly Ser Pro Leu Ile
35 40 45

Thr Asn Asp Gly Val Thr Ile Ala Lys Glu Ile Glu Leu Glu Asp His
50 55 60

Phe Glu Asn Met Gly Ala Lys Leu Val Ser Glu Val Ala Ser Lys Thr
65 70 75 80

Asn Asp Ile Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Thr Gln
85 90 95

Ala Ile Val Arg Glu Gly Leu Lys Asn Val Thr Ala Gly Ala Asn Pro
100 105 110

Ile Gly Ile Arg Arg Gly Ile Glu Thr Ala Val Ser Ala Ala Val Glu
115 120 125

Glu Leu Lys Glu Ile Ala Gln Pro Val Ser Gly Lys Glu Ala Ile Ala
130 135 140

Gln Val Ala Ala Val Ser Ser Arg Ser Glu Lys Val Gly Glu Tyr Ile
145                 150                 155                 160

Ser Glu Ala Met Gly Arg Val Gly Asn Asp Gly Val Ile Thr Ile Glu
                165                 170                 175

Glu Ser Arg Gly Met Glu Thr Glu Leu Glu Val Val Glu Gly Met Gln
            180                 185                 190

Phe Asp Arg Gly Tyr Leu Ser Gln Tyr Met Val Thr Asp Asn Glu Lys
        195                 200                 205

Met Val Ser Glu Leu Glu Asn Pro Tyr Ile Leu Ile Thr Asp Lys Lys
    210                 215                 220

Ile Ser Asn Ile Gln Glu Ile Leu Pro Leu Leu Glu Glu Val Leu Lys
225                 230                 235                 240

Thr Asn Arg Pro Leu Leu Ile Ile Ala Asp Asp Val Asp Gly Glu Ala
                245                 250                 255

Leu Pro Thr Leu Val Leu Asn Lys Ile Arg Gly Thr Phe Asn Val Val
            260                 265                 270

Ala Val Lys Ala Pro Gly Phe Gly Asp Arg Arg Lys Ala Met Leu Glu
        275                 280                 285

Asp Ile Ala Ile Leu Thr Gly Gly Thr Val Val Thr Glu Asp Leu Gly
    290                 295                 300

Leu Asp Leu Lys Asp Ala Thr Met Gln Val Leu Gly Gln Ser Ala Lys
305                 310                 315                 320

Val Thr Val Asp Lys Asp Ser Thr Val Ile Val Glu Gly Ala Gly Asp
                325                 330                 335

Ser Ser Ala Ile Ala Asn Arg Val Ala Ile Ile Lys Ser Gln Met Glu
            340                 345                 350

Ala Thr Thr Ser Asp Phe Asp Arg Glu Lys Leu Gln Glu Arg Leu Ala
        355                 360                 365

Lys Leu Ala Gly Gly Val Ala Val Ile Lys Val Gly Ala Ala Thr Glu
    370                 375                 380

Thr Glu Leu Lys Glu Met Lys Leu Arg Ile Glu Asp Ala Leu Asn Ala
385                 390                 395                 400

Thr Arg Ala Ala Val Glu Glu Gly Ile Val Ser Gly Gly Gly Thr Ala
                405                 410                 415

Leu Val Asn Val Ile Glu Lys Val Ala Ala Leu Lys Leu Asn Gly Asp
420 425 430

Glu Glu Thr Gly Arg Asn Ile Val Leu Arg Ala Leu Glu Glu Pro Val
435 440 445

Arg Gln Ile Ala Tyr Asn Ala Gly Tyr Glu Gly Ser Val Ile Ile Glu
450 455 460

Arg Leu Lys Gln Ser Glu Ile Gly Thr Gly Phe Asn Ala Ala Asn Gly
465 470 475 480

Glu Trp Val Asp Met Val Thr Thr Gly Ile Ile Asp Pro Val Lys Val
485 490 495

Thr Arg Ser Ala Leu Gln Asn Ala Ala Ser Val Ala Ser Leu Ile Leu
500 505 510

Thr Thr Glu Ala Val Val Ala Asn Lys Pro Glu Pro Glu Ala Pro Thr
515 520 525

Ala Pro Ala Met Asp Pro Ser Met Met Gly Gly Phe
530 535 540

<210> 366

<211> 513

<212> PRT

<213> Streptococcus agalactiae

<400> 366

Val Val Glu Asn Leu Glu Lys Pro Ile Gly Val Ser Tyr Lys Asn Ser
1 5 10 15

Pro Ser Met Ser Lys Arg Thr Ala Ile Arg Met Lys Lys Ser Ser Arg
20 25 30

Phe Ser Ile Leu Leu Tyr Ser Val Leu Ser Thr Leu Leu Ala Ile Ala
35 40 45

Asn Pro Leu Leu Thr Tyr Phe Ala Asn Gly Leu Gln Thr Gln Asn Leu
50 55 60

Tyr Thr Gly Leu Met Met Thr Lys Gly Gln Ile Pro Tyr Ser Asp Val
65 70 75 80

Phe Ala Thr Gly Gly Phe Leu Tyr Tyr Val Thr Ile Ala Leu Ser Tyr
85 90 95

Leu Leu Gly Ser Ser Ile Trp Leu Leu Ile Val Gln Phe Ile Ala Tyr
100 105 110

Tyr Val Ser Gly Ile Tyr Phe Tyr Lys Leu Val Tyr Tyr Val Ala Gln
115 120 125

Ser Glu Ile Val Ser Ile Gly Met Thr Leu Ile Phe Tyr Ile Met Asn
130 135 140

Ile Val Leu Gly Phe Gly Gly Met Tyr Pro Ile Gln Trp Ala Leu Pro
145 150 155 160

Phe Met Leu Ile Ser Leu Trp Phe Leu Ile Lys Phe Cys Val Asp Asn
165 170 175

Ile Val Asp Glu Ala Phe Ile Phe Tyr Gly Ile Leu Ala Ala Phe Ser
180 185 190

Leu Phe Ile Asp Pro Gln Thr Leu Ile Phe Trp Leu Cys Ser Phe Val
195 200 205

Leu Leu Thr Ala Thr Asn Ile Lys Gln Lys Gln Ser Leu Arg Gly Phe
210 215 220

Tyr Gln Phe Leu Cys Val Val Phe Gly Met Ile Leu Ile Ala Tyr Thr
225 230 235 240

Val Gly Tyr Phe Met Phe Asn Leu Gln Ile Ile Ser Ser Tyr Ile Asp
245 250 255

Lys Ala Ile Phe Tyr Pro Phe Thr Tyr Phe Ala Arg Thr Asn His Ser
260 265 270

Phe Leu Leu Ser Leu Ala Ile Gln Ile Val Val Leu Leu Gly Ser Gly
275 280 285

Cys Leu Phe Gly Leu Trp Asp Phe Ile Gln Asn Arg Lys Lys Ala Ser
290 295 300

Tyr Gln Ile Gly Leu Asn Phe Ile Ala Cys Ile Phe Ile Ile Tyr Ala
305 310 315 320

Ile Met Ala Ile Phe Ser Arg Asp Phe Asn Leu Tyr His Phe Leu Pro
325 330 335

Ala Leu Pro Phe Gly Leu Leu Leu Thr Ser Asn Lys Ile Thr Ile Leu
340 345 350

Tyr Gln Lys Val Ile Asp Arg Arg Ser His Arg Arg Gln Tyr Phe Ser
355 360 365

Gly Lys Ser Leu Ile Val Asp Leu Phe Val Lys Lys Thr Tyr Tyr Leu
370 375 380

Pro Leu Leu Leu Val Ser Leu Ser Ile Gly Leu Leu Val Tyr Asn Thr
385 390 395 400

Tyr Gln Asn Val Thr Leu Ser Lys Glu Arg Arg Asp Ile Ser His Tyr
405 410 415

Leu Thr Thr Lys Ile Asp Arg Asp Gly Lys Ile Tyr Val Trp Asp Lys
420 425 430

Val Ala Ser Ile Tyr Ser Gln Thr Arg Leu Lys Ser Ala Ser Gln Phe
435 440 445

Val Leu Pro His Ile Asn Thr Ala Gln Lys Asn Asn Glu Lys Ile Leu
450 455 460

Lys Asp Glu Leu Leu Gln His Gly Ala Lys Tyr Phe Ile Leu Asn Lys
465 470 475 480

Asn Glu Lys Leu Pro Asn Glu Leu Lys Ser Asp Ile Lys Lys His Tyr
485 490 495

Gln Glu Val Pro Leu Ser Asn Ile Thr His Phe Val Leu Tyr Arg Phe
500 505 510

Lys

<210> 367

<211> 858

<212> PRT

<213> Streptococcus agalactiae

<400> 367

Met Ala Lys Pro Thr Ile Ser Pro Gly Met Gln Gln Tyr Leu Asp Ile
1 5 10 15

Lys Glu Asn Tyr Pro Asp Ala Phe Leu Leu Phe Arg Met Gly Asp Phe
20 25 30

Tyr Glu Leu Phe Tyr Asp Asp Ala Val Lys Ala Ala Gln Ile Leu Glu
35 40 45

Ile Ser Leu Thr Ser Arg Asn Lys Asn Ala Glu Lys Pro Ile Pro Met
50 55 60

Ala Gly Val Pro Tyr His Ser Ala Gln Gln Tyr Ile Asp Val Leu Val
65                  70                  75                  80

Glu Leu Gly Tyr Lys Val Ala Ile Ala Glu Gln Met Glu Asp Pro Lys
                85                  90                  95

Lys Ala Val Gly Val Val Lys Arg Glu Val Val Gln Val Val Thr Pro
            100                 105                 110

Gly Thr Val Val Glu Ser Thr Lys Pro Asp Ser Ala Asn Asn Phe Leu
        115                 120                 125

Val Ala Ile Asp Ser Gln Asp Gln Gln Thr Phe Gly Leu Ala Tyr Met
    130                 135                 140

Asp Val Ser Thr Gly Glu Phe Gln Ala Thr Leu Leu Thr Asp Phe Glu
145                 150                 155                 160

Ser Val Arg Ser Glu Ile Leu Asn Leu Lys Ala Arg Glu Ile Val Val
                165                 170                 175

Gly Tyr Gln Leu Thr Asp Glu Lys Asn His Leu Leu Thr Lys Gln Met
            180                 185                 190

Asn Leu Leu Leu Ser Tyr Glu Asp Glu Arg Leu Asn Asp Ile His Leu
        195                 200                 205

Ile Asp Glu Gln Leu Thr Asp Leu Glu Ile Ser Ala Ala Glu Lys Leu
    210                 215                 220

Leu Gln Tyr Val His Arg Thr Gln Lys Arg Glu Leu Ser His Leu Gln
225                 230                 235                 240

Lys Val Val His Tyr Glu Ile Lys Asp Tyr Leu Gln Met Ser Tyr Ala
                245                 250                 255

Thr Lys Asn Ser Leu Asp Leu Leu Glu Asn Ala Arg Thr Ser Lys Lys
            260                 265                 270

His Gly Ser Leu Tyr Trp Leu Leu Asp Glu Thr Lys Thr Ala Met Gly
        275                 280                 285

Thr Arg Met Leu Arg Thr Trp Ile Asp Arg Pro Leu Val Ser Met Asn
    290                 295                 300

Arg Ile Lys Glu Arg Gln Asp Ile Ile Gln Val Phe Leu Asp Tyr Phe
305                 310                 315                 320

Phe Glu Arg Asn Asp Leu Thr Glu Ser Leu Lys Gly Val Tyr Asp Ile
                325                 330                 335

Glu Arg Leu Ala Ser Arg Val Ser Phe Gly Lys Ala Asn Pro Lys Asp
340 345 350

Leu Leu Gln Leu Gly Gln Thr Leu Ser Gln Ile Pro Arg Ile Lys Met
355 360 365

Ile Leu Gln Ser Phe Asn Gln Pro Glu Leu Asp Ile Ile Val Asn Lys
370 375 380

Ile Asp Thr Met Pro Glu Leu Glu Ser Leu Ile Asn Thr Ala Ile Ala
385 390 395 400

Pro Glu Ala Gln Ala Thr Ile Thr Glu Gly Asn Ile Ile Lys Ser Gly
405 410 415

Phe Asp Lys Gln Leu Asp Asn Tyr Arg Thr Val Met Arg Glu Gly Thr
420 425 430

Gly Trp Ile Ala Asp Ile Glu Ala Lys Glu Arg Ala Ala Ser Gly Ile
435 440 445

Gly Thr Leu Lys Ile Asp Tyr Asn Lys Lys Asp Gly Tyr Tyr Phe His
450 455 460

Val Thr Asn Ser Asn Leu Ser Leu Val Pro Glu His Phe Phe Arg Lys
465 470 475 480

Ala Thr Leu Lys Asn Ser Glu Arg Tyr Gly Thr Ala Glu Leu Ala Lys
485 490 495

Ile Glu Gly Glu Met Leu Glu Ala Arg Glu Gln Ser Ser Asn Leu Glu
500 505 510

Tyr Asp Ile Phe Met Arg Val Arg Ala Gln Val Glu Ser Tyr Ile Lys
515 520 525

Arg Leu Gln Glu Leu Ala Lys Thr Ile Ala Thr Val Asp Val Leu Gln
530 535 540

Ser Leu Ala Val Val Ala Glu Asn Tyr His Tyr Val Arg Pro Lys Phe
545 550 555 560

Asn Asp Gln His Gln Ile Lys Ile Lys Asn Gly Arg His Ala Thr Val
565 570 575

Glu Lys Val Met Gly Val Gln Glu Tyr Ile Pro Asn Ser Ile Tyr Phe
580 585 590

Asp Ser Gln Thr Asp Ile Gln Leu Ile Thr Gly Pro Asn Met Ser Gly
595 600 605

Lys Ser Thr Tyr Met Arg Gln Leu Ala Leu Thr Val Ile Met Ala Gln
610 615 620

Met Gly Gly Phe Val Ser Ala Asp Glu Val Asp Leu Pro Val Phe Asp
625 630 635 640

Ala Ile Phe Thr Arg Ile Gly Ala Ala Asp Asp Leu Ile Ser Gly Gln
645 650 655

Ser Thr Phe Met Val Glu Met Met Glu Ala Asn Gln Ala Val Lys Arg
660 665 670

Ala Ser Asp Lys Ser Leu Ile Leu Phe Asp Glu Leu Gly Arg Gly Thr
675 680 685

Ala Thr Tyr Asp Gly Met Ala Leu Ala Gln Ser Ile Ile Glu Tyr Ile
690 695 700

His Asp Arg Val Arg Ala Lys Thr Met Phe Ala Thr His Tyr His Glu
705 710 715 720

Leu Thr Asp Leu Ser Glu Gln Leu Thr Arg Leu Val Asn Val His Val
725 730 735

Ala Thr Leu Glu Arg Asp Gly Glu Val Thr Phe Leu His Lys Ile Glu
740 745 750

Ser Gly Pro Ala Asp Lys Ser Tyr Gly Ile His Val Ala Lys Ile Ala
755 760 765

Gly Leu Pro Ile Asp Leu Leu Asp Arg Ala Thr Asp Ile Leu Ser Gln
770 775 780

Leu Glu Ala Asp Ala Val Gln Leu Ile Val Ser Pro Ser Gln Glu Ala
785 790 795 800

Val Thr Ala Asp Leu Asn Glu Glu Leu Asp Ser Glu Lys Gln Gln Gly
805 810 815

Gln Leu Ser Leu Phe Glu Glu Pro Ser Asn Ala Gly Arg Val Ile Glu
820 825 830

Glu Leu Glu Ala Ile Asp Ile Met Asn Leu Thr Pro Met Gln Ala Met
835 840 845

Asn Ala Ile Phe Asp Leu Lys Lys Leu Leu
850 855

<210> 368

<211> 290

<212> PRT

<213> Streptococcus agalactiae

<400> 368

Met Leu Lys Leu Asp Leu Lys Thr Lys Ile Lys Glu Ala Ile Leu Ile
1               5                   10                  15

Ala Phe Gly Val Ala Leu Tyr Thr Phe Gly Phe Val Lys Phe Asn Met
            20                  25                  30

Ala Asn His Leu Ala Glu Gly Gly Ile Ser Gly Val Thr Leu Ile Ile
        35                  40                  45

His Ala Leu Phe Gly Val Asn Pro Ala Leu Ser Ser Leu Leu Leu Asn
    50                  55                  60

Ile Pro Leu Phe Ile Leu Gly Ala Arg Ile Leu Gly Lys Lys Ser Leu
65                  70                  75                  80

Leu Leu Thr Ile Tyr Gly Thr Val Leu Met Ser Phe Phe Met Trp Phe
                85                  90                  95

Trp Gln Gln Ile Pro Val Thr Val Pro Leu Lys Asn Asp Met Met Leu
            100                 105                 110

Val Ala Val Ala Ala Gly Ile Leu Ala Gly Thr Gly Ser Gly Leu Val
        115                 120                 125

Phe Arg Tyr Gly Ala Thr Thr Gly Gly Ala Asp Ile Ile Gly Arg Ile
    130                 135                 140

Val Glu Glu Lys Ser Gly Ile Lys Leu Gly Gln Thr Leu Leu Phe Ile
145                 150                 155                 160

Asp Ala Ile Val Leu Thr Ser Ser Leu Val Tyr Ile Asn Leu Gln Gln
                165                 170                 175

Met Leu Tyr Thr Leu Val Ala Ser Phe Val Phe Ser Gln Val Leu Thr
            180                 185                 190

Asn Val Glu Asn Gly Gly Tyr Thr Val Arg Gly Met Ile Ile Ile Thr
        195                 200                 205

Lys Glu Ser Glu Ser Ala Ala Ala Thr Ile Leu His Glu Ile Asn Arg
    210                 215                 220

Gly Val Thr Phe Leu Arg Gly Gln Gly Ala Tyr Ser Gly Arg Glu His
225                 230                 235                 240

Asp Val Leu Tyr Val Ala Leu Asn Pro Ser Glu Val Arg Asp Val Lys
245 250 255

Glu Ile Met Ala Asp Leu Asp Pro Asp Ala Phe Ile Ser Val Ile Asn
260 265 270

Val Asp Glu Val Ile Ser Ser Asp Phe Lys Ile Arg Arg Arg Asn Tyr
275 280 285

Asp Lys
290

<210> 369

<211> 583

<212> PRT

<213> Streptococcus agalactiae

<400> 369

Met Lys Arg Ser Met Tyr Ala Gly Arg Val Arg Ser Glu His Ile Gly
1 5 10 15

Thr Ser Ile Thr Leu Lys Gly Trp Val Gly Arg Arg Arg Asp Leu Gly
20 25 30

Gly Leu Ile Phe Ile Asp Leu Arg Asp Arg Glu Gly Ile Met Gln Leu
35 40 45

Val Ile Asn Pro Glu Glu Val Ala Ala Ser Val Met Ala Thr Ala Glu
50 55 60

Ser Leu Arg Ser Glu Phe Val Ile Glu Val Ser Gly Val Val Thr Ala
65 70 75 80

Arg Glu Gln Ala Asn Asp Asn Leu Pro Thr Gly Glu Val Glu Leu Lys
85 90 95

Val Gln Glu Leu Ser Val Leu Asn Thr Ser Lys Thr Thr Pro Phe Glu
100 105 110

Ile Lys Asp Gly Ile Glu Ala Asn Asp Asp Thr Arg Met Arg Tyr Arg
115 120 125

Tyr Leu Asp Leu Arg Arg Pro Glu Met Leu Glu Asn Phe Lys Leu Arg
130 135 140

Ala Lys Val Thr His Ser Ile Arg Asn Tyr Leu Asp Asn Leu Glu Phe
145 150 155 160

Ile Asp Val Glu Thr Pro Met Leu Thr Lys Ser Thr Pro Glu Gly Ala
165 170 175

Arg Asp Tyr Leu Val Pro Ser Arg Val Asn Gln Gly His Phe Tyr Ala
180 185 190

Leu Pro Gln Ser Pro Gln Ile Thr Lys Gln Leu Leu Met Asn Ala Gly
195 200 205

Phe Asp Arg Tyr Tyr Gln Ile Val Lys Cys Phe Arg Asp Glu Asp Leu
210 215 220

Arg Gly Asp Arg Gln Pro Glu Phe Thr Gln Val Asp Leu Glu Thr Ser
225 230 235 240

Phe Leu Ser Asp Gln Glu Ile Gln Asp Ile Val Glu Gly Met Ile Ala
245 250 255

Lys Val Met Lys Asp Thr Lys Gly Leu Glu Val Ser Leu Pro Phe Pro
260 265 270

Arg Met Ala Tyr Asp Asp Ala Met Asn Asn Tyr Gly Ser Asp Lys Pro
275 280 285

Asp Thr Arg Phe Asp Met Leu Leu Gln Asp Leu Thr Glu Ile Val Lys
290 295 300

Glu Val Asp Phe Lys Val Phe Ser Glu Ala Ser Val Val Lys Ala Ile
305 310 315 320

Val Val Lys Asp Lys Ala Asp Lys Tyr Ser Arg Lys Asn Ile Asp Lys
325 330 335

Leu Thr Glu Ile Ala Lys Gln Tyr Gly Ala Lys Gly Leu Ala Trp Leu
340 345 350

Lys Tyr Val Asp Asn Thr Ile Ser Gly Pro Val Ala Lys Phe Leu Thr
355 360 365

Ala Ile Glu Gly Arg Leu Thr Glu Ala Leu Gln Leu Glu Asn Asn Asp
370 375 380

Leu Ile Leu Phe Val Ala Asp Ser Leu Glu Val Ala Asn Glu Thr Leu
385 390 395 400

Gly Ala Leu Arg Thr Arg Ile Ala Lys Glu Leu Glu Leu Ile Asp Tyr
405 410 415

Ser Lys Phe Asn Phe Leu Trp Val Val Asp Trp Pro Met Phe Glu Trp
420 425 430

Ser Glu Glu Glu Gly Arg Tyr Met Ser Ala His His Pro Phe Thr Leu
435 440 445

Pro Thr Ala Glu Thr Ala His Glu Leu Glu Gly Asp Leu Ala Lys Val
450 455 460

Arg Ala Val Ala Tyr Asp Ile Val Leu Asn Gly Tyr Glu Leu Gly Gly
465 470 475 480

Gly Ser Leu Arg Ile Asn Gln Lys Asp Thr Gln Glu Arg Met Phe Lys
485 490 495

Ala Leu Gly Phe Ser Ala Glu Ser Ala Gln Glu Gln Phe Gly Phe Leu
500 505 510

Leu Glu Ala Met Asp Tyr Gly Phe Pro Pro His Gly Gly Leu Ala Ile
515 520 525

Gly Leu Asp Arg Phe Val Met Leu Leu Ala Gly Lys Asp Asn Ile Arg
530 535 540

Glu Val Ile Ala Phe Pro Lys Asn Asn Lys Ala Ser Asp Pro Met Thr
545 550 555 560

Gln Ala Pro Ser Leu Val Ser Glu Gln Gln Leu Glu Glu Leu Ser Leu
565 570 575

Thr Val Glu Ser Tyr Glu Asn
580

<210> 370

<211> 151

<212> PRT

<213> Streptococcus agalactiae

<400> 370

Lys Glu Lys Gly Lys Leu Ile Lys Lys Lys Ile Leu Glu Asn Asn Thr
1 5 10 15

Asp Ile Ile Pro Lys Ile Ile Glu Lys Ser Pro Gln Asn Leu Ile Leu
20 25 30

Thr Ser Asn Tyr Asn Arg Val Asn Ile Asp Lys Ile Lys Asn Ile Lys
35 40 45

Asn Phe Asp Lys Gly Phe Glu Leu Gly Phe Pro Leu Phe Glu Lys Gly
50 55 60

Glu Ile Leu Arg Lys Glu Gly Glu Ile Thr Ser Ala Ile Glu Leu Phe
65 70 75 80

Asp Lys Ala Arg Glu Leu Gly Tyr Phe Val Pro Ala Leu Tyr Asn Ser
85 90 95

Tyr Ala Met Ala Phe Arg Lys Ile Lys Asn Tyr Asp Asp Glu Ile Leu
100 105 110

Ile Leu Gln Glu Gly Ile Glu Arg Phe Lys Lys Ser Thr Leu Ser Ser
115 120 125

Asn Ile Asn Pro Lys Thr Ile Asp Arg Trp Ser Thr Arg Ile Ser Arg
130 135 140

Ala Lys Asp Leu Lys Cys Lys
145 150

<210> 371

<211> 225

<212> PRT

<213> Streptococcus agalactiae

<400> 371

Leu Asn Val Lys Lys His His Leu Ala Tyr Gly Ala Ile Thr Leu Val
1 5 10 15

Ala Leu Phe Ser Cys Ile Leu Ala Val Met Val Ile Phe Lys Ser Ser
20 25 30

Gln Val Thr Thr Glu Ser Leu Ser Lys Ala Asp Lys Val Arg Val Ala
35 40 45

Lys Lys Ser Lys Met Thr Lys Ala Thr Ser Lys Ser Lys Val Glu Asp
50 55 60

Val Lys Gln Ala Pro Lys Pro Ser Gln Ala Ser Asn Glu Ala Pro Lys
65 70 75 80

Ser Ser Ser Gln Ser Thr Glu Ala Asn Ser Gln Gln Gln Val Thr Ala
85 90 95

Ser Glu Glu Ala Ala Val Glu Gln Ala Val Val Thr Glu Asn Thr Pro
100 105 110

Ala Thr Ser Gln Ala Gln Gln Ala Tyr Ala Val Thr Glu Thr Thr Tyr
115 120 125

Arg Pro Ala Gln His Gln Thr Ser Gly Gln Val Leu Ser Asn Gly Asn
130 135 140

Thr Ala Gly Ala Ile Gly Ser Ala Ala Ala Ala Gln Met Ala Ala Ala
145 150 155 160

Thr Gly Val Pro Gln Ser Thr Trp Glu His Ile Ile Ala Arg Glu Ser
165 170 175

Asn Gly Asn Pro Asn Val Ala Asn Ala Ser Gly Ala Ser Gly Leu Phe
180 185 190

Gln Thr Met Pro Gly Trp Gly Ser Thr Ala Thr Val Gln Asp Gln Val
195 200 205

Asn Ser Ala Ile Lys Ala Tyr Arg Ala Gln Gly Leu Ser Ala Trp Gly
210 215 220

Tyr
225

<210> 372

<211> 493

<212> PRT

<213> Streptococcus agalactiae

<400> 372

Met Ser Asn Trp Asp Thr Lys Phe Leu Lys Lys Gly Phe Thr Phe Asp
1 5 10 15

Asp Val Leu Leu Ile Pro Ala Glu Ser His Val Leu Pro Asn Glu Val
20 25 30

Asp Met Lys Thr Lys Leu Ala Asp Asn Leu Thr Leu Asn Ile Pro Ile
35 40 45

Ile Thr Ala Ala Met Asp Thr Val Thr Asp Ser Lys Met Ala Ile Ala
50 55 60

Ile Ala Arg Ala Gly Gly Leu Gly Ile Ile His Lys Asn Met Ser Ile
65 70 75 80

Val Asp Gln Ala Glu Glu Val Arg Lys Val Lys Arg Ser Glu Asn Gly
85 90 95

Val Ile Ile Asp Pro Phe Phe Leu Thr Pro Asp Asn Thr Val Ser Glu
100 105 110

Ala Glu Glu Leu Met Gln Asn Tyr Arg Ile Ser Gly Val Pro Ile Val
115 120 125

Glu Thr Leu Glu Asn Arg Lys Leu Val Gly Ile Ile Thr Asn Arg Asp
130 135 140

Met Arg Phe Ile Ser Asp Tyr Lys Gln Leu Ile Ser Glu His Met Thr
145 150 155 160

Ser Gln Asn Leu Val Thr Ala Pro Ile Gly Thr Asp Leu Glu Thr Ala
165 170 175

Glu Arg Ile Leu His Glu His Arg Ile Glu Lys Leu Pro Leu Val Asp
180 185 190

Asp Glu Gly Arg Leu Ser Gly Leu Ile Thr Ile Lys Asp Ile Glu Lys
195 200 205

Val Ile Glu Phe Pro Lys Ala Ala Lys Asp Glu Phe Gly Arg Leu Leu
210 215 220

Val Ala Gly Ala Val Gly Val Thr Ser Asp Thr Phe Glu Arg Ala Glu
225 230 235 240

Ala Leu Phe Glu Ala Gly Ala Asp Ala Ile Val Ile Asp Thr Ala His
245 250 255

Gly His Ser Ala Gly Val Leu Arg Lys Ile Ala Glu Ile Arg Ala His
260 265 270

Phe Pro Asn Arg Thr Leu Ile Ala Gly Asn Ile Ala Thr Ala Glu Gly
275 280 285

Ala Arg Ala Leu Tyr Asp Ala Gly Val Asp Val Val Lys Val Gly Ile
290 295 300

Gly Pro Gly Ser Ile Cys Thr Thr Arg Val Val Ala Gly Val Gly Val
305 310 315 320

Pro Gln Ile Thr Ala Ile Tyr Asp Ala Ala Ala Val Ala Arg Glu Tyr
325 330 335

Gly Lys Thr Ile Ile Ala Asp Gly Gly Ile Lys Tyr Ser Gly Asp Ile
340 345 350

Val Lys Ala Leu Ala Ala Gly Gly Asn Ala Val Met Leu Gly Ser Met
355 360 365

Phe Ala Gly Thr Asp Glu Ala Pro Gly Glu Thr Glu Ile Phe Gln Gly
370 375 380

Arg Lys Phe Lys Thr Tyr Arg Gly Met Gly Ser Ile Ala Ala Met Lys
385 390 395 400

Lys Gly Ser Ser Asp Arg Tyr Phe Gln Gly Ser Val Asn Glu Ala Asn
405 410 415

Lys Leu Val Pro Glu Gly Ile Glu Gly Arg Val Ala Tyr Lys Gly Ser
420 425 430

Val Ala Asp Ile Val Phe Gln Met Leu Gly Gly Ile Arg Ser Gly Met
435 440 445

Gly Tyr Val Gly Ala Ala Asn Ile Lys Glu Leu His Asp Asn Ala Gln
450 455 460

Phe Val Glu Met Ser Gly Ala Gly Leu Lys Glu Ser His Pro His Asp
465 470 475 480

Val Gln Ile Thr Asn Glu Ala Pro Asn Tyr Ser Val His
485 490

<210> 373

<211> 859

<212> PRT

<213> Streptococcus agalactiae

<400> 373

Met Thr Ile Asn His Tyr Lys Leu Arg Ile Pro Tyr Tyr Thr Ile Ser
1 5 10 15

Phe Leu Leu Pro Phe Ile Ile Ile Val Cys Ile Leu Phe Thr Lys Asn
20 25 30

Ile Tyr Trp Gly Ser Pro Thr Thr Ile Leu Ala Ser Asp Gly Phe His
35 40 45

Gln Tyr Val Ile Phe Asn Gln Ala Leu Arg Asn Ile Leu His Gly Ser
50 55 60

Asn Ser Leu Phe Tyr Thr Phe Thr Ser Gly Leu Gly Leu Asn Phe Tyr
65 70 75 80

Ala Leu Ser Ser Tyr Tyr Leu Gly Ser Phe Leu Ser Pro Ile Val Tyr
85 90 95

Phe Phe Asn Leu Lys Asn Met Pro Asp Ala Ile Tyr Leu Leu Thr Ile
100 105 110

Cys Lys Ile Gly Leu Ile Gly Leu Ser Met Phe Val Thr Leu Cys Lys
115 120 125

Arg His Cys Lys Val Asn Arg Val Leu Leu Leu Val Ile Ser Thr Cys
130 135 140

Tyr Ser Leu Met Ser Phe Ser Ile Ser Gln Ile Glu Ile Asn Met Trp
145 150 155 160

Leu Asp Val Phe Ile Leu Ile Pro Leu Val Val Leu Gly Val Asp Gln
165 170 175

Leu Leu Trp Glu Arg Lys Pro Ile Leu Tyr Phe Leu Ser Leu Thr Ala
180 185 190

Leu Phe Ile Gln Asn Tyr Tyr Phe Gly Phe Met Thr Ala Ile Phe Thr
195 200 205

Ser Leu Tyr Phe Ile Val Gln Ile Thr Arg Asn Thr Asp Ser Lys Val
210 215 220

Ala Phe Lys Gln Phe Leu His Phe Thr Phe Leu Ser Leu Leu Ala Gly
225 230 235 240

Met Thr Ser Ser Ile Met Ile Leu Pro Thr Tyr Phe Asp Leu Thr Thr
245 250 255

His Gly Glu Lys Leu Thr Lys Val Ser Lys Met Phe Thr Glu Asn Ser
260 265 270

Trp Tyr Met Asp Leu Phe Ala Lys Asn Met Ile Gly Ala Tyr Asp Thr
275 280 285

Thr Lys Phe Gly Ser Ile Pro Met Ile Tyr Val Gly Leu Leu Pro Leu
290 295 300

Leu Leu Ser Leu Leu Tyr Phe Thr Ile Lys Glu Val Pro Arg Arg Thr
305 310 315 320

Arg Leu Ala Tyr Gly Phe Leu Ile Ile Phe Val Ile Ala Ser Phe Tyr
325 330 335

Ile Thr Pro Leu Asp Leu Phe Trp Gln Gly Met His Ala Pro Asn Met
340 345 350

Phe Leu His Arg Tyr Ser Trp Val Leu Ser Val Leu Ile Cys Leu Leu
355 360 365

Ala Ala Glu Cys Leu Glu Tyr Leu Asp Asn Ile Ser Trp Lys Lys Ile
370 375 380

Leu Gly Val Asn Leu Ile Leu Val Ser Gly Phe Ile Ile Thr Phe Leu
385 390 395 400

Phe Lys Lys His Tyr His Tyr Leu Asn Leu Glu Leu Leu Leu Leu Thr
405 410 415

Leu Thr Phe Leu Ser Ala Tyr Ile Ile Leu Thr Ile Ser Phe Val Ser
420 425 430

Lys Gln Ile Pro Lys Leu Val Phe Tyr Pro Phe Leu Ile Gly Phe Val
435 440 445

Val Leu Glu Met Thr Leu Asn Thr Phe Tyr Gln Leu Asn Ser Leu Asn
450 455 460

Asp Glu Trp Ile Phe Pro Ser Arg Gln Gly Tyr Ala Lys Tyr Asn His
465 470 475 480

Ser Ile Ser Lys Leu Val Arg Lys Thr Glu Arg Asn Asn Ser Thr Phe
485 490 495

Phe Arg Thr Glu Arg Trp Leu Gly Gln Thr Gly Asn Asp Ser Met Lys
500 505 510

Tyr Asn Tyr Asn Gly Ile Ser Gln Phe Ser Ser Ile Arg Asn Arg Ser
515 520 525

Ser Ser Gln Val Leu Asp Arg Leu Gly Phe Lys Ser Asp Gly Thr Asn
530 535 540

Leu Asn Leu Arg Tyr Gln Asn Asn Thr Leu Ile Ala Asp Ser Leu Phe
545 550 555 560

Gly Val Lys Tyr Asn Leu Thr Glu Tyr Pro Phe Asp Lys Phe Gly Phe
565 570 575

Ile Lys Lys Ala Gln Asp Lys Gln Thr Ile Leu Tyr Lys Asn Gln Phe
580 585 590

Ala Ser Gln Leu Ala Ile Leu Thr Asn Gln Val Tyr Gln Asp Lys Pro
595 600 605

Phe Thr Val Asn Thr Leu Asp Asn Gln Thr Thr Leu Leu Asn Gln Leu
610 615 620

Ser Gly Leu Lys Glu Thr Tyr Phe Glu His Leu Ile Pro Asn Ser Val
625 630 635 640

Ser Gly Gln Thr Thr Leu Asn Lys Gln Val Phe Val Lys Lys Asn Lys
645 650 655

Gln Gly Asn Thr Glu Ile Thr Tyr Asn Ile Thr Ile Pro Lys Asn Ser
660 665 670

Gln Leu Tyr Val Ser Met Pro Phe Ile Asn Phe Asn Asn Glu Glu Asn
675 680 685

Lys Ile Val Gln Ile Ser Val Asn Asn Gly Pro Phe Val Pro Asn Thr
690 695 700

Leu Asp Asn Ala Tyr Ser Phe Phe Asn Ile Gly Ser Phe Ala Glu Asn
705 710 715 720

Ser Arg Ile Lys Val Lys Phe Gln Phe Pro His Asn Asp Gln Val Ser
725 730 735

Phe Pro Ile Pro His Phe Tyr Gly Leu Lys Leu Glu Ala Tyr Gln Lys
740 745 750

Ala Met Thr Val Ile Asn Lys Arg Lys Val Lys Val Arg Thr Asp His
755 760 765

Asn Lys Val Ile Ala Asn Tyr Thr Ser Pro Asn Arg Ser Ser Leu Phe
770 775 780

Phe Thr Ile Pro Tyr Asp Arg Gly Trp Lys Ala Tyr Gln Asn Asn Lys
785 790 795 800

Glu Ile Lys Ile Phe Lys Ala Gln Lys Gly Phe Met Lys Ile Asn Ile
805 810 815

Pro Lys Gly Lys Gly Lys Val Thr Leu Ile Phe Ile Pro Tyr Gly Phe
820 825 830

Lys Phe Gly Val Gly Leu Ser Ile Thr Gly Ile Val Leu Phe Thr Val
835 840 845

Tyr Tyr Phe Lys Phe Gly Lys Asn Lys Ile Gly
850 855

<210> 374

<211> 15

<212> PRT

<213> Streptococcus agalactiae

<400> 374

Trp Phe Met Lys His Ser Val Gly Lys Arg His Asn Leu Val Thr
1 5 10 15

<210> 375

<211> 30

<212> PRT

<213> Streptococcus agalactiae

<400> 375

Met Lys Asp His Leu Arg Cys Phe Leu His Tyr Arg Ser Lys Asn Val
1 5 10 15

Gly Lys Asn Gly Thr Arg Leu Lys Gly Gly Lys Pro Asn Asp
20 25 30

<210> 376

<211> 33

<212> PRT

<213> Streptococcus agalactiae

<400> 376

Asp Lys Gln Leu Phe Gln Cys Val Gln Gly Phe Gln Ile Arg Asn Leu
1 5 10 15

Asn Gly Lys Lys His Gly Ile Lys Leu Ile Phe Ile Lys Asn Val Lys
20 25 30

His

<210> 377

<211> 26

<212> PRT

<213> Streptococcus agalactiae

<400> 377

Asn Glu Glu Ala Ile Asp Gly Val Ser Lys Leu Gly Lys Lys Ile Thr
1 5 10 15

Ile Leu Gly Asn Asn Ser Tyr Leu Ser Ser
20 25

<210> 378

<211> 31

<212> PRT

<213> Streptococcus agalactiae

<400> 378

Ile Lys Gln Trp Leu Leu Val Met Lys Lys Met Thr Val Leu Cys Leu
1 5 10 15

Lys Leu Leu Glu Ile Leu Leu Leu Cys Lys Thr Ala Ile Leu Asn
20 25 30

<210> 379

<211> 19

<212> PRT

<213> Streptococcus agalactiae

<400> 379

Arg Arg Ile Ser Asn Asn Leu Gly Val Leu Lys Glu Ala Thr Val Ile
1 5 10 15

His Ala Val

<210> 380

<211> 36

<212> PRT

<213> Streptococcus agalactiae

<400> 380

Glu Leu Cys Leu Lys Leu Ser Asn Val Lys Pro Ile Tyr Met Pro Trp
1 5 10 15

His Phe Glu Gln Ile Ser Leu Lys Lys Gln Val Ser Arg Val Tyr His
20 25 30

Ala Leu Phe Glu
35

<210> 381

<211> 32

<212> PRT

<213>  Streptococcus agalactiae

<400>  381

Arg Ser Cys Phe Ser Arg Cys Tyr Pro Arg Phe Asn Arg Phe Arg Tyr
1               5                   10                  15

His Phe Leu Lys Pro Pro Trp Thr Arg Thr Asn Tyr Cys Lys Arg Tyr
            20                  25                  30

<210>  382

<211>  19

<212>  PRT

<213>  Streptococcus agalactiae

<400>  382

Arg Trp Phe Gly Phe Arg Tyr Asp Asp Gly Arg Lys Phe Ser Phe Thr
1               5                   10                  15

Asn Leu Leu

<210>  383

<211>  22

<212>  PRT

<213>  Streptococcus agalactiae

<400>  383

Pro Leu Lys Ser Leu Ser Met Thr Ser Arg Met Lys Leu Leu Arg Leu
1               5                   10                  15

Ser Gln Arg Lys Ala Met
            20

<210>  384

<211>  30

<212>  PRT

<213>  Streptococcus agalactiae

<400>  384

Arg His Leu Arg Lys Arg Gln Lys Gln Asn His Leu Met Asn Leu Cys
1               5                   10                  15

Phe Leu Cys Ala Val Lys Lys Leu Lys Lys Asp Asn Leu Ile
20 25 30

<210> 385

<211> 30

<212> PRT

<213> Streptococcus agalactiae

<400> 385

Lys Leu Phe Ile Gln Pro Ile Gln Glu Asn Met Lys Gln Pro Ile Glu
1 5 10 15

Ile Ile Ser Asn Tyr Tyr Ala Lys Leu Gly Leu Met Lys Ile
20 25 30

<210> 386

<211> 19

<212> PRT

<213> Streptococcus agalactiae

<400> 386

Tyr Gln Thr Tyr Ser Lys Lys Ala Arg Lys Phe Gly Ser Val Trp Leu
1 5 10 15

Lys Pro Lys

<210> 387

<211> 28

<212> PRT

<213> Streptococcus agalactiae

<400> 387

Thr Leu Leu Phe Gln Ile Leu Leu Leu Leu Ser His Leu Lys Lys Asn
1 5 10 15

Ile Phe Leu Glu Trp Asn Met His Ala Thr Tyr Asn
20 25

<210> 388

<211> 70

<212> PRT

<213> Streptococcus agalactiae

<400> 388

Lys Lys Phe Tyr Glu Ile Ile Leu Ala Thr Lys Tyr His Thr Ser Val
1 5 10 15

Phe Lys Trp Ser Leu Lys Leu Lys Asn Lys Leu Thr Asn Thr Lys Lys
20 25 30

Ile Ser Glu Ala Ser Ser Gly Lys Leu Glu Ile His Leu Glu Gln Gln
35 40 45

Leu Asn Ser Met Pro Lys Val Thr Leu Ala Leu Ile Leu Leu Val Asp
50 55 60

Lys Ser Asn Ala Leu Leu
65 70

<210> 389

<211> 111

<212> PRT

<213> Streptococcus agalactiae

<400> 389

Leu Lys Gln Met Phe Arg Arg Val Leu His Leu Leu Phe Gln Val Val
1 5 10 15

Leu Ile Ala Val Arg Ser Leu Met Lys Met Val Leu Lys Ser Ser Trp
20 25 30

Asp Gly Val Thr Cys Ser Leu Ser Leu Leu Met Arg Ile Ile Gln Tyr
35 40 45

Asp Tyr Lys Val Pro Leu Phe Gln Met Met Met Leu Lys Gly Ser Leu
50 55 60

Val Leu Ser Lys Thr Lys Pro Arg Leu Thr Met Met Met Pro Leu Ile
65 70 75 80

Leu Glu Lys Tyr Leu Lys Gln Ile Thr Ala Leu Val Val Ala Ala Glu
85 90 95

Tyr Leu Lys Val Ile Leu Phe Leu Lys Lys Pro Arg Asp Ser Phe
100 105 110

<210> 390

<211> 13

<212> PRT

<213> Streptococcus agalactiae

<400> 390

Gly Arg Lys Ile Asn Phe Ser Arg Pro Ser Arg Phe Glu
1               5                   10

<210> 391

<211> 27

<212> PRT

<213> Streptococcus agalactiae

<400> 391

Arg Val Lys Tyr Lys Lys Trp Glu Pro Leu Ser Ile Ser Arg Ser Cys
1               5                   10                  15

Tyr Glu Lys Ser Ser Ser Thr Ser Ser Arg Ile
            20                  25

<210> 392

<211> 31

<212> PRT

<213> Streptococcus agalactiae

<400> 392

Thr Trp Ser Arg Cys Cys Ile Pro Arg Cys Tyr Ser Trp Cys Lys Ile
1               5                   10                  15

Arg Arg Ser Asn Gln Cys Phe Gly Arg Trp Thr Ser Ser Phe Gly
            20                  25                  30

<210> 393

<211> 33

<212> PRT

<213> Streptococcus agalactiae

<400> 393

Lys Glu Asn Phe Val Gln Arg Leu Arg Ser Leu Leu Lys Ala Ile Ser
1               5                   10                  15

Lys Asn Ile Ile Ile Tyr Ser Leu Val Ser Leu Pro Leu Ala Arg His
            20                  25                  30

Leu

<210> 394

<211> 59

<212> PRT

<213> Streptococcus agalactiae

<400> 394

Ser Ile Ile Asn Ile Lys Leu Glu Ile Tyr Asp Ile Cys Pro Lys Thr
1               5                   10                  15

Ile Ser Asn Arg Glu Ser Ile His Gly Tyr Arg Lys Leu Leu Pro Arg
            20                  25                  30

Leu Leu Phe Gly Asp Tyr Leu Ser Lys Thr Leu Phe Gln Gly Phe Thr
        35                  40                  45

Ser Asn His Pro Asn Cys Arg Pro Ile Arg Leu
    50                  55

<210> 395

<211> 16

<212> PRT

<213> Streptococcus agalactiae

<400> 395

Leu Ser Phe Arg Arg Ser Arg Arg Ile Gly Ser Ser His Ser Gln Ile
1               5                   10                  15

<210> 396

<211> 14

<212> PRT

<213> Streptococcus agalactiae

<400> 396

Phe Ile Phe Lys Asp Arg Phe Lys Met Arg His Phe Thr Asp
1               5                   10

<210> 397

<211> 74

<212> PRT

<213> Streptococcus agalactiae

<400> 397

Gly Leu Ile Cys Ala Cys Lys Ala Phe Ile Ser Ala Ile Leu Ala Asn
1               5                   10                  15

Leu Phe Cys Ser Ser Val Ile Pro Ile Ala Ser Cys Pro Glu Asn Ile
            20                  25                  30

Cys Ala Lys Pro Arg Thr Arg Phe Ser Ser Thr Ser Asp Ile Val Leu
        35                  40                  45

Ser Pro Ala Lys Tyr Ile Phe Lys Ala Pro Thr Val Leu Ser Phe Ile
    50                  55                  60

Phe Arg Gly Thr Thr Ile Ala Glu Phe Asn
65                  70

<210> 398

<211> 33

<212> PRT

<213> Streptococcus agalactiae

<400> 398

Ser Ser Ser Leu Asp Thr His Tyr Lys His Arg Glu Leu Phe Leu Val
1               5                   10                  15

Ala Asp Ser Leu Gly Ser Leu Trp Leu Ile Leu Leu Val Ala Tyr Phe
            20                  25                  30

Val

<210> 399

<211> 25

<212> PRT

<213>  Streptococcus agalactiae

<400>  399

His Leu Val Pro Thr Gln Tyr His Lys Gln Asn Leu Pro Leu Glu Tyr
1               5                   10                  15

Lys Arg Leu Asn Ala Leu Val His Lys
            20                  25

<210>  400

<211>  24

<212>  PRT

<213>  Streptococcus agalactiae

<400>  400

Ala His Leu His Glu Gly Tyr His Lys Tyr Pro Leu Lys Arg Arg Asn
1               5                   10                  15

Leu Tyr Glu Phe Leu Arg Lys Leu
            20

<210>  401

<211>  23

<212>  PRT

<213>  Streptococcus agalactiae

<400>  401

Pro Leu Lys Glu Leu Arg Glu His Tyr Ile Ile Pro Arg Lys Ile Arg
1               5                   10                  15

Leu Gln Asn Phe Pro His Arg
            20

<210>  402

<211>  21

<212>  PRT

<213>  Streptococcus agalactiae

<400>  402

Lys Tyr Thr Ile Ala Gly Ser Arg Val Thr Gln Arg Arg Pro Ser Phe
1               5                   10                  15

Ser Val Thr Lys Val
20

<210> 403

<211> 19

<212> PRT

<213> Streptococcus agalactiae

<400> 403

Ala Ala Phe Ser Ser Pro Ala Ala Lys Asn Arg Ala Phe Ile Thr Thr
1 5 10 15

Arg Ser Ser

<210> 404

<211> 47

<212> PRT

<213> Streptococcus agalactiae

<400> 404

Ser Met Val Lys Gln Ile Ser Phe Ser Asp His Leu Ile Ser Arg Phe
1 5 10 15

Glu Gly Leu Cys Leu Arg Arg Phe Ser Val Arg Phe Arg Leu Arg Arg
20 25 30

Ser Leu Ser Ser Val Ser Asn Ser Thr Asn Asn Thr Ser Trp Leu
35 40 45

<210> 405

<211> 43

<212> PRT

<213> Streptococcus agalactiae

<400> 405

Tyr His Val Leu Ser Arg Tyr His Leu Asn Pro Leu His Val Leu Gln
1 5 10 15

Ala Leu Tyr Ala His Gln Glu Tyr Val Ile Val Leu Ile Ile His Gln
20 25 30

Arg Glu Leu Phe Tyr Arg Gly Gln Arg Gly Gln
35 40

<210> 406

<211> 18

<212> PRT

<213> Streptococcus agalactiae

<400> 406

Ala Gln Pro Ser Ser Thr Arg Ile Ser Pro Lys Ile Asp Arg Phe Thr
1 5 10 15

Pro Lys

<210> 407

<211> 38

<212> PRT

<213> Streptococcus agalactiae

<400> 407

Trp Asn Arg Thr Ile Asn Tyr Phe Leu Asn Asn Leu Gln Leu Val Thr
1 5 10 15

Asn Ile Lys Leu Pro Thr Arg Lys Ile Phe Gln Ser Gln Asn Lys Phe
20 25 30

Leu Ser Phe Ile Lys Asn
35

<210> 408

<211> 12

<212> PRT

<213> Streptococcus agalactiae

<400> 408

Val Gln Glu Gly His Lys Ile Phe Pro Leu Gln Arg
1 5 10

<210> 409

<211> 29

<212> PRT

<213> Streptococcus agalactiae

<400> 409

Gln Gln Ser Asn Asn Thr Ala Asn Tyr Ser Arg Pro Tyr Lys Pro Trp
1 5 10 15

His Lys Lys Lys Asn Gly Leu Ser Cys Arg Cys Phe Ser
20 25

<210> 410

<211> 83

<212> PRT

<213> Streptococcus agalactiae

<400> 410

Phe Phe Asp Asp Thr Lys Val Asn Ile His Trp Leu Glu Met Phe Ala
1 5 10 15

Val Cys Met Cys Asn Ile Met Trp Gln Cys Thr Asn Ser Ser Ser Leu
20 25 30

Trp Glu Asn Tyr Phe Thr Leu Pro Ile Lys Ala Thr Gly Ser Ile Asp
35 40 45

Ser Arg Tyr Lys Thr Thr Cys Cys Arg Phe Tyr Ile Thr Phe Asn Thr
50 55 60

Gly His Leu Ser Ser Lys Glu Lys Ile Trp Val Leu Thr Cys Ser Lys
65 70 75 80

Gly Leu Val

<210> 411

<211> 81

<212> PRT

<213> Streptococcus agalactiae

<400> 411

Val Tyr Ser Leu Arg Ile Ala Thr Leu Glu Leu Glu Arg Asn Leu Ile
1 5 10 15

Asp Lys Arg Arg Gly Lys Pro Thr Asp Ser Arg Ser Ile Glu Phe Leu
20 25 30

Glu Val Ser Leu Ala Ile Leu Ser Cys Lys Asn Lys Leu Ile Pro Asp
35 40 45

Ile Met Leu Glu Lys Thr Phe Pro Leu Val Ser Ser Glu Ala Lys Ser
50 55 60

Glu Asp Leu Lys Phe Lys Ser Ala Ile Ser Leu Asn Leu Glu Asn Cys
65 70 75 80

Ser

<210> 412

<211> 56

<212> PRT

<213> Streptococcus agalactiae

<400> 412

Gly His Ser Asn Gly Ile Lys Glu Gly Asn Gly Gly Ile Phe Pro Val
1 5 10 15

Phe Cys Ile Ala Ile Thr Ala Thr Arg Phe Arg Phe Thr Ile Asn Gly
20 25 30

Phe Cys Asn Arg Ile Asn Pro Cys Leu Cys His Phe Ile Val Thr Leu
35 40 45

Leu Ser Cys Cys Asn Arg Lys Ser
50 55

<210> 413

<211> 163

<212> PRT

<213> Streptococcus agalactiae

<400> 413

Arg Ile Glu Lys Ala Ile Val Pro Lys Pro Ala Ile Ser Val Leu Met
1 5 10 15

Ile Ile Ser Arg Met Val Leu Gly Thr Pro Glu Lys Glu Pro Val Ile
20 25 30

Cys Ser Ala Asn Gly Ile Ile Ser Ile Val Ile Ala Thr Pro Ala Asp
35 40 45

Ile Glu Ile Gln Met Ser Lys Ala Asp Ile Ile Lys Ala Lys Pro Val
50 55 60

Glu Lys Leu Phe Cys Glu Asn Ser Leu Thr Glu Leu Thr Lys Ala Ala
65 70 75 80

Pro Gly Thr Ile Thr Ile Ser Ala Pro Asn Ile Ile Met Leu Arg Cys
85 90 95

Ser Pro Asn Pro Glu Lys Tyr Asn Lys Leu Ala Leu Lys Ala Thr Thr
100 105 110

Glu Leu Pro Arg Met Val Lys Arg Asn Pro Val Cys Ile Arg Leu Ser
115 120 125

Ile Lys Phe Arg Lys Tyr Pro Lys Ile Lys Pro Val Thr Ala Ala Glu
130 135 140

Asn Glu Ser Asn Lys Glu Leu Pro Lys Ala Lys Glu Lys Leu Pro Ala
145 150 155 160

Pro Gln Lys

<210> 414

<211> 89

<212> PRT

<213> Streptococcus agalactiae

<400> 414

Pro Tyr Ser Val Thr Tyr Ala Ala Pro Val Ile Cys Asn Gly Ala Asp
1 5 10 15

Leu Ala Arg Arg Thr Ala Tyr Ala Met Ser Ser Ser Val Thr Lys Pro
20 25 30

Ser Asp Val Glu Glu Leu Val Thr Ile Gly Asp Arg Thr Lys Arg Phe
35 40 45

Ser Arg Leu Asn Pro Leu Gly Ser Ile Asn Gly Arg Asn Lys Leu Pro
50 55 60

Trp Thr Leu Phe Ile Ser Ala His Arg Pro Leu Ile Ser His Arg Leu
65 70 75 80

Ser Leu Lys Ser Ile Lys Leu Cys Asn
85

<210> 415

<211> 18

<212> PRT

<213> Streptococcus agalactiae

<400> 415

Ala Asn His Asn Asp Lys Asn Asn Thr Ile Ser Val Asn Lys Phe Ser
1 5 10 15

Ala Lys

<210> 416

<211> 51

<212> PRT

<213> Streptococcus agalactiae

<400> 416

Ser Phe Cys Val Phe Cys Cys His Ser Lys Lys Gly Ser Tyr Pro His
1 5 10 15

Pro Lys Gln Ser Ser Trp Ser Ser Arg Phe Asn Ser Arg Ser His Thr
20 25 30

Asn Asp Ile Thr Cys Pro Tyr Arg Cys Ser Lys Ser Ser Cys Lys Gly
35 40 45

Ser Ile Thr
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<210> 417

<211> 30

<212> PRT

<213> Streptococcus agalactiae

<400> 417

Thr Leu Gly Ile Ser Phe Lys Ile Arg Gly Cys His Phe Ser Ala Lys
1 5 10 15

Pro Phe Leu Gly Gly Lys Ser Pro Asp Phe Pro Leu Pro Gly
20 25 30

<210> 418

<211> 60

<212> PRT

<213> Streptococcus agalactiae

<400> 418

Phe Asn Ile Ser Asn Ser Ser Leu Gly Phe Gly Thr Ser Ala Lys Ser
1 5 10 15

Ala Ser Thr Ser Ser Ala Asn Ser Ser Leu Ile Ile Ser Cys Asp Lys
20 25 30

Ala Thr His Ser Leu Gln Met Lys Thr Pro Leu Pro Ala Ile Ile Phe
35 40 45

Phe Thr Ser Ser Trp Leu Leu Pro Gln Asn Glu Gln
50 55 60

<210> 419

<211> 35

<212> PRT

<213> Streptococcus agalactiae

<400> 419

Gly Val Tyr Lys Lys Gln Ser Leu Ser Leu Ile Phe His Gln Ile His
1 5 10 15

Leu Ile Val Tyr His Phe Asp Phe Leu His Asp Arg Phe Val Pro Tyr
20 25 30

Tyr Arg Glu
35

<210> 420

<211> 87

<212> PRT

<213> Streptococcus agalactiae

<400> 420

Ile Phe Leu Arg Ser Val Cys Gly Asn Ser Arg Gln Ala Leu Gly Leu
1               5                   10                  15

Thr Ser Tyr Ile Leu His Lys Leu Ser Ser Pro Lys Asn Gly Gln Gly
            20                  25                  30

Ile Ala Leu Asn Thr Leu Ser Pro Ser Ser Ser Thr Ser Lys Asn Lys
        35                  40                  45

Ser Ser Lys Ala Asp Asn Phe Ile Arg Lys Cys Leu Glu Ile Leu Glu
    50                  55                  60

Ile Ser Ala Ser Val Asn Arg Gly Pro Lys Val Leu Gln Gln Leu Ala
65                  70                  75                  80

His Ala Val Gln Ser Ile Ser
                85

<210> 421

<211> 130

<212> PRT

<213> Streptococcus agalactiae

<400> 421

Ser Arg Ile Ser Thr Ile Thr Ile Pro Ile Arg Ile Ser Pro Thr Phe
1               5                   10                  15

Leu Tyr Arg Glu Asp Phe Ser Ser Gly Leu Lys Gly Ser Phe Gly Leu
            20                  25                  30

Arg Leu Ser Ser Val Lys Tyr Phe Phe Pro Ser Lys Val Tyr Trp Arg
        35                  40                  45

Arg Pro Lys Asn Ile Pro Ile Ala Ala Ser Glu Lys Pro Arg Trp Lys
    50                  55                  60

Phe Thr Ser Cys Pro Arg Tyr Pro Thr Thr Met Gly Glu Ile Lys Ala
65                  70                  75                  80

Pro Arg Leu Ile Pro Lys Thr Lys Ile Leu Lys Pro Ala Ser Arg Arg
                85                  90                  95

Glu Ser Phe Ser Pro Tyr Lys Leu Pro Thr Ile Ser Asp Thr Phe Gly
            100                 105                 110

Phe Asn Ser Pro Val Pro Arg Ile Ile Arg Ala Ile Glu Met Asn Arg
        115                 120                 125

Ala Val
130

<210> 422

<211> 26

<212> PRT

<213> Streptococcus agalactiae

<400> 422

Ser Phe Pro Arg Ser Asn Asn Leu Cys Ala Phe Lys Asp Lys Phe Lys
1 5 10 15

Cys Arg Thr Ser Ser Arg Leu Asp Cys Leu
20 25

<210> 423

<211> 41

<212> PRT

<213> Streptococcus agalactiae

<400> 423

Ile His Ser Phe His Arg Arg Lys Leu Asn His His Gly Lys Leu Asn
1 5 10 15

Leu Tyr His Leu Val Leu Glu Lys Gln Pro Gly Leu Ser Ser Leu Leu
20 25 30

Ile Met Leu Tyr Gln Ser Pro Asp Leu
35 40

<210> 424

<211> 155

<212> PRT

<213> Streptococcus agalactiae

<400> 424

Leu Ser Phe Ser Ile Val Ser His Leu Leu Thr Thr Ile Ile Ile Pro
1 5 10 15

Leu Pro Ala Ser Cys Ala Asn Pro Ala Ile Arg Leu Ser Tyr Ser Arg
20 25 30

Ile Pro Ser Ser Ala Leu Ile Thr Ile Arg Thr Thr Ser Glu Arg Ser
35 40 45

Met Ala Arg Ile Glu Arg Ile Thr Glu Tyr Phe Ser Val Phe Ser Tyr
50 55 60

Thr Leu Pro Asp Leu Arg Ile Pro Ala Val Ser Ile Ile Val Tyr Ser
65 70 75 80

Cys Pro Trp Leu Ser Thr Lys Leu Val Ser Ile Ala Ser Arg Val Val
85 90 95

Pro Ala Thr Gly Leu Ala Ile Thr Arg Ser Ser Pro Arg Met Ala Leu
100 105 110

Ile Lys Leu Asp Phe Pro Thr Phe Gly Arg Pro Ile Lys Leu Lys Arg
115 120 125

Ile Ile Ser Gly Phe Ser Phe Ser Ser Ser Thr Gly Arg Phe Ser Thr
130 135 140

Ile Ala Ser Asn Ile Ser Pro Val Pro Ile Pro
145 150 155

<210> 425

<211> 24

<212> PRT

<213> Streptococcus agalactiae

<400> 425

Cys Pro Ser Ser Asp Ile Ala Gly Ile Asn Phe Thr Lys Asn Ser Gly
1 5 10 15

Lys Ile Asp Lys Gln Thr Val Thr
20

<210> 426

<211> 32

<212> PRT

<213> Streptococcus agalactiae

<400> 426

Pro Phe Leu Arg Asn His Phe His Asn Asn Glu Thr Ser Thr Lys Phe
1 5 10 15

Phe Ser Asp Ser Thr Lys Ser Arg Ile Gly Asn Thr Cys His Arg Cys
20 25 30

<210> 427

<211> 50

<212> PRT

<213> Streptococcus agalactiae

<400> 427

Ala Ser Thr Gly Ser Ala Ala Asn Pro Gln Thr Thr Pro Gly Lys Leu
1 5 10 15

Leu Gln Ala Ser Ile Ala Pro Ile Pro Val Pro Gln Pro Val Ile Thr
20 25 30

Lys Ser Ala Ala Pro Leu Leu Ser Lys Ile Ala Val Ser Lys Pro Phe
35 40 45

Cys Thr
50

<210> 428

<211> 47

<212> PRT

<213> Streptococcus agalactiae

<400> 428

Ala Met Pro Lys Arg Cys Phe Ile Pro Pro Glu Tyr Asp Glu Ile Phe
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Phe Leu Pro Thr Ser Pro Lys Pro Thr Ser Ser Ser Asn Leu Gly Ile
20 25 30

Ser Cys Leu Ala Phe Phe Leu Ser Thr Pro Phe Lys Val Ala Ile
35 40 45

<210> 429

<211> 49

<212> PRT

<213> Streptococcus agalactiae

<400> 429

Leu Leu Leu Ile Leu Lys Asn Pro Asp Thr Thr His Asn Thr Thr Ile
1 5 10 15

Lys Arg Gln Pro Asn Lys Pro Pro Lys Val Leu Arg Lys Arg Thr Glu
20 25 30

Lys Lys Ser Ile Lys Leu Met Lys Arg Ile Pro Ile Asn His Val Ala
35 40 45

Pro

<210> 430

<211> 44

<212> PRT

<213> Streptococcus agalactiae

<400> 430

Asn Phe Lys Ala Arg Pro Pro Gly Val Val Ser Gly Leu Pro Asn Ile
1 5 10 15

Thr Pro Thr Phe Ser Leu Asn Trp Leu Ile Lys Ile Ala Ile Val Phe
20 25 30

Val Leu Leu Met Asp Ala Asp Asn Leu Arg Ile Ala
35 40

<210> 431

<211> 47

<212> PRT

<213> Streptococcus agalactiae

<400> 431

Lys Arg Val Gly Ile Cys His Ile Tyr His Val Ser Gln Ser Ser Cys
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Phe His Asn Asn Lys Phe Ser Arg Tyr Phe Thr Gln Phe Ser Phe Asn
20 25 30

Ile Ile Val His Ser Ile Phe Leu Ser Gln Tyr Phe Ser Phe Trp
35 40 45

<210> 432

<211> 79

<212> PRT

<213> Streptococcus agalactiae

<400> 432

Asn Ser Thr Thr Ser Ala Ser Leu Ile Ser Gly Leu Ile Ser Ser Arg
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Ser Gly Arg Arg Val Asn Glu Pro Ser Ser Phe Ser Ala Ser Asn Asp
            20                  25                  30

Thr Lys Ala Gly Arg Pro Lys Val Ala Ser Thr Ala Ser Arg Ile Ala
        35                  40                  45

Gly Thr Phe Ile Asp Phe Ser Arg Thr Glu Ile Thr Cys Pro Gly Val
    50                  55                  60

Thr Arg Tyr Asp Gly Ile Ser Thr Arg Leu Pro Ser Thr Arg Ile
65                  70                  75

<210> 433

<211> 37

<212> PRT

<213> Streptococcus agalactiae

<400> 433

Thr Arg Pro Leu Val Glu Ile Leu Val Asp Lys Leu Ala Pro Tyr Lys
1               5                   10                  15

Glu Ala Asn Phe Ser Arg Asn Ser Cys Thr Leu Gly Tyr Leu Ala Phe
            20                  25                  30

Ala Val Thr Asn Ile
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<210> 434

<211> 287

<212> PRT

<213> Streptococcus agalactiae

<400> 434

Arg Thr Arg Asn Ala Ile Arg Tyr Pro Lys Ala Ser Ser Gly Asp Tyr
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Gly Thr Lys Arg Glu Ile Ile Thr Ala Asn Lys Asp Lys Tyr Ser Ile
20 25 30

Ser Lys Met Cys Arg Trp Leu Asn Met Pro Arg Ser Ser Tyr Tyr Tyr
35 40 45

Gln Ala Val Glu Ser Val Ser Lys Thr Glu Phe Glu Glu Thr Ile Lys
50 55 60

Arg Ile Phe Leu Asp Ser Glu Ser Arg Tyr Gly Ser Arg Lys Ile Lys
65 70 75 80

Ile Cys Leu Asn Asn Glu Gly Ile Thr Leu Ser Arg Arg Arg Ile Arg
85 90 95

Arg Ile Met Lys Arg Leu Asn Leu Val Ser Val Tyr Gln Lys Ala Thr
100 105 110

Phe Lys Pro His Ser Arg Gly Lys Asn Glu Ala Pro Ile Pro Asn His
115 120 125

Leu Asp Arg Gln Phe Lys Gln Glu Arg Pro Leu Gln Ala Leu Val Thr
130 135 140

Asp Leu Thr Tyr Val Arg Val Gly Asn Arg Trp Ala Tyr Val Cys Leu
145 150 155 160

Ile Ile Asp Leu Tyr Asn Arg Glu Ile Ile Gly Leu Ser Leu Gly Trp
165 170 175

His Lys Thr Ala Glu Leu Val Lys Gln Ala Ile Gln Ser Ile Pro Tyr
180 185 190

Ala Leu Thr Lys Val Lys Met Phe His Ser Asp Arg Gly Lys Glu Phe
195 200 205

Asp Asn Gln Leu Ile Asp Glu Ile Leu Glu Ala Phe Gly Ile Thr Arg
210 215 220

Ser Leu Ser Gln Ala Gly Cys Pro Tyr Asp Asn Ala Val Ala Glu Ser
225 230 235 240

Thr Tyr Arg Ala Phe Lys Ile Glu Phe Val Tyr Gln Glu Thr Phe Gln
245 250 255

Ser Leu Glu Glu Leu Ala Leu Lys Thr Glu Lys Ala Thr Leu Phe Cys
260 265 270

Thr Thr Phe Ile Lys Cys Cys Leu Phe Arg Phe Leu Pro Met Leu
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<210> 435

<211> 2367

<212> DNA

<213> Streptococcus agalactiae

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<210> 436

<211> 2802

<212> DNA

<213> Streptococcus agalactiae

<400> 436
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<210> 437

<211> 3150

<212> DNA

<213> Streptococcus agalactiae

<400> 437

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<210> 438

<211> 279

<212> DNA

<213> Streptococcus agalactiae

<400> 438
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gaaaagatgc agcggaagct taagaacaaa gaaaaataa 279

<210> 439

<211> 384

<212> DNA

<213> Streptococcus agalactiae

<400> 439
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gagattttat tatattcttt tttgttaaat cgtttaagag agccattaga ttttattcaa 180

aaaggctatg atgataatga agatacctat gttcacttta aggtcgaaga tttatgtgaa 240

ctactcaacc agagtaagac aaccgttatt tccttgaaga aaaggttagc tcaatatggt 300

ttgatagaag aagtgaaagc aggtagtcac cagccgaatc gtatttattt aacagataaa 360

ttagttccat atattaaggg gtaa 384

<210> 440

<211> 1329

<212> DNA

<213> Streptococcus agalactiae

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<210> 441

<211> 2367

<212> DNA

<213> Streptococcus agalactiae

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gaagaacgta ggcaagctca acgttaa 2367

<210> 442

<211> 2802

<212> DNA

<213> Streptococcus agalactiae

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<210> 443
<211> 3150
<212> DNA
<213> Streptococcus agalactiae

<400> 443
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gtcagaaaaa ccataagaaa cttttttcag ctgatgaagg gtttcatagg tgatagagag 180
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<210> 444

<211> 279

<212> DNA

<213> Streptococcus agalactiae

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<210> 445
<211> 384
<212> DNA
<213> Streptococcus agalactiae

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<210> 446
<211> 1329
<212> DNA
<213> Streptococcus agalactiae

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<210> 447

<211> 1389

<212> DNA

<213> Streptococcus agalactiae

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tcaattacta acttaggtat gtttggtact aagacgttta acccaattat caatcaaccg 1200
aactcagcaa tccttggagt aggcgctact attccgactc caacagtggt tgatggtgaa 1260
attgtagctc gaccaatcat ggcaatgtgt ttaacaattg accaccgtat tgttgatgga 1320
atgaatggtg ctaagtttat ggttgatctt aagaacttaa tggaaaaccc atttggttta 1380
cttatttga 1389

<210> 448

<211> 1596

<212> DNA

<213> Streptococcus agalactiae

<400> 448
atgtctagtt ttaatagaaa aaaacttaag tttttgggta tatctttggc gactctaaca 60
gccaccacag ttaccctggt tgcctgtggt aatgagtcaa agaactctgg agataataaa 120
gttattaatt ggtatattcc tactgaaatc agtacattgg acatttcaaa gaatacagat 180
gcttattcaa acttagctat aggtaattca ggcagcaatt tacttagaat tgataaagag 240
ggcaaaccaa aacccgattt agctaaaaaa gtatccgttt cttctgatgg tcttacttat 300
actgctacac ttcgtgataa tttaaaatgg tcagatggaa gcaaactaag cgctgaagat 360
tttgtttaca catggcggag aatagttgat cctaaaactg catctgaata tgcttacttg 420
gcgacagaat cgcacctttt aaatgctgat aagattaatt ctggagatat taaagattta 480
aataaacttg gtgtaacagc taaaggcaat caagtgacct ttaaattgac aagtccatgc 540
cctcaattta aatattattt agccttctct aattttatgc ctcaaaaaca atcgtatgtt 600
gaaaaagttg gtaaagatta tggtacaaca tcaaaaaatc aaatttactc aggtccttac 660
cttgttaagg attggaatgg ttcaaatggt aaatttaaat tagtcaaaaa taaatattat 720
tgggattcta aacatgttaa aacaaatagt gtcatagttc aaactatcaa aaaaccagat 780
actgcagttc aaatgtacaa gcaaggtcag attgattttg ctgaaatatc aggaacttct 840
gctatttata accaaactgg ttcggttaaa gcattgacaa atcagaaaat taggcaagct 900
ttgaatttag cgactgatcg taaaggtgtt gttaaagcgg cagttgatac aggttcaact 960
cctgctgaat ctctggtccc taaaaaatta gccaaattac ctaatggtga ggatctttcc 1020
aagtatactg ccccaggtta tacgtataat acaagtaaag ctcaaaaact ttttaaagaa 1080

ggtcttgctg aggttggtca gtcatctctc aagttaacaa tcacagctga ttcggactct 1140
ccagcagcta aaaatgctgt tgactatgtg aaatctacat gggagagtgc tttgcctggt 1200
ctaactgttg aagaaaaatt tgttactttc aagcaacgcc ttgaagatgc aaaaaatgaa 1260
aattttgatg tcgtgctctt ctcatgggga ggagattatc cagaaggatc aactttctat 1320
gggttattca cgactaattc tgcgtataat tatggtaaat tttcttctaa agagtatgac 1380
aatgcctatc aaaaggcaat tactactgac gccttgaaac caggagatgc cgctaatgat 1440
tacaaaactg ctgaaaaagc tttatttgat caatcatatt ataacccagt ttattaccta 1500
gggaaaaaag gactccaaaa ttctaaatta aaggggttgg taagaaattc aactggtttg 1560
aatgttgatt ttacttatgc ttataagaca gaataa 1596

<210> 449

<211> 788

<212> PRT

<213> Streptococcus agalactiae

<400> 449

Met Asp Val Ser Ser Ser Pro Asn Ile Thr Phe Met Leu Gln Tyr Thr
1 5 10 15

Glu Ala Asn Pro Gln Tyr Val Asp Tyr Thr Asn Arg Glu Glu Ala Val
20 25 30

Lys Ile Asp Glu Glu Leu Ser Leu Glu Thr Asn Arg Gln Met Ile Glu
35 40 45

Gly Leu Thr Glu Asp Glu Leu Thr Arg Ile Gln Glu Ala Val Pro Glu
50 55 60

Thr Gln Leu Asn Phe Arg Glu Tyr Ile Asp Tyr Met Asn Arg Ser Tyr
65 70 75 80

Ala Thr Glu Glu Gln Ser Lys Glu Leu Thr Ala Ile Phe Thr Gln Glu
85 90 95

Ala Asp Tyr Leu Gln Lys Leu Arg Leu Ile Asp Leu Lys Asn Lys Leu
100 105 110

Glu Ser Ala Tyr Gln Asn Gly Ser Leu Leu Trp Gln Gly Val Ile Ser
115 120 125

Phe Asp Asn Ala Phe Leu Ala Glu Gln Gly Leu Tyr Asp Val Ala Thr
130 135 140

Gly Gln Val Asp Gln Lys Ala Ile Lys Ala Val Met Arg Asp Met Met
145 150 155 160

Pro Thr Leu Ile Gln Lys Glu Gly Leu Ser Asp Ser Ala Phe Trp Trp
165 170 175

Gly Asn Ile His Leu Asn Thr Asp Asn Ile His Ile His Phe Gly Leu
180 185 190

Ser Glu Val Glu Ser Asn Arg Glu Lys Ile Phe Tyr Gln Pro Arg Gly
195 200 205

Arg Met Glu Tyr Lys Gly Asn Phe Ser Gln Lys Thr Ile Asn Arg Phe
210 215 220

Lys Ser Gly Val Tyr His Gly Leu Leu Lys Glu Glu Thr Arg Ser Asn
225 230 235 240

Leu Leu Arg Lys Glu Gln Ile Leu Ala Asn Leu Lys Ala Asp Phe Ile
245 250 255

Thr Ser Ile Tyr Gln Lys Asp Lys Ile Thr Ser Ser Ala Glu Lys Asn
260 265 270

Phe Leu Glu Gln Ala Tyr Asn His Leu Pro Leu Asn Lys Lys Trp Arg
275 280 285

Tyr Gly Ser Asn Ala Arg Asp Phe Ala Val Ser Lys Phe Phe Leu Asp
290 295 300

Arg Tyr Leu Asp Ser Tyr Leu Asn Asn Glu Gly Ser Ala Ala Tyr Gln
305 310 315 320

Glu Phe Leu Lys Glu Thr Arg Asp Phe Leu Gln Thr Tyr Glu Gly Val
325 330 335

Tyr Ser Ala Glu Lys Asn Lys Ile Tyr Glu Lys Leu Arg Lys Val Asp
340 345 350

Gly Gln Thr Ile Arg Thr Leu Ala Glu Ser Lys Gly Tyr Asp Leu Glu
355 360 365

His His Leu Ala Arg Arg Val Met Asp Leu Arg Glu Arg Leu Ala Asn
370 375 380

Asn Ile Leu Arg Ser Phe Arg Glu Ala Ala Pro Gln Ile Gln Asp Val
385 390 395 400

Gln Leu Glu Lys Asn Leu Glu Ser Phe Ser Val Leu Asn Gln Lys Lys
405 410 415

Ile Leu Glu Gln His Pro Glu Ala Ser Val Val Lys Ser Gln Lys Ala
420 425 430

Trp Gln Lys Leu Gly Tyr Phe Val Lys Ala Gly Glu Gln Pro Leu Glu
435 440 445

Ile Ile Arg Pro Val Tyr Lys Ser Tyr Asp Lys His Gly Lys Gly Ile
450 455 460

Gly Arg Pro Glu Phe Val Ser Asp Thr Val Tyr Asp Ile Ser Gln Leu
465 470 475 480

Thr Glu Asn Ile Gln Leu Lys Ser Leu Thr Leu Lys Asp Leu Ser Leu
485 490 495

Phe Ser Ser Asn Glu Leu Lys Glu Leu Val Asp Ala Ala Lys Leu Lys
500 505 510

Thr Asn Pro Thr Glu Arg Glu Arg Arg Glu Leu Gly Thr Tyr Arg Tyr
515 520 525

Ala Leu Lys Leu Ser Ile Leu Glu Ser Ser Gln Lys Glu Leu Gln Val
530 535 540

Arg Gln Lys Leu Leu Glu Gln Val Gln Pro Leu Ala Ser Asp Gln Pro
545 550 555 560

Phe Leu Asp Phe Lys Lys Gln Leu Ile Ala Gln Glu Leu Gln Ala Ile
565 570 575

Ala Leu Gln Leu Thr Pro Asn Tyr Lys Leu Ser Glu Asp Asp Lys Ala
580 585 590

Leu Lys Asn Arg Leu Lys Arg Gln Phe Glu Asp Ser Val Ala Leu Pro
595 600 605

Val Ser Lys Ala Thr Pro Gly Ala Ile Gln Leu Pro Ile Arg Gln Leu
610 615 620

Trp Thr Glu Leu Gly Leu Val His His Ile Gln Asp Glu Asn Ile Leu
625 630 635 640

Thr Leu Leu Lys Gly Thr Ser Thr Thr Lys Gln Ala Tyr Ile Glu Glu
645 650 655

Leu Gln Thr His Ile Ser Ile Phe Gln Leu Lys Tyr Gln Ile Asn Asn
660 665 670

Arg Asn Lys Gln Ile Ser Gln Leu Ser Asp Glu Ala Thr Ile Lys Glu
675 680 685

Met Arg Ile Ala Asn Ala Lys Gly Phe Ser Glu Leu Lys Arg Leu Tyr
690 695 700

Asp Thr Leu Gln Pro Ser Asp Asp Gly Gln Asn Gln Ile Ser Gln Ala
705 710 715 720

Val Ser Lys Gln Leu Gln Glu Arg Lys Val Ile Lys Lys Ala Gln Leu
725 730 735

Gln Gln Thr Gln Arg Ser Gly Lys Ile Asn Thr Asp Phe Met Arg Gln
740 745 750

Leu Thr Ala Ser Leu Asn Arg Ser Gln Gln Ala Ser Lys Lys Ala Leu
755 760 765

Met Glu Arg Ala Arg Ser Asp Glu Arg Glu Glu Gln Glu Glu Arg Arg
770 775 780

Gln Ala Gln Arg
785

<210> 450

<211> 933

<212> PRT

<213> Streptococcus agalactiae

<400> 450

Met Asn Ser Asn Thr Lys Gly His Gly Phe Phe Arg Lys Ser Lys Ala
1 5 10 15

Tyr Gly Leu Val Cys Ala Ile Ala Leu Ala Gly Ala Phe Thr Leu Ala
20 25 30

Thr Ser Gln Val Ser Ala Asp Gln Val Thr Thr Gln Ala Thr Thr Gln
35 40 45

Thr Val Thr Gln Asn Gln Ala Glu Thr Val Thr Ser Thr Gln Leu Asp
50 55 60

Lys Ala Val Ala Thr Ala Lys Lys Ala Ala Val Ala Val Thr Thr Thr
65 70 75 80

Pro Ala Val Asn His Ala Thr Thr Thr Asp Ala Gln Ala Asp Leu Ala
85 90 95

Asn Gln Thr Gln Ala Val Lys Asp Val Thr Ala Lys Ala Gln Ala Asn
100 105 110

Thr Gln Ala Ile Lys Asp Ala Thr Ala Glu Asn Ala Lys Ile Asp Ala
115 120 125

Glu Asn Lys Ala Glu Ala Glu Arg Val Ala Lys Glu Asn Lys Glu Gly
130 135 140

Gln Ala Ala Val Asp Ala Arg Asn Lys Ala Gly Gln Ala Ala Val Asp
145 150 155 160

Ala Arg Asn Lys Ala Lys Gln Gln Ala Gln Asp Asp Gln Lys Ala Lys
165 170 175

Ile Asp Ala Glu Asn Lys Ala Glu Ser Gln Arg Val Ser Gln Leu Asn
180 185 190

Ala Gln Asn Lys Ala Lys Ile Asp Ala Glu Asn Lys Asp Ala Gln Ala
195 200 205

Lys Ala Asn Ala Thr Asn Ala Gln Leu Gln Lys Asp Tyr Gln Ala Lys
210 215 220

Leu Ala Glu Ile Lys Ser Val Glu Ala Tyr Asn Ala Gly Val Arg Gln
225 230 235 240

Arg Asn Lys Asp Ala Gln Ala Lys Ala Asp Ala Thr Asn Ala Gln Leu
245 250 255

Gln Lys Asp Tyr Gln Ala Lys Leu Ala Leu Tyr Asn Gln Ala Leu Lys
260 265 270

Ala Lys Ala Glu Ala Asp Lys Gln Ser Ile Asn Asn Val Ala Phe Asp
275 280 285

Ile Lys Ala Gln Ala Lys Gly Val Asp Asn Ala Glu Tyr Gly Asn Ser
290 295 300

Ile Met Thr Ala Lys Thr Lys Pro Asp Gly Ser Phe Glu Phe Asn His
305 310 315 320

Asp Met Ile Asp Gly Val Lys Thr Ile Gly Tyr Gly Lys Leu Thr Gly
325 330 335

Lys Val Asn His His Tyr Val Ala Asn Lys Asp Gly Ser Val Thr Ala
340 345 350

Phe Val Asp Ser Val Thr Leu Tyr Lys Tyr Glu Tyr Arg Asn Val Ala
355 360 365

Gln Asn Ala Ala Val Asn Gln Asn Ile Val Phe Arg Val Leu Thr Lys
370 375 380

Asp Gly Arg Pro Ile Phe Glu Lys Ala His Asn Gly Asn Lys Thr Phe
385 390 395 400

Ala Glu Thr Leu Asn Lys Thr Leu Gln Leu Asn Leu Lys Tyr Glu Leu
405 410 415

Lys Pro His Ala Ser Ser Gly Asn Val Glu Val Phe Lys Ile His Asp
420 425 430

Asp Trp Val His Asp Thr His Gly Ser Ala Leu Val Ser Tyr Val Asn
435 440 445

Asn Asn Asp Ala Val Pro Asn Val Val Ile Pro Glu Arg Pro Thr Pro
450 455 460

Pro Lys Pro Val Lys Val Thr Pro Glu Ala Glu Lys Pro Val Pro Glu
465 470 475 480

Lys Pro Val Glu Pro Lys Leu Val Thr Pro Thr Leu Lys Thr Tyr Thr
485 490 495

Pro Val Lys Phe Ile Pro Arg Glu Tyr Lys Pro Glu Pro Ile Thr Pro
500 505 510

Glu Thr Phe Thr Pro Glu Lys Phe Thr Pro Ala Gln Pro Lys Val Lys
515 520 525

Pro His Val Ser Ile Pro Glu Lys Ile Asn Tyr Ser Val Ser Val His
530 535 540

Pro Val Leu Val Pro Ala Ala Asn Pro Ser Lys Ala Val Ile Asp Glu
545 550 555 560

Ala Gly Gln Ser Val Asn Gly Lys Thr Val Leu Pro Asn Ala Thr Leu
565 570 575

Asp Tyr Val Ala Lys Gln Asn Phe Ser Gln Tyr Lys Gly Ile Lys Ala
580 585 590

Ser Ala Glu Ala Ile Ala Lys Gly Phe Ala Phe Val Asp Gln Pro Asn
595 600 605

Glu Ala Leu Ala Glu Leu Thr Val Lys Ser Ile Lys Ala Ser Asn Gly
610 615 620

Asp Asp Val Ser Ser Leu Leu Glu Met Arg His Val Leu Ser Lys Asp
625 630 635 640

Thr Leu Asp Gln Lys Leu Gln Ser Leu Ile Lys Glu Ala Gly Ile Ser
645 650 655

Pro Val Gly Glu Phe Tyr Met Trp Thr Ala Lys Asp Pro Gln Ala Phe
660 665 670

Tyr Lys Ala Tyr Val Gln Lys Gly Leu Asp Ile Thr Tyr Asn Leu Ser
675 680 685

Phe Lys Ile Lys Ala Asn Phe Thr Lys Gly Gln Ile Lys Asn Gly Val
690 695 700

Ala Gln Ile Asp Phe Gly Asn Gly Tyr Thr Gly Asn Ile Val Val Asn
705 710 715 720

Asp Val Thr Val Pro Glu Val His Lys Asp Ile Leu Asp Lys Glu Asp
725 730 735

Gly Lys Ser Ile Asn Asn Ser Thr Val Lys Leu Gly Asp Glu Val Thr
740 745 750

Tyr Lys Leu Glu Gly Trp Val Val Pro Ala Asn Arg Gly Tyr Asp Leu
755 760 765

Phe Glu Tyr Lys Phe Val Asp Gln Leu Gln His Thr His Asp Leu Tyr
770 775 780

Leu Arg Asp Lys Val Val Ala Lys Val Asp Val Thr Leu Lys Asp Gly
785 790 795 800

Thr Val Ile Lys Lys Gly Thr Asn Leu Gly Glu Tyr Thr Glu Thr Val
805 810 815

Tyr Asn Lys Thr Thr Gly His Tyr Glu Leu Ala Phe Lys Lys Glu Phe
820 825 830

Leu Ala Lys Val Ser Arg Glu Ser Glu Phe Gly Ala Asp Asp Phe Ile
835 840 845

Val Val Lys Arg Ile Lys Ala Gly Asp Val Tyr Asn Thr Ala Asp Leu
850 855 860

Tyr Val Asn Gly Tyr Lys Val Lys Ser Glu Ala Val Val Thr His Thr
865 870 875 880

Thr Glu Lys Ser Lys Pro Val Glu Pro Gln Lys Ala Thr Pro Lys Ala
885 890 895

Pro Ala Lys Gly Leu Pro Ser Thr Gly Glu Ala Ser Met Thr Pro Leu
900 905 910

Thr Ala Ile Gly Ala Ile Ile Leu Ser Ala Leu Gly Leu Ala Gly Phe
915 920 925

Lys Lys Arg Gln Lys
930

<210> 451

<211> 1049

<212> PRT

<213> Streptococcus agalactiae

<400> 451

Met Phe Ser Trp Leu Glu Ala Leu Tyr Tyr Thr Leu Ile Gln Leu Ala
1 5 10 15

Lys Val Asn Arg Leu Asn Ala Leu Phe Leu Val Ser Val Val Gly Tyr
20 25 30

Leu Cys Tyr Gln Gly Ile Lys Leu Val Arg Lys Thr Ile Arg Asn Phe
35 40 45

Phe Gln Leu Met Lys Gly Phe Ile Gly Asp Arg Glu Asn Ile Lys Lys
50 55 60

Cys Ile Lys Asn Lys Lys Glu Ala Leu Val His Ser Trp Lys His Arg
65 70 75 80

Gln Asp Ile Asp Trp Lys Ser Thr Gly Lys Asp Lys Ser Lys Gln Leu
85 90 95

Trp Asn Leu Met Lys Arg Leu Ala Thr Val Ala Pro Ser Phe Leu Phe
100 105 110

Leu Leu Leu Gly Asn Val Leu Phe Arg Leu Ile Tyr Gln Leu Pro Phe
115 120 125

Val Lys Gln Asp Arg Lys Arg Phe Asp Lys Glu Met Lys Pro Leu Leu
130 135 140

Tyr Phe Lys Asn Tyr Arg Ser Phe Val Phe Met Gly Ile Gly Phe Ser
145 150 155 160

Phe Ile Ala Phe Ile Leu Thr Asn Tyr Phe Val Thr Val Leu Arg Ala
165 170 175

Ala Ile Arg Phe Leu Tyr Phe Ser Ile Met Thr Leu Arg Asp Asn Ser
180 185 190

Gln Val Val Ser Phe Asn Val Asp Ser Leu Leu Ile Gln Asn Leu Phe
195 200 205

Asn Ala Arg Val Phe Val Ile Ala Pro Ile Leu Ala Val Pro Ile Phe
    210                 215                 220

Leu Ile Gly Leu Val Val Ala Trp Arg Ser Ala Trp Val Asn Phe Glu
225                 230                 235                 240

Gln Tyr Arg Asp Tyr Asn His Asn Glu Glu Gly Asp Asp Arg Phe Ala
                245                 250                 255

Thr Val Lys Glu Ile His Gln Gln Tyr Lys Lys Val Pro Asn Lys Thr
            260                 265                 270

Glu Thr Tyr Pro Gly Glu Gly Gly Val Pro Val Leu His Glu Thr Arg
        275                 280                 285

Lys Asn Leu Thr Gly Leu Thr Leu Lys Ser Gln Met Leu Trp Gln Asn
    290                 295                 300

Arg Thr Phe Ser Arg Tyr Leu Thr Asn Ala Glu Arg Ile Leu Gly Leu
305                 310                 315                 320

Leu Ser Thr Pro Ser Gly Asp Tyr Tyr Ile Asp Asp Ser Thr Thr Asn
                325                 330                 335

Leu Ile Thr Met Gly Ile Thr Arg Ser Gly Lys Gly Glu Ala His Ile
            340                 345                 350

Ala Pro Ile Ile Asp Ile Asn Ser Arg Ala Glu Ile Gln Pro Ser Leu
        355                 360                 365

Ile Ile Ala Asp Pro Lys Gly Glu His Tyr Gln Ser Ser Tyr Lys Thr
    370                 375                 380

Met Arg Arg Arg Gly Tyr Asp Val Asn Val Leu Ser Phe Gln Asn Met
385                 390                 395                 400

Asp Trp Ser Met Ser Tyr Asn Pro Leu Ala Leu Ala Ile Ala Ala Ala
                405                 410                 415

Lys Lys Gly Tyr Tyr Glu Met Thr Gln Thr Arg Val Asn Ala Val Ala
            420                 425                 430

Glu Ala Ile Tyr Arg Lys Thr Lys Pro Gly Ser Gly Asn Gly Asn Ala
        435                 440                 445

Lys Tyr Trp Glu Asp Thr Ser Ile Ser Leu Phe Asn Ala Ile Ala Met
    450                 455                 460

Ala Leu Met Asp Arg Ala Asn Glu Thr Val Arg Asn Gly Glu Thr Asp
465                 470                 475                 480

Ala Trp Asp Thr Val Thr Val Arg Asn Ile Ala Lys Phe Leu Thr Asp
485 490 495

Leu Gly Ser Glu Glu Val Phe Val Asn Asp Phe Gly Glu Ile Val Glu
500 505 510

Asn Pro Asp Lys Asn Gln Gln Val Lys Lys Lys Ser Lys Ile Thr Val
515 520 525

Tyr Phe Asp Asn Leu Arg Lys Ile Asn Gln Glu Gln Phe Ser Lys Phe
530 535 540

Arg Asp Met Ala Asp Leu Asn Phe Arg Ser Ser Asp Phe Ala Ser Glu
545 550 555 560

Glu Thr Lys Gly Asn Val Phe Ser Ser Met Met Ser Gly Ile Asn Leu
565 570 575

Phe Leu Gln Asp Asn Ile Ala Lys Leu Thr Ser Lys Asn Ser Ile Asp
580 585 590

Leu Glu Ser Val Gly Phe Pro Arg Arg Leu Ser Ile Lys Phe Arg Ser
595 600 605

Ser Ser Asn Val Ala Met Arg Asn Glu Tyr Thr His Lys Thr Ala Lys
610 615 620

Val Thr Ile Thr Ser Gln Ala Val Trp Gly Lys Thr Thr Lys Gln Val
625 630 635 640

Ile His Val Asp Ala Ala Thr Ala Leu Ile Asp Gly Glu Gly Tyr Leu
645 650 655

Thr Tyr Val Ile Glu Pro Gln Leu Pro Asp Gln Phe Leu Val Thr Ile
660 665 670

Asp Phe Asn His Glu Asn Asn Gly Gly Ser Ala Ile Arg His Lys Thr
675 680 685

Phe Gln Phe Ser Ala Glu Lys Val Tyr Lys Lys Arg Gly Asn Val Ile
690 695 700

Thr Leu Asp Asp Tyr Thr Lys Lys Pro Val Leu Asp His Ile Lys Val
705 710 715 720

Thr Val Leu Asn Lys Gln Asp Asp Asn Leu Leu Gln Lys Glu Asp Ile
725 730 735

Asp Leu Ile Tyr Ser Asp Asn Pro Lys Val Ile Tyr Leu Val Thr Pro
740 745 750

Pro Asn Arg Thr Glu Tyr Asn Ser Ile Val Ser Leu Phe Leu Asp Gln
755 760 765

Leu Phe Asn Ala Asn Tyr Glu Leu Ala Leu Ser Asn Gly Arg Lys Cys
770 775 780

Val Asn Arg Ile Leu His Ile Leu Asp Glu Phe Thr Asn Ile Pro Ala
785 790 795 800

Ile Pro His Met Asp Thr Lys Ile Ser Ile Gly Leu Gly Gln Asn Ile
805 810 815

Leu Tyr Tyr Leu Trp Ile Gln Asn Leu Lys Gln Leu Val Ser Glu Tyr
820 825 830

Gly Glu Asn Thr Ala Glu Thr Ile Arg Glu Asn Cys Ser Leu Lys Val
835 840 845

Tyr Ile Lys Ser Thr Ala Pro Ala Thr Asn Glu Tyr Phe Ser Lys Glu
850 855 860

Leu Gly Thr Arg Thr Ile Thr Arg Arg Arg Arg Ser Ser Asn Ile Leu
865 870 875 880

Asp Glu Ala Asn Pro Asn Val Ser Ile Glu Asn Pro Arg Gln Glu Leu
885 890 895

Leu Thr Pro Thr Gln Leu Ser Lys Leu Gln Glu Gly Glu Ala Val Ile
900 905 910

Leu Arg Gly Val Lys Gly Arg Asp Asn Ala Gly Arg Lys Ile Thr Thr
915 920 925

Asp Pro Ile Phe Leu His Glu Lys Thr Ser Leu Pro Tyr Arg Tyr Met
930 935 940

Phe Leu Gln Glu Glu Phe Asp Gln Ser Met Ala Leu Ala Asp Ile Pro
945 950 955 960

Val Glu Ser Gly His Arg Asp Leu Asp Leu Gln Asp Ile Ala Val Gly
965 970 975

Ala Gln Ser Thr Phe Asn Lys Ile Ile Asp Trp Arg Met Ala Leu Thr
980 985 990

Asp Arg Met Arg Thr Asn Gly Lys Ile Pro Gln Leu Ala Ser Arg Lys
995 1000 1005

Gln Thr Ile Lys Ala Leu Ser Gln Ser Gln Phe Thr Ser Pro Ala
1010 1015 1020

Asp Leu Thr Gln Ala Val Ile Ala Glu Val Phe Asp Glu Glu Asp
1025 1030 1035

Asp Asp Asp Leu Phe Phe Val Asp Asp Val Met
1040 1045

<210> 452

<211> 92

<212> PRT

<213> Streptococcus agalactiae

<400> 452

Met Thr Asp Asn Arg Phe Ala Gln Leu Lys Glu Asn Phe Glu Lys Gly
1 5 10 15

Ser Pro Lys Arg Arg Val Pro Thr Ser Arg Pro Ile Ala Ala Gln Lys
20 25 30

Ala Pro Glu Ser Tyr Asn Lys Lys Gly Arg Tyr Pro Phe Ser Leu His
35 40 45

Gln Asp Val Arg Tyr Asp Lys Leu Glu Ala Leu Val Ala Tyr His Gly
50 55 60

Ala Lys Ser Ala Ser Asp Tyr Leu Glu Arg Leu Ile Val Gln Glu Trp
65 70 75 80

Glu Lys Met Gln Arg Lys Leu Lys Asn Lys Glu Lys
85 90

<210> 453

<211> 127

<212> PRT

<213> Streptococcus agalactiae

<400> 453

Met Ala Tyr Leu Ser Lys Leu Ser Asp Leu Asp Pro Ser Leu Met Asp
1 5 10 15

Ala Asp Ser Glu Gln Ile Tyr Ile Pro Lys Val Leu Phe Glu His Asn
20 25 30

Asp Phe Lys Gly Leu Thr Tyr Lys Glu Ile Leu Leu Tyr Ser Phe Leu
35 40 45

Leu Asn Arg Leu Arg Glu Pro Leu Asp Phe Ile Gln Lys Gly Tyr Asp
50 55 60

Asp Asn Glu Asp Thr Tyr Val His Phe Lys Val Glu Asp Leu Cys Glu
65 70 75 80

Leu Leu Asn Gln Ser Lys Thr Thr Val Ile Ser Leu Lys Lys Arg Leu
85 90 95

Ala Gln Tyr Gly Leu Ile Glu Glu Val Lys Ala Gly Ser His Gln Pro
100 105 110

Asn Arg Ile Tyr Leu Thr Asp Lys Leu Val Pro Tyr Ile Lys Gly
115 120 125

<210> 454

<211> 442

<212> PRT

<213> Streptococcus agalactiae

<400> 454

Met Thr Ile Phe Asp Glu Arg Glu Leu Lys Glu Arg Phe Thr His Glu
1 5 10 15

Asn Arg Val Ser Phe Tyr Glu Phe Val Ala Lys Tyr Asp Ala Gln Met
20 25 30

Val Pro Val Met Lys Ala Lys Gly Tyr Arg Cys Ile His Ser Met Glu
35 40 45

Arg Thr Val Val Phe Thr Phe Gly Glu Phe Thr Ile Arg Arg Arg Arg
50 55 60

Trp Gln Lys Gly Glu His Trp Val Val Pro Val Asp Glu Lys Leu Gly
65 70 75 80

Leu Lys Lys Asn Val Arg Tyr Ser Leu Glu Phe Met Tyr Gln Ile Ala
85 90 95

Ser Leu Ala Thr Met Met Pro Tyr Glu Lys Val Ile Lys Val Val Gln
100 105 110

Met Met Tyr Cys Ile Val Ile Thr Lys Pro Thr Val Val Lys Ala Val
115 120 125

Lys Ile Ser Arg Glu Leu Leu Lys Glu Lys Glu Ala Tyr Arg Phe Phe
130 135 140

Asp Glu Asp Ile Pro Val Asp Lys Glu Pro Val Asp Met Ile Tyr Leu
145 150 155 160

Glu Gly Asp Gly Val Met Val Lys Ala Arg Glu Glu Gly Leu Asp Asn
165 170 175

Arg Asn Val Asp Leu Ser His Phe Val Val His Thr Gly Ser Gln Lys
180 185 190

Val Gly Ser Asn Arg Phe Val Leu Gln Asn Lys Lys Glu Phe Val Ser
195 200 205

Leu Asp Asn Arg Gln Thr Arg Gln Lys Ile Leu Asp Tyr Leu Tyr Asn
210 215 220

His Phe Tyr Ile Ala Pro Asn Thr Leu Leu Ile Thr Asn Ser Asp Gly
225 230 235 240

Gly His Gly Tyr Thr Pro Tyr Val Phe Lys Glu Ile Ala Lys Ala Leu
245 250 255

Lys Val Lys Gln His Glu His Phe Trp Asp Arg Tyr His Val Asn Glu
260 265 270

Lys Ile Lys Ser Phe Phe Lys Leu Tyr Pro Val Glu Leu Met Thr Gly
275 280 285

Ala Phe Gln Ser Ile Lys Gln His Asp Lys Glu Lys Leu Arg Thr Val
290 295 300

Leu Asp Thr Thr Glu Ala Leu Ile Leu Met Glu Glu Glu Met Glu Gly
305 310 315 320

Phe Asn Gln Phe Lys Arg Lys Leu Leu Asn Asn Phe Gln Tyr Thr Lys
325 330 335

Ser Ala Glu Leu Arg Gly Phe Ser Arg Ala Gly Ile Gly Val Met Glu
340 345 350

Ser Gln His Arg Lys Ile Thr Tyr Arg Met Lys Lys Arg Gly Met Tyr
355 360 365

Trp Thr Ile Gln Gly Ala Glu Thr Met Ser Gln Leu Ile Val Leu Ser
370 375 380

Tyr Glu Gly Gln Leu Arg Asp Leu Phe Phe Gly Ser Trp Arg Glu Asp
385 390 395 400

Tyr Gln Lys Tyr Gln Glu Leu Glu Asn Leu Ser Ala Gly Lys Ile Lys
405 410 415

His Glu Gln Asn Lys Ile Asn Lys Arg Tyr Asp Leu Gln Thr Leu Gly
420 425 430

Arg Leu Arg Tyr Gly Arg His Arg Asn Leu
435 440

<210> 455

<211> 788

<212> PRT

<213> Streptococcus agalactiae

<400> 455

Met Asp Val Ser Ser Ser Pro Asn Ile Thr Phe Met Leu Gln Tyr Thr
1 5 10 15

Glu Ala Asn Pro Gln Tyr Val Asp Tyr Thr Asn Arg Glu Glu Ala Val
20 25 30

Lys Ile Asp Glu Glu Leu Ser Leu Glu Thr Asn Arg Gln Met Ile Glu
35 40 45

Gly Leu Thr Glu Asp Glu Leu Thr Arg Ile Gln Glu Ala Val Pro Glu
50 55 60

Thr Gln Leu Asn Phe Arg Glu Tyr Ile Asp Tyr Met Asn Arg Ser Tyr
65 70 75 80

Ala Thr Glu Glu Gln Ser Lys Glu Leu Thr Ala Ile Phe Thr Gln Glu
85 90 95

Ala Asp Tyr Leu Gln Lys Leu Arg Leu Ile Asp Leu Lys Asn Lys Leu
100 105 110

Glu Ser Ala Tyr Gln Asn Gly Ser Leu Leu Trp Gln Gly Val Ile Ser
115 120 125

Phe Asp Asn Ala Phe Leu Ala Glu Gln Gly Leu Tyr Asp Val Ala Thr
130 135 140

Gly Gln Val Asp Gln Lys Ala Ile Lys Ala Val Met Arg Asp Met Met
145 150 155 160

Pro Thr Leu Ile Gln Lys Glu Gly Leu Ser Asp Ser Ala Phe Trp Trp
165 170 175

Gly Asn Ile His Leu Asn Thr Asp Asn Ile His Ile His Phe Gly Leu
180 185 190

Ser Glu Val Glu Ser Asn Arg Glu Lys Ile Phe Tyr Gln Pro Arg Gly
195 200 205

Arg Met Glu Tyr Lys Gly Asn Phe Ser Gln Lys Thr Ile Asn Arg Phe
210 215 220

Lys Ser Gly Val Tyr His Gly Leu Leu Lys Glu Glu Thr Arg Ser Asn
225 230 235 240

Leu Leu Arg Lys Glu Gln Ile Leu Ala Asn Leu Lys Ala Asp Phe Ile
245 250 255

Thr Ser Ile Tyr Gln Lys Asp Lys Ile Thr Ser Ser Ala Glu Lys Asn
260 265 270

Phe Leu Glu Gln Ala Tyr Asn His Leu Pro Leu Asn Lys Lys Trp Arg
275 280 285

Tyr Gly Ser Asn Ala Arg Asp Phe Ala Val Ser Lys Phe Phe Leu Asp
290 295 300

Arg Tyr Leu Asp Ser Tyr Leu Asn Asn Glu Gly Ser Ala Ala Tyr Gln
305 310 315 320

Glu Phe Leu Lys Glu Thr Arg Asp Phe Leu Gln Thr Tyr Glu Gly Val
325 330 335

Tyr Ser Ala Glu Lys Asn Lys Ile Tyr Glu Lys Leu Arg Lys Val Asp
340 345 350

Gly Gln Thr Ile Arg Thr Leu Ala Glu Ser Lys Gly Tyr Asp Leu Glu
355 360 365

His His Leu Ala Arg Arg Val Met Asp Leu Arg Glu Arg Leu Ala Asn
370 375 380

Asn Ile Leu Arg Ser Phe Arg Glu Ala Ala Pro Gln Ile Gln Asp Val
385 390 395 400

Gln Leu Glu Lys Asn Leu Glu Ser Phe Ser Val Leu Asn Gln Lys Lys
405 410 415

Ile Leu Glu Gln His Pro Glu Ala Ser Val Val Lys Ser Gln Lys Ala
420 425 430

Trp Gln Lys Leu Gly Tyr Phe Val Lys Ala Gly Glu Gln Pro Leu Glu
435 440 445

Ile Ile Arg Pro Val Tyr Lys Ser Tyr Asp Lys His Gly Lys Gly Ile
450 455 460

Gly Arg Pro Glu Phe Val Ser Asp Thr Val Tyr Asp Ile Ser Gln Leu
465 470 475 480

Thr Glu Asn Ile Gln Leu Lys Ser Leu Thr Leu Lys Asp Leu Ser Leu
485 490 495

Phe Ser Ser Asn Glu Leu Lys Glu Leu Val Asp Ala Ala Lys Leu Lys
500 505 510

Thr Asn Pro Thr Glu Arg Glu Arg Arg Glu Leu Gly Thr Tyr Arg Tyr
515 520 525

Ala Leu Lys Leu Ser Ile Leu Glu Ser Ser Gln Lys Glu Leu Gln Val
530 535 540

Arg Gln Lys Leu Leu Glu Gln Val Gln Pro Leu Ala Ser Asp Gln Pro
545 550 555 560

Phe Leu Asp Phe Lys Lys Gln Leu Ile Ala Gln Glu Leu Gln Ala Ile
565 570 575

Ala Leu Gln Leu Thr Pro Asn Tyr Lys Leu Ser Glu Asp Asp Lys Ala
580 585 590

Leu Lys Asn Arg Leu Lys Arg Gln Phe Glu Asp Ser Val Ala Leu Pro
595 600 605

Val Ser Lys Ala Thr Pro Gly Ala Ile Gln Leu Pro Ile Arg Gln Leu
610 615 620

Trp Thr Glu Leu Gly Leu Val His His Ile Gln Asp Glu Asn Ile Leu
625 630 635 640

Thr Leu Leu Lys Gly Thr Ser Thr Thr Lys Gln Ala Tyr Ile Glu Glu
645 650 655

Leu Gln Thr His Ile Ser Ile Phe Gln Leu Lys Tyr Gln Ile Asn Asn
660 665 670

Arg Asn Lys Gln Ile Ser Gln Leu Ser Asp Glu Ala Thr Ile Lys Glu
675 680 685

Met Arg Ile Ala Asn Ala Lys Gly Phe Ser Glu Leu Lys Arg Leu Tyr
690 695 700

Asp Thr Leu Gln Pro Ser Asp Asp Gly Gln Asn Gln Ile Ser Gln Ala
705 710 715 720

Val Ser Lys Gln Leu Gln Glu Arg Lys Val Ile Lys Lys Ala Gln Leu
725 730 735

Gln Gln Thr Gln Arg Ser Gly Lys Ile Asn Thr Asp Phe Met Arg Gln
740 745 750

Leu Thr Ala Ser Leu Asn Arg Ser Gln Gln Ala Ser Lys Lys Ala Leu
755 760 765

Met Glu Arg Ala Arg Ser Asp Glu Arg Glu Glu Gln Glu Glu Arg Arg
770 775 780

Gln Ala Gln Arg
785

<210> 456

<211> 933

<212> PRT

<213> Streptococcus agalactiae

<400> 456

Met Asn Ser Asn Thr Lys Gly His Gly Phe Phe Arg Lys Ser Lys Ala
1 5 10 15

Tyr Gly Leu Val Cys Ala Ile Ala Leu Ala Gly Ala Phe Thr Leu Ala
20 25 30

Thr Ser Gln Val Ser Ala Asp Gln Val Thr Thr Gln Ala Thr Thr Gln
35 40 45

Thr Val Thr Gln Asn Gln Ala Glu Thr Val Thr Ser Thr Gln Leu Asp
50 55 60

Lys Ala Val Ala Thr Ala Lys Lys Ala Ala Val Ala Val Thr Thr Thr
65 70 75 80

Pro Ala Val Asn His Ala Thr Thr Thr Asp Ala Gln Ala Asp Leu Ala
85 90 95

Asn Gln Thr Gln Ala Val Lys Asp Val Thr Ala Lys Ala Gln Ala Asn
100 105 110

Thr Gln Ala Ile Lys Asp Ala Thr Ala Glu Asn Ala Lys Ile Asp Ala
115 120 125

Glu Asn Lys Ala Glu Ala Glu Arg Val Ala Lys Glu Asn Lys Glu Gly
130 135 140

Gln Ala Ala Val Asp Ala Arg Asn Lys Ala Gly Gln Ala Ala Val Asp
145 150 155 160

Ala Arg Asn Lys Ala Lys Gln Gln Ala Gln Asp Asp Gln Lys Ala Lys
165 170 175

Ile Asp Ala Glu Asn Lys Ala Glu Ser Gln Arg Val Ser Gln Leu Asn
180 185 190

Ala Gln Asn Lys Ala Lys Ile Asp Ala Glu Asn Lys Asp Ala Gln Ala
195 200 205

Lys Ala Asn Ala Thr Asn Ala Gln Leu Gln Lys Asp Tyr Gln Ala Lys
210 215 220

Leu Ala Glu Ile Lys Ser Val Glu Ala Tyr Asn Ala Gly Val Arg Gln
225 230 235 240

Arg Asn Lys Asp Ala Gln Ala Lys Ala Asp Ala Thr Asn Ala Gln Leu
245 250 255

Gln Lys Asp Tyr Gln Ala Lys Leu Ala Leu Tyr Asn Gln Ala Leu Lys
260 265 270

Ala Lys Ala Glu Ala Asp Lys Gln Ser Ile Asn Asn Val Ala Phe Asp
275 280 285

Ile Lys Ala Gln Ala Lys Gly Val Asp Asn Ala Glu Tyr Gly Asn Ser
290 295 300

Ile Met Thr Ala Lys Thr Lys Pro Asp Gly Ser Phe Glu Phe Asn His
305 310 315 320

Asp Met Ile Asp Gly Val Lys Thr Ile Gly Tyr Gly Lys Leu Thr Gly
325 330 335

Lys Val Asn His His Tyr Val Ala Asn Lys Asp Gly Ser Val Thr Ala
340 345 350

Phe Val Asp Ser Val Thr Leu Tyr Lys Tyr Glu Tyr Arg Asn Val Ala
355 360 365

Gln Asn Ala Ala Val Asn Gln Asn Ile Val Phe Arg Val Leu Thr Lys
370 375 380

Asp Gly Arg Pro Ile Phe Glu Lys Ala His Asn Gly Asn Lys Thr Phe
385 390 395 400

Ala Glu Thr Leu Asn Lys Thr Leu Gln Leu Asn Leu Lys Tyr Glu Leu
405 410 415

Lys Pro His Ala Ser Ser Gly Asn Val Glu Val Phe Lys Ile His Asp
420 425 430

Asp Trp Val His Asp Thr His Gly Ser Ala Leu Val Ser Tyr Val Asn
435 440 445

Asn Asn Asp Ala Val Pro Asn Val Val Ile Pro Glu Arg Pro Thr Pro
450 455 460

Pro Lys Pro Val Lys Val Thr Pro Glu Ala Glu Lys Pro Val Pro Glu
465 470 475 480

Lys Pro Val Glu Pro Lys Leu Val Thr Pro Thr Leu Lys Thr Tyr Thr
485 490 495

Pro Val Lys Phe Ile Pro Arg Glu Tyr Lys Pro Glu Pro Ile Thr Pro
500 505 510

Glu Thr Phe Thr Pro Glu Lys Phe Thr Pro Ala Gln Pro Lys Val Lys
515 520 525

Pro His Val Ser Ile Pro Glu Lys Ile Asn Tyr Ser Val Ser Val His
530 535 540

Pro Val Leu Val Pro Ala Ala Asn Pro Ser Lys Ala Val Ile Asp Glu
545 550 555 560

Ala Gly Gln Ser Val Asn Gly Lys Thr Val Leu Pro Asn Ala Thr Leu
565 570 575

Asp Tyr Val Ala Lys Gln Asn Phe Ser Gln Tyr Lys Gly Ile Lys Ala
580 585 590

Ser Ala Glu Ala Ile Ala Lys Gly Phe Ala Phe Val Asp Gln Pro Asn
595 600 605

Glu Ala Leu Ala Glu Leu Thr Val Lys Ser Ile Lys Ala Ser Asn Gly
610 615 620

Asp Asp Val Ser Ser Leu Leu Glu Met Arg His Val Leu Ser Lys Asp
625 630 635 640

Thr Leu Asp Gln Lys Leu Gln Ser Leu Ile Lys Glu Ala Gly Ile Ser
645 650 655

Pro Val Gly Glu Phe Tyr Met Trp Thr Ala Lys Asp Pro Gln Ala Phe
660 665 670

Tyr Lys Ala Tyr Val Gln Lys Gly Leu Asp Ile Thr Tyr Asn Leu Ser
675 680 685

Phe Lys Ile Lys Ala Asn Phe Thr Lys Gly Gln Ile Lys Asn Gly Val
690 695 700

Ala Gln Ile Asp Phe Gly Asn Gly Tyr Thr Gly Asn Ile Val Val Asn
705 710 715 720

Asp Val Thr Val Pro Glu Val His Lys Asp Ile Leu Asp Lys Glu Asp
725 730 735

Gly Lys Ser Ile Asn Asn Ser Thr Val Lys Leu Gly Asp Glu Val Thr
740 745 750

Tyr Lys Leu Glu Gly Trp Val Val Pro Ala Asn Arg Gly Tyr Asp Leu
755 760 765

Phe Glu Tyr Lys Phe Val Asp Gln Leu Gln His Thr His Asp Leu Tyr
770 775 780

Leu Arg Asp Lys Val Val Ala Lys Val Asp Val Thr Leu Lys Asp Gly
785 790 795 800

Thr Val Ile Lys Lys Gly Thr Asn Leu Gly Glu Tyr Thr Glu Thr Val
805 810 815

Tyr Asn Lys Thr Thr Gly His Tyr Glu Leu Ala Phe Lys Lys Glu Phe
820 825 830

Leu Ala Lys Val Ser Arg Glu Ser Glu Phe Gly Ala Asp Asp Phe Ile
835 840 845

Val Val Lys Arg Ile Lys Ala Gly Asp Val Tyr Asn Thr Ala Asp Leu
850 855 860

Tyr Val Asn Gly Tyr Lys Val Lys Ser Glu Ala Val Val Thr His Thr
865 870 875 880

Thr Glu Lys Ser Lys Pro Val Glu Pro Gln Lys Ala Thr Pro Lys Ala
885 890 895

Pro Ala Lys Gly Leu Pro Ser Thr Gly Glu Ala Ser Met Thr Pro Leu
900 905 910

Thr Ala Ile Gly Ala Ile Ile Leu Ser Ala Leu Gly Leu Ala Gly Phe
915 920 925

Lys Lys Arg Gln Lys
930

<210> 457

<211> 1049

<212> PRT

<213> Streptococcus agalactiae

<400> 457

Met Phe Ser Trp Leu Glu Ala Leu Tyr Tyr Thr Leu Ile Gln Leu Ala
1 5 10 15

Lys Val Asn Arg Leu Asn Ala Leu Phe Leu Val Ser Val Val Gly Tyr
20 25 30

Leu Cys Tyr Gln Gly Ile Lys Leu Val Arg Lys Thr Ile Arg Asn Phe
35 40 45

Phe Gln Leu Met Lys Gly Phe Ile Gly Asp Arg Glu Asn Ile Lys Lys
50 55 60

Cys Ile Lys Asn Lys Lys Glu Ala Leu Val His Ser Trp Lys His Arg
65 70 75 80

Gln Asp Ile Asp Trp Lys Ser Thr Gly Lys Asp Lys Ser Lys Gln Leu
85 90 95

Trp Asn Leu Met Lys Arg Leu Ala Thr Val Ala Pro Ser Phe Leu Phe
100 105 110

Leu Leu Leu Gly Asn Val Leu Phe Arg Leu Ile Tyr Gln Leu Pro Phe
115 120 125

Val Lys Gln Asp Arg Lys Arg Phe Asp Lys Glu Met Lys Pro Leu Leu
130 135 140

Tyr Phe Lys Asn Tyr Arg Ser Phe Val Phe Met Gly Ile Gly Phe Ser
145 150 155 160

Phe Ile Ala Phe Ile Leu Thr Asn Tyr Phe Val Thr Val Leu Arg Ala
165 170 175

Ala Ile Arg Phe Leu Tyr Phe Ser Ile Met Thr Leu Arg Asp Asn Ser
180 185 190

Gln Val Val Ser Phe Asn Val Asp Ser Leu Leu Ile Gln Asn Leu Phe
195 200 205

Asn Ala Arg Val Phe Val Ile Ala Pro Ile Leu Ala Val Pro Ile Phe
210 215 220

Leu Ile Gly Leu Val Val Ala Trp Arg Ser Ala Trp Val Asn Phe Glu
225 230 235 240

Gln Tyr Arg Asp Tyr Asn His Asn Glu Glu Gly Asp Asp Arg Phe Ala
245 250 255

Thr Val Lys Glu Ile His Gln Gln Tyr Lys Lys Val Pro Asn Lys Thr
260 265 270

Glu Thr Tyr Pro Gly Glu Gly Gly Val Pro Val Leu His Glu Thr Arg
275 280 285

Lys Asn Leu Thr Gly Leu Thr Leu Lys Ser Gln Met Leu Trp Gln Asn
290 295 300

Arg Thr Phe Ser Arg Tyr Leu Thr Asn Ala Glu Arg Ile Leu Gly Leu
305 310 315 320

Leu Ser Thr Pro Ser Gly Asp Tyr Tyr Ile Asp Asp Ser Thr Thr Asn
325 330 335

Leu Ile Thr Met Gly Ile Thr Arg Ser Gly Lys Gly Glu Ala His Ile
340 345 350

Ala Pro Ile Ile Asp Ile Asn Ser Arg Ala Glu Ile Gln Pro Ser Leu
355 360 365

Ile Ile Ala Asp Pro Lys Gly Glu His Tyr Gln Ser Ser Tyr Lys Thr
370 375 380

Met Arg Arg Arg Gly Tyr Asp Val Asn Val Leu Ser Phe Gln Asn Met
385 390 395 400

Asp Trp Ser Met Ser Tyr Asn Pro Leu Ala Leu Ala Ile Ala Ala Ala
405 410 415

Lys Lys Gly Tyr Tyr Glu Met Thr Gln Thr Arg Val Asn Ala Val Ala
420 425 430

Glu Ala Ile Tyr Arg Lys Thr Lys Pro Gly Ser Gly Asn Gly Asn Ala
435 440 445

Lys Tyr Trp Glu Asp Thr Ser Ile Ser Leu Phe Asn Ala Ile Ala Met
450 455 460

Ala Leu Met Asp Arg Ala Asn Glu Thr Val Arg Asn Gly Glu Thr Asp
465 470 475 480

Ala Trp Asp Thr Val Thr Val Arg Asn Ile Ala Lys Phe Leu Thr Asp
485 490 495

Leu Gly Ser Glu Glu Val Phe Val Asn Asp Phe Gly Glu Ile Val Glu
500 505 510

Asn Pro Asp Lys Asn Gln Gln Val Lys Lys Lys Ser Lys Ile Thr Val
515 520 525

Tyr Phe Asp Asn Leu Arg Lys Ile Asn Gln Glu Gln Phe Ser Lys Phe
530 535 540

Arg Asp Met Ala Asp Leu Asn Phe Arg Ser Ser Asp Phe Ala Ser Glu
545 550 555 560

Glu Thr Lys Gly Asn Val Phe Ser Ser Met Met Ser Gly Ile Asn Leu
565 570 575

Phe Leu Gln Asp Asn Ile Ala Lys Leu Thr Ser Lys Asn Ser Ile Asp
580 585 590

Leu Glu Ser Val Gly Phe Pro Arg Arg Leu Ser Ile Lys Phe Arg Ser
595 600 605

Ser Ser Asn Val Ala Met Arg Asn Glu Tyr Thr His Lys Thr Ala Lys
610 615 620

Val Thr Ile Thr Ser Gln Ala Val Trp Gly Lys Thr Thr Lys Gln Val
625 630 635 640

Ile His Val Asp Ala Ala Thr Ala Leu Ile Asp Gly Glu Gly Tyr Leu
645 650 655

Thr Tyr Val Ile Glu Pro Gln Leu Pro Asp Gln Phe Leu Val Thr Ile
660 665 670

Asp Phe Asn His Glu Asn Asn Gly Gly Ser Ala Ile Arg His Lys Thr
675 680 685

Phe Gln Phe Ser Ala Glu Lys Val Tyr Lys Lys Arg Gly Asn Val Ile
690 695 700

Thr Leu Asp Asp Tyr Thr Lys Lys Pro Val Leu Asp His Ile Lys Val
705 710 715 720

Thr Val Leu Asn Lys Gln Asp Asp Asn Leu Leu Gln Lys Glu Asp Ile
725 730 735

Asp Leu Ile Tyr Ser Asp Asn Pro Lys Val Ile Tyr Leu Val Thr Pro
740 745 750

Pro Asn Arg Thr Glu Tyr Asn Ser Ile Val Ser Leu Phe Leu Asp Gln
755 760 765

Leu Phe Asn Ala Asn Tyr Glu Leu Ala Leu Ser Asn Gly Arg Lys Cys
770 775 780

Val Asn Arg Ile Leu His Ile Leu Asp Glu Phe Thr Asn Ile Pro Ala
785 790 795 800

Ile Pro His Met Asp Thr Lys Ile Ser Ile Gly Leu Gly Gln Asn Ile
805 810 815

Leu Tyr Tyr Leu Trp Ile Gln Asn Leu Lys Gln Leu Val Ser Glu Tyr
820 825 830

Gly Glu Asn Thr Ala Glu Thr Ile Arg Glu Asn Cys Ser Leu Lys Val
835 840 845

Tyr Ile Lys Ser Thr Ala Pro Ala Thr Asn Glu Tyr Phe Ser Lys Glu
850 855 860

Leu Gly Thr Arg Thr Ile Thr Arg Arg Arg Arg Ser Ser Asn Ile Leu
865 870 875 880

Asp Glu Ala Asn Pro Asn Val Ser Ile Glu Asn Pro Arg Gln Glu Leu
885 890 895

Leu Thr Pro Thr Gln Leu Ser Lys Leu Gln Glu Gly Glu Ala Val Ile
900 905 910

Leu Arg Gly Val Lys Gly Arg Asp Asn Ala Gly Arg Lys Ile Thr Thr
915 920 925

Asp Pro Ile Phe Leu His Glu Lys Thr Ser Leu Pro Tyr Arg Tyr Met
930 935 940

Phe Leu Gln Glu Glu Phe Asp Gln Ser Met Ala Leu Ala Asp Ile Pro
945 950 955 960

Val Glu Ser Gly His Arg Asp Leu Asp Leu Gln Asp Ile Ala Val Gly
965 970 975

Ala Gln Ser Thr Phe Asn Lys Ile Ile Asp Trp Arg Met Ala Leu Thr
980 985 990

Asp Arg Met Arg Thr Asn Gly Lys Ile Pro Gln Leu Ala Ser Arg Lys
995 1000 1005

Gln Thr Ile Lys Ala Leu Ser Gln Ser Gln Phe Thr Ser Pro Ala
1010 1015 1020

Asp Leu Thr Gln Ala Val Ile Ala Glu Val Phe Asp Glu Glu Asp
1025 1030 1035

Asp Asp Asp Leu Phe Phe Val Asp Asp Val Met
1040 1045

<210> 458

<211> 92

<212> PRT

<213> Streptococcus agalactiae

<400> 458

Met Thr Asp Asn Arg Phe Ala Gln Leu Lys Glu Asn Phe Glu Lys Gly
1               5                   10                  15

Ser Pro Lys Arg Arg Val Pro Thr Ser Arg Pro Ile Ala Ala Gln Lys
            20                  25                  30

Ala Pro Glu Ser Tyr Asn Lys Lys Gly Arg Tyr Pro Phe Ser Leu His
        35                  40                  45

Gln Asp Val Arg Tyr Asp Lys Leu Glu Ala Leu Val Ala Tyr His Gly
    50                  55                  60

Ala Lys Ser Ala Ser Asp Tyr Leu Glu Arg Leu Ile Val Gln Glu Trp
65                  70                  75                  80

Glu Lys Met Gln Arg Lys Leu Lys Asn Lys Glu Lys
                85                  90

<210> 459

<211> 127

<212> PRT

<213> Streptococcus agalactiae

<400> 459

Met Ala Tyr Leu Ser Lys Leu Ser Asp Leu Asp Pro Ser Leu Met Asp
1               5                   10                  15

Ala Asp Ser Glu Gln Ile Tyr Ile Pro Lys Val Leu Phe Glu His Asn
            20                  25                  30

Asp Phe Lys Gly Leu Thr Tyr Lys Glu Ile Leu Leu Tyr Ser Phe Leu
        35                  40                  45

Leu Asn Arg Leu Arg Glu Pro Leu Asp Phe Ile Gln Lys Gly Tyr Asp
    50                  55                  60

Asp Asn Glu Asp Thr Tyr Val His Phe Lys Val Glu Asp Leu Cys Glu
65                  70                  75                  80

Leu Leu Asn Gln Ser Lys Thr Thr Val Ile Ser Leu Lys Lys Arg Leu
                85                  90                  95

Ala Gln Tyr Gly Leu Ile Glu Glu Val Lys Ala Gly Ser His Gln Pro
100 105 110

Asn Arg Ile Tyr Leu Thr Asp Lys Leu Val Pro Tyr Ile Lys Gly
115 120 125

<210> 460

<211> 442

<212> PRT

<213> Streptococcus agalactiae

<400> 460

Met Thr Ile Phe Asp Glu Arg Glu Leu Lys Glu Arg Phe Thr His Glu
1 5 10 15

Asn Arg Val Ser Phe Tyr Glu Phe Val Ala Lys Tyr Asp Ala Gln Met
20 25 30

Val Pro Val Met Lys Ala Lys Gly Tyr Arg Cys Ile His Ser Met Glu
35 40 45

Arg Thr Val Val Phe Thr Phe Gly Glu Phe Thr Ile Arg Arg Arg Arg
50 55 60

Trp Gln Lys Gly Glu His Trp Val Val Pro Val Asp Glu Lys Leu Gly
65 70 75 80

Leu Lys Lys Asn Val Arg Tyr Ser Leu Glu Phe Met Tyr Gln Ile Ala
85 90 95

Ser Leu Ala Thr Met Met Pro Tyr Glu Lys Val Ile Lys Val Val Gln
100 105 110

Met Met Tyr Cys Ile Val Ile Thr Lys Pro Thr Val Val Lys Ala Val
115 120 125

Lys Ile Ser Arg Glu Leu Leu Lys Glu Lys Glu Ala Tyr Arg Phe Phe
130 135 140

Asp Glu Asp Ile Pro Val Asp Lys Glu Pro Val Asp Met Ile Tyr Leu
145 150 155 160

Glu Gly Asp Gly Val Met Val Lys Ala Arg Glu Glu Gly Leu Asp Asn
165 170 175

Arg Asn Val Asp Leu Ser His Phe Val Val His Thr Gly Ser Gln Lys
180 185 190

Val Gly Ser Asn Arg Phe Val Leu Gln Asn Lys Lys Glu Phe Val Ser
195 200 205

Leu Asp Asn Arg Gln Thr Arg Gln Lys Ile Leu Asp Tyr Leu Tyr Asn
210 215 220

His Phe Tyr Ile Ala Pro Asn Thr Leu Leu Ile Thr Asn Ser Asp Gly
225 230 235 240

Gly His Gly Tyr Thr Pro Tyr Val Phe Lys Glu Ile Ala Lys Ala Leu
245 250 255

Lys Val Lys Gln His Glu His Phe Trp Asp Arg Tyr His Val Asn Glu
260 265 270

Lys Ile Lys Ser Phe Phe Lys Leu Tyr Pro Val Glu Leu Met Thr Gly
275 280 285

Ala Phe Gln Ser Ile Lys Gln His Asp Lys Glu Lys Leu Arg Thr Val
290 295 300

Leu Asp Thr Thr Glu Ala Leu Ile Leu Met Glu Glu Glu Met Glu Gly
305 310 315 320

Phe Asn Gln Phe Lys Arg Lys Leu Leu Asn Asn Phe Gln Tyr Thr Lys
325 330 335

Ser Ala Glu Leu Arg Gly Phe Ser Arg Ala Gly Ile Gly Val Met Glu
340 345 350

Ser Gln His Arg Lys Ile Thr Tyr Arg Met Lys Lys Arg Gly Met Tyr
355 360 365

Trp Thr Ile Gln Gly Ala Glu Thr Met Ser Gln Leu Ile Val Leu Ser
370 375 380

Tyr Glu Gly Gln Leu Arg Asp Leu Phe Phe Gly Ser Trp Arg Glu Asp
385 390 395 400

Tyr Gln Lys Tyr Gln Glu Leu Glu Asn Leu Ser Ala Gly Lys Ile Lys
405 410 415

His Glu Gln Asn Lys Ile Asn Lys Arg Tyr Asp Leu Gln Thr Leu Gly
420 425 430

Arg Leu Arg Tyr Gly Arg His Arg Asn Leu
435 440

<210> 461

<211> 462

<212> PRT

<213> Streptococcus agalactiae

<400> 461

Met Ala Val Glu Ile Ile Met Pro Lys Leu Gly Val Asp Met Gln Glu
1 5 10 15

Gly Glu Ile Leu Glu Trp Lys Lys Gln Val Gly Asp Val Val Asn Glu
20 25 30

Gly Asp Val Leu Leu Glu Ile Met Ser Asp Lys Thr Asn Met Glu Ile
35 40 45

Glu Ala Glu Asp Ser Gly Val Leu Leu Lys Ile Thr His Gly Asn Gly
50 55 60

Asp Val Val Pro Val Thr Glu Thr Ile Gly Tyr Ile Gly Ala Glu Gly
65 70 75 80

Glu Glu Val Thr Glu Ala Ser Ser Ser Glu Asn Thr Ser Val Glu Glu
85 90 95

Asn Ala Thr Gln Val Thr Ser Glu Pro Glu Lys Val Glu Glu Thr Ser
100 105 110

Glu Pro Ser Val Pro Ala Ala Thr Ser Gly Glu Lys Val Arg Ala Thr
115 120 125

Pro Ala Ala Arg Lys Leu Ala Arg Glu Met Ser Ile Asp Leu Ala Leu
130 135 140

Val Ser Gly Thr Gly Ala Asn Gly Arg Val His Arg Glu Asp Val Glu
145 150 155 160

Ser Phe Lys Gly Ala Gln Pro Arg Ile Thr Pro Leu Ala Arg Arg Ile
165 170 175

Ala Glu Asp Gln Gly Val Asp Ile Ala Glu Ile Thr Gly Ser Gly Ile
180 185 190

Arg Gly Lys Ile Val Lys Asn Asp Val Leu Ala Ala Met Ser Pro Gln
195 200 205

Ala Ala Glu Ala Pro Val Glu Thr Lys Ala Thr Pro Thr Thr Glu Glu
210 215 220

Lys Gln Leu Pro Glu Gly Val Glu Val Ile Lys Met Ser Ala Met Arg
225 230 235 240

Lys Ala Ile Ser Lys Gly Met Thr Asn Ser Tyr Leu Thr Ala Pro Ser
245 250 255

Phe Thr Leu Asn Tyr Asp Ile Asp Met Thr Glu Met Met Ala Leu Arg
260 265 270

Lys Lys Leu Ile Asp Pro Ile Met Ala Lys Thr Gly Leu Lys Val Ser
275 280 285

Phe Thr Asp Leu Ile Gly Met Ala Val Val Lys Thr Leu Met Lys Pro
290 295 300

Glu His Arg Tyr Leu Asn Ala Ser Leu Ile Asn Asp Ala Gln Glu Ile
305 310 315 320

Glu Leu His Asn Phe Val Asn Ile Gly Ile Ala Val Gly Leu Asp Asp
325 330 335

Gly Leu Ile Val Pro Val Val His Asn Ala Asp Gln Met Ser Leu Ser
340 345 350

Asp Phe Val Ile Ala Ser Lys Asp Val Ile Lys Lys Thr Gln Glu Gly
355 360 365

Lys Leu Lys Ser Ala Glu Met Ser Gly Ser Thr Phe Ser Ile Thr Asn
370 375 380

Leu Gly Met Phe Gly Thr Lys Thr Phe Asn Pro Ile Ile Asn Gln Pro
385 390 395 400

Asn Ser Ala Ile Leu Gly Val Gly Ala Thr Ile Pro Thr Pro Thr Val
405 410 415

Val Asp Gly Glu Ile Val Ala Arg Pro Ile Met Ala Met Cys Leu Thr
420 425 430

Ile Asp His Arg Ile Val Asp Gly Met Asn Gly Ala Lys Phe Met Val
435 440 445

Asp Leu Lys Asn Leu Met Glu Asn Pro Phe Gly Leu Leu Ile
450 455 460

<210> 462

<211> 531

<212> PRT

<213> Streptococcus agalactiae

<400> 462

Met Ser Ser Phe Asn Arg Lys Lys Leu Lys Phe Leu Gly Ile Ser Leu
1               5                   10                  15

Ala Thr Leu Thr Ala Thr Thr Val Thr Leu Val Ala Cys Gly Asn Glu
            20                  25                  30

Ser Lys Asn Ser Gly Asp Asn Lys Val Ile Asn Trp Tyr Ile Pro Thr
        35                  40                  45

Glu Ile Ser Thr Leu Asp Ile Ser Lys Asn Thr Asp Ala Tyr Ser Asn
    50                  55                  60

Leu Ala Ile Gly Asn Ser Gly Ser Asn Leu Leu Arg Ile Asp Lys Glu
65                  70                  75                  80

Gly Lys Pro Lys Pro Asp Leu Ala Lys Lys Val Ser Val Ser Ser Asp
                85                  90                  95

Gly Leu Thr Tyr Thr Ala Thr Leu Arg Asp Asn Leu Lys Trp Ser Asp
            100                 105                 110

Gly Ser Lys Leu Ser Ala Glu Asp Phe Val Tyr Thr Trp Arg Arg Ile
        115                 120                 125

Val Asp Pro Lys Thr Ala Ser Glu Tyr Ala Tyr Leu Ala Thr Glu Ser
    130                 135                 140

His Leu Leu Asn Ala Asp Lys Ile Asn Ser Gly Asp Ile Lys Asp Leu
145                 150                 155                 160

Asn Lys Leu Gly Val Thr Ala Lys Gly Asn Gln Val Thr Phe Lys Leu
                165                 170                 175

Thr Ser Pro Cys Pro Gln Phe Lys Tyr Tyr Leu Ala Phe Ser Asn Phe
            180                 185                 190

Met Pro Gln Lys Gln Ser Tyr Val Glu Lys Val Gly Lys Asp Tyr Gly
        195                 200                 205

Thr Thr Ser Lys Asn Gln Ile Tyr Ser Gly Pro Tyr Leu Val Lys Asp
    210                 215                 220

Trp Asn Gly Ser Asn Gly Lys Phe Lys Leu Val Lys Asn Lys Tyr Tyr
225                 230                 235                 240

Trp Asp Ser Lys His Val Lys Thr Asn Ser Val Ile Val Gln Thr Ile
                245                 250                 255

Lys Lys Pro Asp Thr Ala Val Gln Met Tyr Lys Gln Gly Gln Ile Asp
            260                 265                 270

Phe Ala Glu Ile Ser Gly Thr Ser Ala Ile Tyr Asn Gln Thr Gly Ser
275 280 285

Val Lys Ala Leu Thr Asn Gln Lys Ile Arg Gln Ala Leu Asn Leu Ala
290 295 300

Thr Asp Arg Lys Gly Val Val Lys Ala Ala Val Asp Thr Gly Ser Thr
305 310 315 320

Pro Ala Glu Ser Leu Val Pro Lys Lys Leu Ala Lys Leu Pro Asn Gly
325 330 335

Glu Asp Leu Ser Lys Tyr Thr Ala Pro Gly Tyr Thr Tyr Asn Thr Ser
340 345 350

Lys Ala Gln Lys Leu Phe Lys Glu Gly Leu Ala Glu Val Gly Gln Ser
355 360 365

Ser Leu Lys Leu Thr Ile Thr Ala Asp Ser Asp Ser Pro Ala Ala Lys
370 375 380

Asn Ala Val Asp Tyr Val Lys Ser Thr Trp Glu Ser Ala Leu Pro Gly
385 390 395 400

Leu Thr Val Glu Glu Lys Phe Val Thr Phe Lys Gln Arg Leu Glu Asp
405 410 415

Ala Lys Asn Glu Asn Phe Asp Val Val Leu Phe Ser Trp Gly Gly Asp
420 425 430

Tyr Pro Glu Gly Ser Thr Phe Tyr Gly Leu Phe Thr Thr Asn Ser Ala
435 440 445

Tyr Asn Tyr Gly Lys Phe Ser Ser Lys Glu Tyr Asp Asn Ala Tyr Gln
450 455 460

Lys Ala Ile Thr Thr Asp Ala Leu Lys Pro Gly Asp Ala Ala Asn Asp
465 470 475 480

Tyr Lys Thr Ala Glu Lys Ala Leu Phe Asp Gln Ser Tyr Tyr Asn Pro
485 490 495

Val Tyr Tyr Leu Gly Lys Lys Gly Leu Gln Asn Ser Lys Leu Lys Gly
500 505 510

Leu Val Arg Asn Ser Thr Gly Leu Asn Val Asp Phe Thr Tyr Ala Tyr
515 520 525

Lys Thr Glu
530